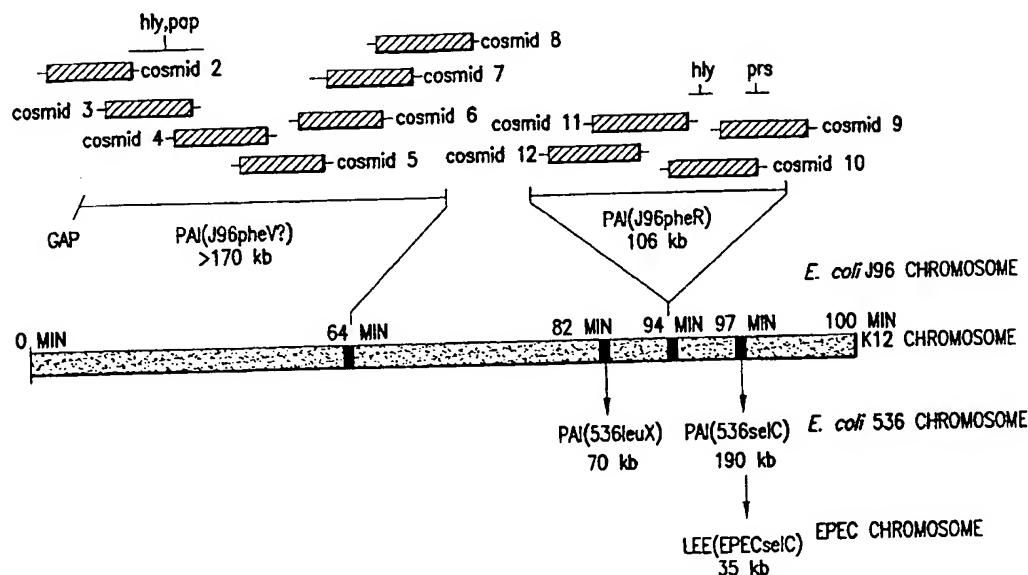




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(54) Title: THERMOSTABLE POLYMERASES HAVING ALTERED FIDELITY



(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

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Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

Background of the Invention

Field of the Invention

5 The present invention relates to novel genes located in two chromosomal regions within *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs).

Related Background Art

10 *Escherichia coli* (*E. coli*) is a normal inhabitant of the intestine of humans and various animals. Pathogenic *E. coli* strains are able to cause infections of the intestine (intestinal *E. coli* strains) and of other organs such as the urinary tract (uropathogenic *E. coli*) or the brain (extraintestinal *E. coli*). Intestinal pathogenic *E. coli* are a well established and leading cause of severe infantile diarrhea in the developing world. Additionally, cases of newborn meningitis and sepsis have
15 been attributed to *E. coli* pathogens.

 In contrast to non-pathogenic isolates, pathogenic *E. coli* produce pathogenicity factors which contribute to the ability of strains to cause infectious diseases (Mühdorfer, I. and Hacker, J., *Microb. Pathogen.* 16:171-181 1994). Adhesions facilitate binding of pathogenic bacteria to host tissues. Pathogenic
20 *E. coli* strains also express toxins including haemolysins, which are involved in the destruction of host cells, and surface structures such as O-antigens, capsules or membrane proteins, which protect the bacteria from the action of phagocytes or the complement system (Ritter, *et al.*, *Mol. Microbiol.* 17:109-212 1995).

 The genes coding for pathogenicity factors of intestinal *E. coli* are located
25 on large plasmids, phage genomes or on the chromosome. In contrast to intestinal *E. coli*, pathogenicity determinants of uropathogenic and other extraintestinal *E. coli* are, in most cases, located on the chromosome. *Id.*

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Large chromosomal regions in pathogenic bacteria that encode adjacently located virulence genes have been termed *pathogenicity islands* ("PAIs"). PAIs are indicative of large fragments of DNA which comprise a group of virulence genes behaving as a distinct molecular and functional unit much like an island within the bacterial chromosome. For example, intact PAIs appear to transfer between organisms and confer complex virulence properties to the recipient bacteria.

Chromosomal PAIs in bacterial cells have been described in increasing detail over recent years. For example, J. Hacker and co-workers described two large, unstable regions in the chromosome of uropathogenic *Escherichia coli* strain 536 as PAI-I and PAI-II (Hacker J., *et al.*, *Microbiol. Pathog.* 8:213-25 1990). Hacker found that PAI-I and PAI-II containing virulence regions can be lost by spontaneous deletion due to recombination events. Both of these PAIs were found to encode multiple virulence genes, and their loss resulted in reduced hemolytic activity, serum resistance, mannose-resistant hemagglutination, uroepithelial cell binding, and mouse virulence of the *E. coli*. (Knapp, S *et al.*, *J. Bacteriol.* 168:22-30 1986). Therefore, pathogenicity islands are characterized by their ability to confer complex virulence phenotypes to bacterial cells.

In addition to *E. coli*, specific deletion of large virulence regions has been observed in other bacteria such as *Yersinia pestis*. For example, Fetherston and co-workers found that a 102-kb region of the *Y. pestis* chromosome lost by spontaneous deletion resulted in the loss of many *Y. pestis* virulence phenotypes. (Fetherston, J.D. and Perry, R.D., *Mol. Microbiol.* 13:697-708 1994, Fetherston, *et al.*, *Mol. Microbiol.* 6:2693-704 1992). In this instance, the deletion appeared to be due to recombination within 2.2-kb repetitive elements at both ends of the 102-kb region.

It is possible that deletion of PAIs may benefit the organism by modulating bacterial virulence or genome size during infection. PAIs may also represent foreign DNA segments that were acquired during bacterial evolution that conferred important pathogenic properties to the bacteria. Observed flanking

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repeats, as observed in *Y. pestis* for example, may suggest a common mechanism by which these virulence genes were integrated into the bacterial chromosomes.

Integration of the virulence genes into bacterial chromosomes was further elucidated by the discovery and characterization of a locus of enterocyte effacement (the LEE locus) in enteropathogenic *E. coli* (McDaniel, *et al.*, *Proc. Natl Acad. Sci. (USA)* 92:1664-8 1995). The LEE locus comprises 35-kb and encodes many genes required for these bacteria to "invade" and degrade the apical structure of enterocytes causing diarrhea. Although the LEE and PAI-I loci encode different virulence genes, these elements are located at the exact same site in the *E. coli* genome and contain the same DNA sequence within their right-hand ends, thus suggesting a common mechanism for their insertion.

Besides being found in enteropathogenic *E. coli*, the LEE element is also present in rabbit diarrheal *E. coli*, *Hafnia alvei*, and *Citrobacter freundii* biotype 4280, all of which induce attaching and effacing lesions on the apical face of enterocytes. The LEE locus appears to be inserted in the bacterial chromosome as a discrete molecular and functional virulence unit in the same fashion as PAI-I, PAI-II, and *Yersinia* PAI.

Along these same lines, a 40-kb *Salmonella typhimurium* PAI was characterized on the bacterial chromosome which encodes genes required for *Salmonella* entry into nonphagocytic epithelial cells of the intestine (Mills, D.M., *et al.*, *Mol. Microbiol.* 15:749-59 1995). Like the LEE element, this PAI confers to *Salmonella* the ability to invade intestinal cells, and hence may likewise be characterized as an "invasion" PAI.

The pathogenicity islands described above all possess the common feature of conferring complex virulence properties to the recipient bacteria. However, they may be separated into two types by their respective contributions to virulence. PAI-I, PAI-II, and the *Y. pestis* PAI confer multiple virulence phenotypes, while the LEE and the *S. typhimurium* "invasion" PAI encode many genes specifying a single, complex virulence process.

It is advantageous to characterize closely-related bacteria that contain or do not contain the PAI by the isolation of a discrete molecular and functional unit

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on the bacterial chromosome. Since the presence versus the absence of essential virulence genes can often distinguish closely-related virulent versus avirulent bacterial strains or species, experiments have been conducted to identify virulence loci and potential PAIs by isolating DNA sequences that are unique to virulent bacteria (Bloch, C.A., *et al.*, *J Bacteriol.* 176:7121-5 1994, Groisman, E.A., *EMBO J.* 12:3779-87 1993).

At least two PAIs are present in *E. coli* J96. These PAIs, PAI IV and PAI V are linked to tRNA loci but at sites different from those occupied by other known *E. coli* PAIs. Swenson *et al.*, *Infect. and Immun.* 64:3736-3743 (1996).

The era of true comparative genomics has been ushered in by high through-put genomic sequencing and analysis. The first two complete bacterial genome sequences, those of *Haemophilus influenzae* and *Mycoplasma genitalium* were recently described (Fleischmann, R.D., *et al.*, *Science* 269:496 (1995); Fraser, C.M., *et al.*, *Science* 270:397 (1995)). Large scale DNA sequencing efforts also have produced an extensive collection of sequence data from eukaryotes, including *Homo sapiens* (Adams, M.D., *et al.*, *Nature* 377:3 (1995)) and *Saccharomyces cerevisiae* (Levy, J., *Yeast* 10:1689 (1994)).

The need continues to exist for the application of high through-put sequencing and analysis to study genomes and subgenomes of infectious organisms. Further, a need exists for genetic markers that can be employed to distinguish closely-related virulent and avirulent strains of a given bacteria.

Summary of the Invention

The present invention is based on the high through-put, random sequencing of cosmid clones covering two pathogenic islands (PAIs) of uropathogenic *Escherichia coli* strain J96 (O4:K6; *E. coli* J96). PAIs are large fragments of DNA which comprise pathogenicity determinants. PAI IV is located approximately at 64 min (near *pheV*) on the *E. coli* chromosome and is greater than 170 kilobases in size. PAI V is located at approximately 94 min (at *pheR*) on the *E. coli* chromosome and is approximately 106 kb in size. These PAIs

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differ in location from the PAIs described by Hacker and colleagues for uropathogenic strain 536 (PAI I, 82 minutes {*selC*} and PAI II, 97 minutes {*leuX*}).

5 The location of the PAIs relative to one another and the cosmid clones covering the J96 PAIs is shown in Figure 1. The present invention relates to the nucleotide sequences of 142 fragments of DNA (contigs) covering the PAI IV and PAI V regions of the *E. coli* J96 chromosome. The nucleotide sequences shown in SEQ ID NOs: 1 through 142 were obtained by shotgun sequencing eleven *E. coli* J96 subclones, which were deposited in two pools on September 23, 1996 at
10 the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession numbers 97726 (includes 7 cosmid clones covering PAI (IV) and 97727 (includes 4 cosmid clones covering PAI V). The deposited sets or "pools" of clones are more fully described in Example 1. In addition, *E. coli* strain J96 was also deposited at the American Type Culture
15 Collection on September 23, 1996, and given accession number 98176.

Three hundred fifty-one open reading frames have been thus far identified in the 142 contigs described by SEQ ID NOs: 1 through 142. Thus, the present invention is directed to isolated nucleic acid molecules comprising open reading frames (ORFs) encoding *E. coli* J96 PAI proteins, and fragments of said nucleic
20 acid molecules.

The present invention also relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of *E. coli* J96 PAI proteins. Further embodiments include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical,
25 and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an *E. coli* J96 PAI ORF described herein, and fragments of said nucleic acid molecules.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention and fragments thereof, host cells containing the recombinant vectors, as well as methods for
30

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making such vectors and host cells for *E. coli* J96 PAI protein production by recombinant techniques.

5 The invention further provides isolated polypeptides encoded by the *E. coli* J96 PAI ORFs or fragments of said ORFs. It will be recognized that some amino acid sequences of the polypeptides described herein can be varied without significant effect on the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

10 In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope-bearing portion is an immunogenic or antigenic epitope useful for raising antibodies.

15 The invention further provides a vaccine comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*, such as strain J96.

20 The invention also provides a method of eliciting a protective immune response in an animal comprising administering to the animal the above-described vaccine.

25 The invention further provides a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for one or more of:

(a) polynucleic acids encoding an open reading frame listed in Tables 1-4 or a fragment of said polynucleic acid;

(b) full length or mature polypeptides encoded for by an open reading frame listed in Tables 1-4; or

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(c) antibodies specific to polypeptides encoded for by an open reading frame listed in Tables 1-4.

The invention further provides a nucleic acid probe for the detection of the presence of one or more *E. coli* PAI nucleic acids (nucleic acids encoding one or more ORFs as listed in Tables 1-4) in a sample from an individual comprising one or more nucleic acid molecules sufficient to specifically detect under stringent hybridization conditions the presence of the above-described molecule in the sample.

The invention also provides a method of detecting *E. coli* PAI nucleic acids in a sample comprising:

- a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and
- b) detecting the presence of the probe bound to an *E. coli* PAI nucleic acid.

The invention further provides a kit for detecting the presence of one or more *E. coli* PAI nucleic acids in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

The invention also provides a diagnostic kit for detecting the presence of pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antibodies.

The invention also provides a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antigens.

Brief Description of the Figures

Figure 1 is a schematic diagram of cosmid clones derived from *E. coli* J96 pathogenicity island and map positions of known *E. coli* PAIs (not drawn to scale). The gray bar represents the *E. coli* K-12 chromosome with minute demarcations of PAI junction points located above the bar. *E. coli* J96 overlapping cosmid clones are represented by hatched bars (overlap not drawn to

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scale) with positions of *hly*, *pap*, and *prs* operons indicated above bar. The PAIs and estimated sizes are shown above and below the K-12 chromosome map.

Figure 2 is a block diagram of a computer system 102 that can be used to implement the computer-based systems of present invention.

5

Detailed Description of the Invention

The present invention is based on high through-put, random sequencing of a uropathogenic strain of *Escherichia coli*. The DNA sequences of contiguous DNA fragments covering the pathogenicity islands, PAI IV (also referred to as PAI_{J96(pheV)}) and PAI V (also referred to as PAI_{J96(pheU)}) from the chromosome of the *E. coli* uropathogenic strain, J96 (04:K6) were determined. The sequences were used for DNA and protein sequence similarity searches of the database.

The primary nucleotide sequences generated by shotgun sequencing cosmid clones of the PAI IV and PAI V regions of the *E. coli* chromosome are provided in SEQ ID NOs:1 through 142. These sequences represent contiguous fragments of the PAI DNA. As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system. The present invention provides the nucleotide sequences of SEQ ID NOs:1 through 142, or representative fragments thereof, in a form that can be readily used, analyzed, and interpreted by a skilled artisan. Within these 142 sequences, there have been thus far identified 351 open reading frames (ORFs) that are described in greater detail below.

As used herein, a "representative fragment" refers to *E. coli* J96 PAI protein-encoding regions (also referred to herein as open reading frames or ORFs), expression modulating fragments, and fragments that can be used to diagnose the presence of *E. coli* in a sample. A non-limiting identification of such representative fragments is provided in Tables 1 through 6, preferably in Tables 1 through 4. As described in detail below, representative fragments of the present invention further include nucleic acid molecules having a nucleotide sequence at least 95% identical, preferably at least 96%, 97%, 98%, or 99%

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identical, to an ORF identified in Tables 1 through 6, or more preferably Tables 1 through 4.

As indicated above, the nucleotide sequence information provided in SEQ ID NOs:1 through 142 was obtained by sequencing cosmid clones covering the PAIs located on the chromosome of *E. coli* J96 using a megabase shotgun sequencing method. The sequences provided in SEQ ID NOs:1 through 142 are highly accurate, although not necessarily a 100% perfect, representation of the nucleotide sequences of contiguous stretches of DNA (contigs) which include the ORFs located on the two pathogenicity islands of *E. coli* J96. As discussed in detail below, using the information provided in SEQ ID NOs:1 through 142 and in Tables 1 through 6 together with routine cloning and sequencing methods, one of ordinary skill in the art would be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *E. coli* J96 PAI proteins. In rare instances, this may reveal a nucleotide sequence error present in the nucleotide sequences disclosed in SEQ ID NOs: 1 through 142. Thus, once the present invention is made available (i.e., once the information in SEQ ID NOs: 1 through 142 and in Tables 1 through 6 is made available), resolving a rare sequencing error would be well within the skill of the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler™ can be used as an aid during visual inspection of nucleotide sequences.

Even if all of the rare sequencing errors were corrected, it is predicted that the resulting nucleotide sequences would still be at least about 99.9% identical to the reference nucleotide sequences in SEQ ID NOs: 1 through 142. Thus, the present invention further provides nucleotide sequences that are at least 99.9% identical to the nucleotide sequence of SEQ ID NOs: 1 through 142 in a form which can be readily used, analyzed and interpreted by the skilled artisan. Methods for determining whether a nucleotide sequence is at least 99.9% identical to a reference nucleotide sequence of the present invention are described below.

Nucleic Acid Molecules

The present invention is directed to isolated nucleic acid fragments of the PAIs of *E. coli* J96. Such fragments include, but are not limited to, nucleic acid molecules encoding polypeptides, nucleic acid molecules that modulate the expression of an operably linked ORF (hereinafter expression modulating fragments (EMFs)), and nucleic acid molecules that can be used to diagnose the presence of *E. coli* in a sample (hereinafter diagnostic fragments (DFs)).

By "isolated nucleic acid molecule(s)" is intended a nucleic acid molecule, DNA or RNA, that has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells, purified (partially or substantially) DNA molecules in solution, and nucleic acid molecules produced synthetically. Isolated RNA molecules include *in vitro* RNA transcripts of the DNA molecules of the present invention.

In one embodiment, *E. coli* J96 PAI DNA can be mechanically sheared to produce fragments about 15-20 kb in length, which can be used to generate an *E. coli* J96 PAI DNA library by insertion into lambda clones as described in Example 1 below. Primers flanking an ORF described in Tables 1 through 6 can then be generated using the nucleotide sequence information provided in SEQ ID NOs: 1 through 142. The polymerase chain reaction (PCR) is then used to amplify and isolate the ORF from the lambda DNA library. PCR cloning is well known in the art. Thus, given SEQ ID NOs: 1 through 142, and Tables 1 through 6, it would be routine to isolate any ORF or other representative fragment of the *E. coli* J96 PAI subgenomes. Isolated nucleic acid molecules of the present invention include, but are not limited to, single stranded and double stranded DNA, and single stranded RNA, and complements thereof.

Tables 1 through 6 herein describe ORFs in the *E. coli* J96 PAI cosmid clone library.

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Tables 1 and 3 list, for PAI IV and PAI V, respectively, a number of ORFs that putatively encode a recited protein based on homology matching with protein sequences from an organism listed in the Table. Tables 1 and 3 indicate the location of ORFs (i.e., the position) by reference to its position within the one of the 142 *E. coli* J96 contigs described in SEQ ID NOs: 1 through 142. Column 1 of Tables 1 and 3 provides the Sequence ID Number (SEQ ID NO) of the contig in which a particular open reading frame is located. Column 2 numerically identifies a particular ORF on a particular contig (SEQ ID NO) since many contigs comprise a plurality of ORFs. Columns 3 and 4 indicate an ORF's position in the nucleotide sequence (contig) provided in SEQ ID NOs: 1 through 142 by referring to start and stop positions in the contig sequence.

One of ordinary skill in the art will appreciate that the ORFs may be oriented in opposite directions in the *E. coli* chromosome. This is reflected in columns 3 and 4. For these ORFs, the sense strand is complementary to the actual sequence given. The corresponding sense-strand of the ORF must be read as the 5'-3' complement of the antisense strand actually shown in the Sequence Listing, wherein the location is specified 3'-5'.

Column 5 provides a database accession number to a homologous protein identified by a similarity search of public sequence databases (*see, infra*). Column 6 describes the matching protein sequence and the source organism is identified in brackets. Column 7 of Tables 1 and 3 indicates the percent similarity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 of Tables 1 and 3 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. The concepts of percent identity and percent similarity of two polypeptide sequences are well understood in the art and are described in more detail below. Identified genes can frequently be assigned a putative cellular role category adapted from Riley (*see, Riley, M., Microbiol. Rev. 57:862 (1993)*). Column 9 of Tables 1 and 3 provides the nucleotide length of the open reading frame.

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Tables 2 and 4, below, provide ORFs of *E. coli* J96 PAI IV and PAI V, respectively, that did not elicit a homology match with a known sequence from either *E. coli* or another organism. As above, the first column in Tables 2 and 4 provides the contig in which the ORF is located and the second column numerically identifies a particular ORF in a particular contig. Columns 3 and 4 identify an ORF's position in one of SEQ ID NOS: 1 through 142 by reference to start and stop nucleotides.

Tables 5 and 6, below, provide the *E. coli* J96 PAI IV ORFs and PAI V ORFs, respectively, identified by the present inventors that provided a significant match to a previously published *E. coli* protein. Columns 1-6 correspond to columns 1-6 appearing in Tables 1 and 3. Column 7 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 indicates the length of the high-scoring segment pair (HSP). Column 9 provides the nucleotide length of the open reading frame.

As used herein, "open reading frame" or "ORF" refers to the nucleotide sequences as described in Tables 1 through 6. In Tables 1 through 6, each ORF is designated by a nucleotide sequence start position and stop position according to numbering of contig nucleotides in the Sequence Listing provided (Contig ID = SEQ ID NO).

In a first embodiment, the invention comprises a nucleotide sequence described in Tables 1 through 4 which begins with the nucleotide following the last nucleotide of an upstream stop codon (first nucleotide of the "ORF"), an initiation codon, in-frame putative polypeptide-encoding sequence, and nucleotides of an in-frame stop codon.

In a second embodiment, the invention comprises a nucleotide sequence of Tables 1 through 4 which contains an initiation codon (*e.g.* a methionine or valine codon) on their 5' end and a stop codon on their 3' end. The sequences of this embodiment are present within the nucleotide sequence described in Tables 1 through 4 by start and stop position as numbered in the Sequence Listing. To

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determine the 5' start position of this embodiment, one simply reads 5' to 3' from the designated 5' end position until an initiation codon is found.

In a third embodiment, the invention comprises a nucleotide sequence of the second embodiment, except that the 3' stop codon is not present.

5 In a fourth embodiment, the invention comprises a nucleotide sequence encoding a putative protein which is a sequence of Tables 1 through 4 excluding sequence encoding amino acids subject to removal by post-translational processing and sequences 3' of the last codon coding for an amino acid present in the putative polypeptide (*e.g.*, sequences not containing the stop codon and
10 encoding the mature form of the polypeptide).

Certain embodiments of the invention may therefore either include or exclude initiation codons for methionine or valine and either include or exclude the stop codon.

Further details concerning the algorithms and criteria used for homology
15 searches are provided in the Examples below. A skilled artisan can readily identify ORFs in the *Escherichia coli* J96 cosmid library other than those listed in Tables 1 through 6, such as ORFs that are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

20 Isolated nucleic acid molecules of the present invention include DNA molecules having a nucleotide sequence substantially different than the nucleotide sequence of an ORF described in Tables 1 through 4, but which, due to the degeneracy of the genetic code, still encode a *E. coli* J96 PAI protein. The genetic code is well known in the art. Thus, it would be routine to generate such
25 degenerate variants.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of an *E. coli* protein encoded by an ORF described in Table 1 through 4. Non-naturally occurring variants may be produced using art-known mutagenesis
30 techniques and include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more

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nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *E. coli* protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an ORF described in Tables 1 through 6, preferably 1 through 4. By a polynucleotide having a nucleotide sequence at least, for example, 95% identical to the reference *E. coli* ORF nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the ORF sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference ORF nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleotide sequence of an *E. coli* J96 PAI ORF can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, *Advances in Applied Mathematics* 2: 482-489 (1981),

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to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

Preferred are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence of an *E. coli* J96 PAI ORF that encode a functional polypeptide. By a "functional polypeptide" is intended a polypeptide exhibiting activity similar, but not necessarily identical, to an activity of the protein encoded by the *E. coli* J96 PAI ORF. For example, the *E. coli* ORF [Contig ID 84, ORF ID 3 (84/3)] encodes a hemolysin. Thus, a "functional polypeptide" encoded by a nucleic acid molecule having a nucleotide sequence, for example, 95% identical to the nucleotide sequence of 84/3, will also possess hemolytic activity. As the skilled artisan will appreciate, assays for determining whether a particular polypeptide is "functional" will depend on which ORF is used as the reference sequence. Depending on the reference ORF, the assay chosen for measuring polypeptide activity will be readily apparent in light of the role categories provided in Tables 1, 3, 5 and 6.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of a reference ORF will encode a functional polypeptide. In fact, since degenerate variants all encode the same amino acid sequence, this will be clear to the skilled artisan even without performing a comparison assay for protein activity. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a functional polypeptide. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not

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likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie, J.U. *et al.*, *supra*, and the references cited therein.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated nucleic acid molecule having the nucleotide sequence of an *E. coli* J96 PAI ORF is intended fragments at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length that are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of an *E. coli* J96 PAI ORF. By a fragment at least 20 nt in length, for example, is intended fragments that include 20 or more contiguous bases from the nucleotide sequence of an *E. coli* J96 PAI ORF. Since *E. coli* ORFs are listed in Tables 1 through 6 and the sequences of the ORFs have been provided within the contig sequences of SEQ ID NOs: 1 through 142, generating

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such DNA fragments would be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes from the PAI DNA that is incorporated into the deposited pools of cosmid clones. Alternatively, such fragments could be generated synthetically.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of an *E. coli* J96 PAI protein. Methods for determining such epitope-bearing portions are described in detail below.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide that hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, an ORF described in Tables 1 through 6, preferably an ORF described in Tables 1, 2, 3 or 4. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5 x SSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 x SSC at about 65°C.

By a polynucleotide that hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., a *E. coli* ORF), for instance, a portion 50-500 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of an *E. coli* J96 PAI ORF.

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By "expression modulating fragment" (EMF), is intended a series of nucleotides that modulate the expression of an operably linked, putative polypeptide-encoding region (encoding region). A sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments that induce the expression of an operably linked encoding region in response to a specific regulatory factor or physiological event. EMF sequences can be identified within the *E. coli* genome by their proximity to the encoding regions within ORFs described in Tables 1 through 6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken 5' from any one of the encoding regions of ORFs of Tables 1 through 6 will modulate the expression of an operably linked 3' encoding region in a fashion similar to that found within the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to the fragments of the *E. coli* J96 PAI subgenome that are between two encoding regions herein described. Alternatively, EMFs can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site 5' to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence that is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed

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host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

By a "diagnostic fragment" (DF), is intended a series of nucleotides that selectively hybridize to *E. coli* sequences. DFs can be readily identified by identifying unique sequences within the *E. coli* J96 PAI subgenome, or by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format for amplification or hybridization selectivity.

Each of the ORFs of the *E. coli* J96 PAI subgenome disclosed in Tables 1 through 4, and EMFs found 5' to the encoding regions of the ORFs, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of uropathogenic *E. coli* in a sample. This is especially the case with the fragments or ORFs of Table 2 and 4 which will be highly selective for uropathogenic *E. coli* J96, and perhaps other uropathogenic or extraintestinal strains that include one or more PAIs.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the

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sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

Vectors and Host Cells

The present invention further provides recombinant constructs comprising one or more fragments of the *E. coli* J96 PAIs. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which, for example, an *E. coli* J96 PAI ORF is inserted. The vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the encoding region of an ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrec99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments (preferably an ORF) of the *E. coli* J96 PAIs described herein. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a

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lower eukaryotic host cell, such as a yeast cell, or the host cell can be a procaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). Host cells containing, for example, an *E. coli* J96 PAI ORF can be used conventionally to produce the encoded protein.

Polypeptides and Fragments

The invention further provides isolated polypeptides having the amino acid sequence encoded by an *E. coli* PAI ORF described in Tables 1 through 6, preferably Tables 1 through 4, or a peptide or polypeptide comprising a portion of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

It will be recognized in the art that some amino acid sequences of *E. coli* polypeptides can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the invention further includes variations of polypeptides encoded for by ORFs listed in Tables 1 through 6 which show substantial pathogenic activity or which include regions of particular *E. coli* PAI proteins such as the protein portions discussed below. Such mutants include deletions, insertions,

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inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

5 Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

10 As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (i.e., are not likely to have a significant deleterious effect on a function) can be found in Bowie, J.U., *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990).

15 Thus, the fragment, derivative or analog of a polypeptide encoded by an ORF described in one of Tables 1 through 6, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic
20 code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as an IgG Fc
25 fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

30 Of particular interest are substitutions of charged amino acids with another charged amino acid and with neutral or negatively charged amino acids. The latter results in proteins with reduced positive charge to improve the

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characteristics of said proteins. The prevention of aggregation is highly desirable. Aggregation of proteins not only results in a loss of activity but can also be problematic when preparing pharmaceutical formulations, because they can be immunogenic. (Pinckard *et al.*, *Clin Exp. Immunol.* 2:331-340 (1967); Robbins *et al.*, *Diabetes* 36:838-845 (1987); Cleland *et al.* *Crit. Rev. Therapeutic Drug Carrier Systems* 10:307-377 (1993)).

The replacement of amino acids can also change the selectivity of binding to cell surface receptors. Ostade *et al.*, *Nature* 361:266-268 (1993) describes certain mutations resulting in selective binding of TNF- α to only one of the two known types of TNF receptors. Thus, proteins encoded for by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6, and that bind to a cell surface receptor, may include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation.

As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 7).

TABLE 7. Conservative Amino Acid Substitutions

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

Amino acids in the proteins encoded by ORFs of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science* 244:1081-1085 (1989)). The latter procedure introduces single
5 alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding or *in vitro*, or *in vitro* proliferative activity. Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.*
10 224:899-904 (1992) and de Vos *et al.* *Science* 255:306-312 (1992)).

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the polypeptides can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

15 The polypeptides of the present invention include the polypeptide encoded by the ORFs listed in Tables 1-6, preferably Tables 1-4, as well as polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above, and also include portions of such polypeptides with at least 30 amino acids
20 and more preferably at least 50 amino acids.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive,
25 Madison, WI 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman (*Advances in Applied Mathematics* 2:482-489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example,
30 95% "identical" to a reference amino acid sequence of a polypeptide is intended

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that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of said polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence encoded by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6 can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The polypeptide of the present invention could be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art.

As described in detail below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting pathogenic protein expression as described below or as

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agonists and antagonists capable of enhancing or inhibiting protein function of important proteins encoded by the ORFs of the present invention. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" protein binding proteins which are also candidate agonist and antagonist according to the present invention. The yeast two hybrid system is described in Fields and Song, *Nature* 340:245-246 (1989).

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen *et al.*, *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R.A. (1983) Antibodies that react with predetermined sites on proteins. *Science* 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. Sutcliffe *et al.*,

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5 *supra*, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

10 Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe *et al.*, *supra*, at 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, for instance, Wilson *et al.*, *Cell* 37:767-778 (1984) at 777. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods well known in the art.

25 Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including 30 the entire amino acid sequence of a polypeptide of the invention, also are

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considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks. Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA* 82:5131-5135. This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten *et al.* (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten *et al.*, *supra*, at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe *et al.*, *supra*; Wilson *et al.*, *supra*; Chow, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle, F. J. *et al.*, *J. Gen. Virol.* 66:2347-2354 (1985).

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Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al.* *supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction

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with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to
10 Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) on Peralkylated Oligopeptide Mixtures discloses linear C₁-C₇-alkyl peralkylated
15 oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

20 The entire disclosure of each document cited in this section on "Polypeptides and Peptides" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, *E. coli* PAI polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG),
25 resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, e.g., for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins (EP A 394,827; Traunecker *et al.*, *Nature* 331:84-86 (1988)). Fusion proteins that have a disulfide-linked dimeric structure due to
30 the IgG part can also be more efficient in binding and neutralizing other

molecules than the monomeric *E. coli* J96 PAI proteins or protein fragments alone (Fountoulakis *et al.*, *J. Biochem* 270:3958-3964 (1995)).

Vaccines

In another embodiment, the present invention relates to a vaccine, preferably in unit dosage form, comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit a protective immune response in an animal to pathogenic *E. coli*. Antigens of *E. coli* J96 PAI IV and V may be obtained from polypeptides encoded for by the ORFs listed in Tables 1-6, particularly Tables 1-4, using methods well known in the art.

In a preferred embodiment, the antigens are *E. coli* J96 PAI IV or PAI V proteins that are present on the surface of pathogenic *E. coli*. In another preferred embodiment, the pathogenic *E. coli* J96 PAI IV or PAI V protein-antigen is conjugated to an *E. coli* capsular polysaccharide (CP), particularly to capsular polypeptides that are more prevalent in pathogenic strains, to produce a double vaccine. CPs, in general, may be prepared or synthesized as described in Schneerson *et al. J. Exp. Med.* 152:361-376 (1980); Marburg *et al. J. Am. Chem. Soc.* 108:5282 (1986); Jennings *et al., J. Immunol.* 127:1011-1018 (1981); and Beuvery *et al., Infect. Immunol.* 40:39-45 (1983). In a further preferred embodiment, the present invention relates to a method of preparing a polysaccharide conjugate comprising: obtaining the above-described *E. coli* J96 PAI antigen; obtaining a CP or fragment from pathogenic *E. coli*; and conjugating the antigen to the CP or CP fragment.

In a preferred embodiment, the animal to be protected is selected from the group consisting of humans, horses, deer, cattle, pigs, sheep, dogs, and chickens. In a more preferred embodiment, the animal is a human or a dog.

In a further embodiment, the present invention relates to a prophylactic method whereby the incidence of pathogenic *E. coli*-induced symptoms are

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decreased in an animal, comprising administering to the animal the above-described vaccine, wherein the vaccine is administered in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*. This vaccination method is contemplated to be useful in protecting against severe diarrhea (pathogenic intestinal *E. coli* strains), urinary tract infections (uropathogenic *E. coli*) and infections of the brain (extraintestinal *E. coli*). The vaccine of the invention is used in an effective amount depending on the route of administration. Although intra-nasal, subcutaneous or intramuscular routes of administration are preferred, the vaccine of the present invention can also be administered by an oral, intraperitoneal or intravenous route. One skilled in the art will appreciate that the amounts to be administered for any particular treatment protocol can be readily determined without undue experimentation. Suitable amounts are within the range of 2 micrograms of the protein per kg body weight to 100 micrograms per kg body weight.

The vaccine can be delivered through a vector such as BCG. The vaccine can also be delivered as naked DNA coding for target antigens.

The vaccine of the present invention may be employed in such dosage forms as capsules, liquid solutions, suspensions or elixirs for oral administration, or sterile liquid forms such as solutions or suspensions. Any inert carrier is preferably used, such as saline, phosphate-buffered saline, or any such carrier in which the vaccine has suitable solubility properties. The vaccines may be in the form of single dose preparations or in multi-dose flasks which can be used for mass vaccination programs. Reference is made to Remington's *Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, Osol (ed.) (1980); and *New Trends and Developments in Vaccines*, Voller *et al.* (eds.), University Park Press, Baltimore, MD (1978), for methods of preparing and using vaccines.

The vaccines of the present invention may further comprise adjuvants which enhance production of antibodies and immune cells. Such adjuvants include, but are not limited to, various oil formulations such as Freund's complete adjuvant (CFA), the dipeptide known as MDP, saponins (ex. *Quillajasaponin* fraction QA-21, U.S. Patent No. 5,047,540), aluminum hydroxide, or lymphatic

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cytokines. Freund's adjuvant is an emulsion of mineral oil and water which is mixed with the immunogenic substance. Although Freund's adjuvant is powerful, it is usually not administered to humans. Instead, the adjuvant alum (aluminum hydroxide) may be used for administration to a human. Vaccine may be absorbed onto the aluminum hydroxide from which it is slowly released after injection. The vaccine may also be encapsulated within liposomes according to Fullerton, U.S. Patent No. 4,235,877.

Protein Function

Each ORF described in Tables 1 and 3 possesses a biological role similar to the role associated with the identified homologous protein. This allows the skilled artisan to determine a function for each identified coding sequence. For example, a partial list of the *E. coli* protein functions provided in Tables 1 and 3 includes many of the functions associated with virulence of pathogenic bacterial strains. These include, but are not limited to adhesins, excretion pathway proteins, O-antigen/carbohydrate modification, cytotoxins and regulators. A more detailed description of several of these functions is provided in Example 1 below.

Diagnostic Assays

In another preferred embodiment, the present invention relates to a method of detecting pathogenic *E. coli* nucleic acid in a sample comprising:

- a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and
- b) detecting the presence of the probe bound to pathogenic *E. coli* nucleic acid.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* nucleic acid in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

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In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antibodies.

5 In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antigens.

10 The present invention provides methods to identify the expression of an ORF of the present invention, or homolog thereof, in a test sample, using one of the antibodies of the present invention. Such methods involve incubating a test sample with one or more of the antibodies of the present invention and assaying for binding of the antibodies to components within the test sample.

15 In a further embodiment, the present invention relates to a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for a nucleic acid, protein, polypeptide-antigen or antibody specific to one of the ORFs described in Tables 1-4 herein from *E. coli* J96 PAI IV or V. Analysis of nucleic acid specific to pathogenic *E. coli* can be by PCR techniques or hybridization techniques (cf. *Molecular Cloning: A Laboratory*
20 *Manual, second edition*, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989; Ereemeeva *et al.*, *J. Clin. Microbiol.* 32:803-810 (1994) which describes differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA).

25 Proteins or antibodies specific to pathogenic *E. coli* may be identified as described in *Molecular Cloning: A Laboratory Manual, second edition*, Sambrook *et al.*, eds., Cold Spring Harbor Laboratory (1989). More specifically, antibodies may be raised to *E. coli* J96 PAI proteins as generally described in *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988). *E. coli* J96 PAI-specific antibodies can also be obtained from
30 infected animals (Mather, T. *et al.*, *JAMA* 205:186-188 (1994)).

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In another embodiment, the present invention relates to an antibody having binding affinity specifically to an *E. coli* J96 PAI antigen as described above. The *E. coli* J96 PAI antigens of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, a peptide can be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well as fragments of these antibodies. The invention further includes single chain antibodies. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques, for example, such fragments include but are not limited to: the F(ab')₂ fragment; the Fab' fragments, Fab fragments, and Fv fragments.

Of special interest to the present invention are antibodies to pathogenic *E. coli* antigens which are produced in humans, or are "humanized" (i.e. non-immunogenic in a human) by recombinant or other technology. Humanized antibodies may be produced, for example by replacing an immunogenic portion of an antibody with a corresponding, but non-immunogenic portion (i.e. chimeric antibodies) (Robinson, R.R. *et al.*, International Patent Publication PCT/US86/02269; Akira, K. *et al.*, European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison, S.L. *et al.*, European Patent Application 173,494; Neuberger, M.S. *et al.*, PCT Application WO 86/01533; Cabilly, S. *et al.*, European Patent Application 125,023; Better, M. *et al.*, *Science* 240:1041-1043 (1988); Liu, A.Y. *et al.*, *Proc. Natl. Acad. Sci. USA* 84:3439-3443 (1987); Liu, A.Y. *et al.*, *J. Immunol.* 139:3521-3526 (1987); Sun, L.K. *et al.*, *Proc. Natl. Acad. Sci. USA* 84:214-218 (1987); Nishimura, Y. *et al.*, *Canc. Res.* 47:999-1005 (1987); Wood, C.R. *et al.*, *Nature* 314:446-449 (1985); Shaw *et al.*, *J. Natl. Cancer Inst.* 80:1553-1559 (1988). General reviews of "humanized" chimeric antibodies are provided by Morrison, S.L. (*Science*, 229:1202-1207 (1985)) and by Oi, V.T. *et al.*, *BioTechniques* 4:214 (1986)). Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones, P.T. *et al.*, *Nature* 321:552-525 (1986); Verhoeyan *et al.*,

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Science 239:1534 (1988); Beidler, C.B. *et al.*, *J. Immunol.* 141:4053-4060 (1988)).

In another embodiment, the present invention relates to a hybridoma which produces the above-described monoclonal antibody. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "*Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*," Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods* 35:1-21 (1980)).

In another embodiment, the present invention relates to a method of detecting a pathogenic *E. coli* antigen in a sample, comprising: a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and b) detecting the presence of said antibody bound to the antigen. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard, *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands

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(1985); and *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988).

5 The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein
10 extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is capable with the system utilized.

In another embodiment, the present invention relates to a method of detecting the presence of antibodies to pathogenic *E. coli* in a sample, comprising: a) contacting the sample with an above-described antigen, under conditions such that immunocomplexes form, and b) detecting the presence of
15 said antigen bound to the antibody. In detail, the methods comprise incubating a test sample with one or more of the antigens of the present invention and assaying whether the antigen binds to the test sample.

In another embodiment of the present invention, a kit is provided which contains all the necessary reagents to carry out the previously described methods
20 of detection. The kit may comprise: i) a first container means containing an above-described antibody, and ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting
25 the presence of bound antibodies. Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits.

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One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

Screening Assay for Binding Agents

5 Using the isolated proteins described herein, the present invention further provides methods of obtaining and identifying agents that bind to a protein encoded by an *E. coli* J96 PAI ORF or to a fragment thereof.

The method involves:

- 10 (a) contacting an agent with an isolated protein encoded by a *E. coli* J96 PAI ORF, or an isolated fragment thereof; and
- (b) determining whether the agent binds to said protein or said fragment.

15 The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques. For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by an ORF of the present invention.

20 Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific

25 peptide sequence in order to generate rationally designed anti-peptide ligands, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides, In *Synthetic Peptides, A User's Guide*, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry* 28:9230-8 (1989).

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In addition to the foregoing, one class of agents of the present invention, can be used to control gene expression through binding to one of the ORF encoding regions or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed and selected. Targeting the encoding region or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF encoding region or multiple encoding regions that rely on the same EMF for expression control.

One class of DNA binding agents are those that contain nucleotide base residues that hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives having base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251: 1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Computer Related Embodiments

The nucleotide sequence provided in SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to the sequences provided in SEQ ID NOs: 1 through 142, can be "provided" in

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a variety of media to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, that contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NOs: 1 through 142, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NOs: 1 through 142. Such a manufacture provides the *E. coli* J96 PAI subgenomes or a subset thereof (e.g., one or more *E. coli* J96 PAI open reading frame (ORF)) in a form that allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *E. coli* J96 PAI subgenome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, one or more nucleotide sequences of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on

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computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of dataprocessor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to SEQ ID NOs: 1 through 142, in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the *E. coli* J96 PAI subgenome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the *E. coli* J96 PAI subgenome and are useful in producing commercially important proteins such as enzymes used in modifying surface O-antigens of bacteria. A comprehensive list of ORFs encoding commercially important *E. coli* J96 PAI proteins is provided in Tables 1 through 6.

The present invention provides a DNA sequence - gene database of pathogenicity islands (PAIs) for *E. coli* involved in infectious diseases. This database is useful for identifying and characterizing the basic functions of new virulence genes for *E. coli* involved in uropathogenic and extraintestinal diseases. The database provides a number of novel open reading frames that can be selected for further study as described herein.

Selectable insertion mutations in plasmid subclones encoding PAI genes with potentially significant phenotypes for *E. coli* uropathogenesis and sepsis can

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be isolated. The mutations are then crossed back into wild type, uropathogenic *E. coli* by homologous recombination to create wild-type strains specifically altered in the targeted gene. The significance of the genes to *E. coli* pathogenesis is assessed by *in vitro* assays and *in vivo* murine models of sepsis/peritonitis and ascending urinary tract infection.

New virulence genes and PAI sites in uropathogenic *E. coli* may be identified by the transposon signature-tagged mutagenesis system and negative selection of *E. coli* mutants avirulent in murine models of ascending urinary tract infection or peritonitis.

Epidemiological investigations of new virulence genes and PAIs may be used to test for their occurrence in the genomes of other pathogenic and opportunistic members of the Enterobacteriaceae.

One can choose from the ORFs included in SEQ ID NOs: 1 through 142, using Tables 1 through 6 as a useful guidepost for selecting, as candidates for targeted mutagenesis, a limited number of candidate genes within the PAIs based on their homology to virulence, export or regulation genes in other pathogens. For the large number of apparent genes within the PAIs that do not share sequence similarity to any entries in the database, the transposon signature-tagged mutagenesis method developed by David Holden's laboratory can be employed as an independent means of virulence gene identification.

Allelic knock-outs are constructed using different *pir*-dependent suicide vectors (Swihart, K.A. and R.A. Welch, *Infect. Immun.* 58:1853-1869 (1990)). In addition, two different animal model systems can be employed for assessment of pathogenic determinants. The initial identification of *E. coli* hemolysin as a virulence factor came from the construction of isogenic *E. coli* strains that were tested in a rat model of intra-abdominal sepsis (Welch, R.A. *et al.*, *Nature (London)* 294:665-667 (1981)). The ascending UTI (Urinary Tract Infection) mouse model was also successfully performed with allelic knock-outs of the *hpmA* hemolysin of *Proteus mirabilis* (Swihart, K.A. and R.A. Welch, *Infect. Immun.* 58:1853-1869 (1990)).

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The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *E. coli* J96 PAI subgenome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *E. coli* genome that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

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As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the *E. coli* J96 PAI subgenome, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequence and the homologous *E. coli* J96 PAI sequence identified using a search means as described above, and an output means for outputting the identified homologous *E. coli* J96 PAI sequence. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *E. coli* J96 PAI subgenome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

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E. coli J96 PAI subgenomes. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) can be used to identify open reading frames within the *E. coli* J96 PAI subgenome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

One application of this embodiment is provided in Figure 2. Figure 2 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114 once inserted in the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108 during execution.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

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Experimental

Example 1: High Through-put Sequencing of Cosmid Clones Covering PAI IV and PAI V in E. coli J96

5 The complete DNA sequence of the pathogenicity islands, PAI IV and PAI V (respectively >170 kb and ~110 kb), from uropathogenic *E. coli* strain, J96 (O4:K6) was determined using a strategy, cloning and sequencing method, data collection and assembly software essentially identical to those used by the TIGR group for determining the sequence of the *Haemophilus influenzae* genome (Fleischmann, R.D., *et al.*, *Science* 269:496 (1995)). The sequences were then
10 used for DNA and protein sequence similarity searches of the databases as described in Fleischmann, *Id.*

The analysis of the genetic information found within the PAIs of *E. coli* J96 was facilitated by the use of overlapping cosmid clones possessing these unique segments of DNA. These cosmid clones were previously constructed and
15 mapped (as further described below) as an overlapping set in the laboratory of Dr. Doug Berg (Washington University). A gap exists between the left portion of cosmid 2 and the end of the PAI IV that would represent the *pheV* junction to the *E. coli* K-12 genome.

Uropathogenic strain *E. coli* J96 (O4:K6) was used as a source of
20 chromosomal DNA for construction of a cosmid library. *E. coli* K-12 DH5 α and DH12 (Gibco/BRL, Gaithersburg, Md.) were used as hosts for maintaining cosmid and plasmid clones. The cosmid library of *E. coli* J96 DNA was constructed essentially as described by Bukanow & Berg (*Mol. Microbiol* 11:509-523 (1994)). DNA was digested with *Sau3A*I under conditions that generated
25 fragments with an average size of 40 to 50 kb and electrophoresed through 1% agarose gels. Fragments of 35 to 50 kb were isolated and cloned into Lorist 6 vector that had been linearized with *Bam*III and treated with bacterial alkaline phosphatase to block self-ligation. (Lorist 6 is a 5.2-kb moderate-copy-number cosmid vector with T7 and SP6 promoters close to the cloning site.) Cloned

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DNA was packaged in lambda phage particles *in vitro* by using a commercial kit (Amersham, Arlington Heights, IL) and cosmid-containing phage particles were used to transduce *E. coli* DH5 α . Transductant colonies were transferred to 150 μ L of Luria-Bertani broth supplemented with kanamycin in 96-well microtiter plates and grown overnight at 37°C with shaking. Two sets of clones, one for each PAI were ultimately assembled, as previously described (Swenson *et al.*, *Infection and Immunity* 64:3736-3743 (1996)), fully incorporated by reference herein).

The two sets of clones contain eleven sub-clones that were employed in the sequencing method described below. One set of four overlapping cosmid clones covers the *prs*-containing PAI V, ATCC Deposit No. 97727, deposited September 23, 1996. A second set of seven subclones covers much of the *pap*-containing PAI V, ATCC Deposit No. 97726, deposited September 23, 1996. See Figure 1.

A high through-put, random sequencing method (Fleischmann *et al.*, *Science* 269:496 (1995); Fraser *et al.*, *Science* 270:397 (1995)) was used to obtain the sequences for 142 (contigs) fragments of *E. coli* J96 PAIs. All clones were sequenced from both ends to aid in the eventual ordering of contigs during the sequence assembly process. Briefly, random libraries of ~ 2 kb clones covering the two J96 PAIs were constructed, ~ 2,800 clones were subjected to automated sequencing (~ 450 nt/clone) and preliminary assemblies of the sequences accomplished which result in 142 contigs for each of the two PAIs that total 95 and 135 kb respectively. The estimated sizes of the PAI IV and PAI V based on the overlapping cosmid clones are 1.7×10^5 and 1.1×10^5 bp respectively. The 142 sequences were assembled by means of the TIGR Assembler (Fleischmann *et al.*; Fraser *et al.*; Sutton *et al.*, *Genome Sci. Tech.* 1:9 (1995)). Sequence and physical gaps were closed using a combination of strategies (Fleischmann *et al.*; Fraser *et al.*). Presently the average depth of sequencing for each base assembled in the contigs is 6-fold. The tentative identity of many genes based on sequence homology is covered in Tables 1, 3, 5 and 6.

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Open reading frames (ORFs) and predicted protein-coding regions were identified as described (Fleischmann *et al.*; Fraser *et al.*) with some modification. In particular, the statistical prediction of uropathogenic *E. coli* J96 pathogenicity island genes was performed with GeneMark (Borodovsky, M. & McIninch, J. Comput. Chem. 17:123 (1993)). Regular GeneMark uses nonhomogeneous Markov models derived from a training set of coding sequences and ordinary Markov models derived from a training set of noncoding sequences. The ORFs in Tables 1-6 were identified by GeneMark using a second-order Markov model trained from known *E. coli* coding regions and known *E. coli* non-coding regions.

Among the important genes that are implicated in the virulence of *E. coli* J96 PAIs are adhesins, excretion pathway proteins, proteins that participate in alterations of the O-antigen in the PAIs, cytotoxins, and two-component (membrane sensor/DNA binding) proteins.

I. Adhesins. It is believed that the principal adhesin determinants involved in uropathogenicity that are present within PAIs of uropathogenic *E. coli* are the pili encoded by the *pap*-related operons (Hultgren *et al.*, Infect. Immun. 50:370-377 (1993), Stromberg *et al.*, EMBO J 9:2001-2010 (1990), High *et al.*, Infect. Immun. 56:513-517 (1988)) and the distantly related afimbrial adhesins (Labigne-Roussel *et al.*, Infect. Immun. 46:251-259 (1988)). The presence of two of these (*pap*, and *prs*) has been confirmed. In addition potential genes for five other adhesins including *sla* (described above), AIDA-I (diffuse adherence-DEAC), *hra* (heat resistant hemagglutinin-ETEC), *fha* (filamentous hemagglutinin- *Bordetella pertussis*) and the arg-gingipain proteinase of *Porphyromonas gingivalis* have been found.

II. Type II exoprotein secretion pathway. Highly significant statistics support the presence of multiple genes involved in the type II exoprotein pathway. Curiously, perhaps two different determinants appear to be present in PAI IV where one set of genes has the highest sequence similarity to *eps*-like genes (*Vibrio cholerae* Ctx export) and the other has greatest similarity to *exe* genes (*Aeromonas hydrophila* aerolysin and protease export). At present, the assembly of contigs involving these potential genes is incomplete. Thus, it is

uncertain if two separate and complete determinants are present. However, it is clear that these genes are newly discovered and novel to pathogenic *E. coli* because the derived sequences do not have either the *bfp* or *hop* genes as the highest matches. The gene products that are the target of the type II export pathway are not evident at this time.

Within PAI IV there are sequences which suggest genes very similar to *secD* and *secF*. These two linked genes encode homologous products that are localized to the inner membrane and are hypothesized to play a late role in the translocation of leader-peptide containing proteins across the inner membrane of gram-negative bacteria. In addition, in each PAI, sequences are found that are reminiscent of the heat-shock *htrA/degA* gene that encodes a periplasmic protease. They may perform endochaperone-like function as Pugsley *et al.* have hypothesized for different exoprotein pathways.

III. O-antigen/capsule/carbohydrate modification (Nod genes). J96 has the O4. The O-antigen portion of lipopolysaccharide is encoded by *rfb* genes that are located at 45 min. on the *E. coli* chromosome. We have found in both PAIs a cumulative total of five possible *rfb*-like genes which could participate alterations of the O-antigen in the PAIs. Overall these data suggest that PAIs provide the genetic potential for greater change of the cell surface for uropathogenic *E. coli* strains than what was previously known.

The apparent capsule type for strain J96 is a non-sialic acid K6-type. Sequence similarity "hits" were made in PAI IV region to two region-1 capsule genes, *kpsS* and *kpsE* involved in the stabilization of polysaccharide synthesis and polysaccharide export across the inner membrane. This is not altogether surprising based on the genetic mapping of the *kps* locus to *serA* at 63 minutes on the genome of the K1 capsular type of *E. coli*. This suggests that these *kps*-like genes either are participating in the K6-biosynthesis or perhaps are involved in complex carbohydrate export for other purposes.

An intriguing discovery are the hits made on genes involved in bacteria-plant interactions by *Rhizobium*, *Bradyrhizobium* and *Agrobacterium*. Four potential genes identified thus far share significant sequence similarity to genes

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encoding products that modify lipo-oligosaccharides that influence nodule morphogenesis on legume roots. These are: ORF140, carbamyl phosphate synthetase; nodulation protein 1265; phosphate-regulatory protein; and an ORF at a plant-inducible locus in *Agrobacterium*. To date there are no descriptions in the literature of such gene products being utilized by human or animal bacterial pathogens for the purposes of modification or secretion of extracellular carbohydrate. However, the sequence similarity to the capsular region-2 genes and to lipooligosaccharide biosynthetic genes in *Rhizobium* spp has been recently noted by Petit (1995).

IV. Cytotoxins. Besides the previously known hemolysin and CNF toxins in the PAIs, in each PAI sequences similar to the *shlBA* operon (cosmid 5 and 12) were found for a cytolytic toxin from *Serratia marcescens* and *Proteus mirabilis*. Ironically, the *P. mirabilis* hemolysin (HpmA) member of this family of toxins was discovered by Uphoff and Welch (1990), but not thought to exist in other members of the Enterobacteriaceae (Swihart (1990)). A *shlB*-like transporter does also appear to be involved in the export of the filamentous hemagglutinin of *Bordetella pertussis* which was described above and a cell surface adhesin of *Haemophilus influenzae*. It has been demonstrated that cosmid #5 of *E. coli* J96 encodes an extracellular protein that is ~180 kDa and cross-reactive to polyclonal antisera to the *P. mirabilis* HpmA hemolysin. Thus, there is evidence suggesting there is new member of this family of proteins in extraintestinal *E. coli* isolates. In addition, there is also a hit on the FhaC hemolysin-like gene within the PAI V although its statistical significance for the sequence thus far available is only 0.0043.

V. Regulators. A common regulatory motif in bacteria are the two-component (membrane sensor/DNA binding) proteins. In numerous instances in pathogenic bacteria, external signals in the environment cause membrane-bound protein kinases to phosphorylate a cytoplasmic protein which in turn acts as either a negative or positive effector of transcription of large sets of operons. On cosmid 11 representing PAI V were found, in two different *Pst*I clones, sequences

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for two-component regulators (similar probabilities for OmpR/ AIGB and separately RcsC, probabilities at the 10^{-22} level).

In addition, the phosphoglycerate transport system (*pgtA*, *pgtC*, and *pgtP*) including the *pgtB* regulator is present in PAI IV. This transport system which was originally described in *S. typhimurium* is not appreciated as a component of any pathogenic *E. coli* genome. The operon had been previously mapped at 49 minutes, near or within one of the *S. typhimurium* chromosome specific-loops not present in the K-12 genome. It should be noted that the *E. coli* K-12 *glpT* gene product is similar to *pgtP* gene product (37% identity), but the *E. coli* J96 genes are clearly homologs to the *pgt* genes and their linkage within the middle of PAI IV element (cosmid #4) is suspicious.

VI. Mobile genetic elements. There are numerous sequences that share similarity to genes found on insertion elements, plasmids and phages. The temperate bacteriophage P4 inserts within tRNA loci in the *E. coli* chromosome. The hypothesis was made that PAIs are the result of bacteriophage P4-virulence gene recombination events (Blum *et al.*, *Infect. Immun.* 62:606-614 (1994). Data supporting this hypothesis was found during our sequencing with the identification of P4-like sequences in each of the PAIs (cosmids 7 and 9). This is a very important preliminary result which supports the hypothesis that PAIs can be identified by common sequence or genetic elements. However, there are indications that multiple mobile genetic elements involved in the evolution of the J96 PAIs. Conjugal plasmid-related sequences may also be present at two different locations (F factor and RI plasmid). Sequences for multiple transposable elements are present that are likely to have originated from different bacterial genera (Tn1000, IS630, IS911, IS100, IS21, IS 1203, IS5376 (*B. stearothersophilus*) and RHS). Of particular interest is IS100, which was originally identified in *Yersinia pestis* (Fetherston *et al.*, *Mol. Microbiol.* 6:2693-2704 (1992)). The presence of IS100 is significant because it has been associated with the termini of a large chromosomal element encoding pigmentation and some aspect of virulence in *Y. pestis*. This element undergoes spontaneous deletions similar to the PAIs from *E. coli* 536 (Fetherston *et al.*, *Mol. Microbiol.*

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6:2693-2704 (1992)) and appears to participate in plasmid-chromosome rearrangements. This element was not previously known to be in genera outside of *Yersinia*.

5 The discovery of the apparent *att* site for bacteriophage P2 in the PAIs is interesting. P2 acts as a helper phage for the P4 satellite phage. The P2 *att* site is at 44 min in the K-12 genome. The significance of this hit is unknown at present, but may be explained as either a cloning artifact (some K-12 fragments in the *Pst* I library of cosmid 5) or evidence of some curious chromosomal-P4/P2 phage history. It may indicate that the J96 PAIs are composites of multiple
10 smaller PAIs.

Example 2: Preparation of PCR Primers and Amplification of DNA

Various fragments of the sequenced *E. coli* J96 PAIs, such as those disclosed in Tables 1 through 6 can be used, in accordance with the present invention, to prepare PCR primers. The PCR primers are preferably at least 15
15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers are useful during PCR cloning of the ORFs described herein.

Example 3: Gene expression from DNA Sequences Corresponding to ORFs

20 A fragment of an *E. coli* J96 PAI (preferably, a protein-encoding sequence provided in Tables 1 through 6) is introduced into an expression vector using conventional technology (techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art). Commercially available vectors
25 and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper

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protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Pat. No. 5,082,767, which is hereby incorporated by reference.

5 The following is provided as one exemplary method to generate polypeptide(s) from a cloned ORF of an *E. coli* J96 PAI whose sequence is provided in SEQ ID NOs: 1 through 142. A poly A sequence can be added to the construct by, for example, splicing out the poly A sequence from pSG5 (Stratagene) using BglII and Sall restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use
10 in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *E. coli* J96 PAI DNA is obtained by PCR from the bacterial vector using
15 oligonucleotide primers complementary to the *E. coli* J96 PAI DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *E. coli* J96 PAI DNA 3' primer, taking care to ensure that the *E. coli* J96 PAI DNA is positioned such that its followed with the poly A sequence. The purified fragment obtained from the
20 resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions
25 outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface.

30 Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *E. coli* J96 PAI DNA

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sequence are injected into mice to generate antibody to the polypeptide encoded by the *E. coli* J96 PAI DNA.

If antibody production is not possible, the *E. coli* J96 PAI DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as a chimeric with, for example, β -globin. Antibody to β -globin is used to purify the chimeric. Corresponding protease cleavage sites engineered between the β -globin gene and the *E. coli* J96 PAI DNA are then used to separate the two polypeptide fragments from one another after translation. One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene). This vector encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides may additionally be produced from either construct using *in vitro* translation systems such as In vitro Express™ Translation Kit (Stratagene).

Example 4

E. coli Expression of an E. coli J96 PAI ORF and protein purification

An *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified using PCR oligonucleotide primers designed from the nucleotide sequences flanking the selected ORF and/or from portions of the ORF's NH₂- or COOH-terminus. Additional nucleotides containing restriction sites to facilitate cloning are added to the 5' and 3' sequences, respectively.

The restriction sites are selected to be convenient to restriction sites in the bacterial expression vector pQE60. The bacterial expression vector pQE60 is used for bacterial expression in this example. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible

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promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., *supra*, and suitable single restriction enzyme cleavage sites. These elements are arranged such that a DNA fragment encoding a polypeptide may be inserted in such a way as to produce that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of an *E. coli* J96 PAI is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the *E. coli* protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

The amplified *E. coli* J96 PAI DNA fragments and the vector pQE60 are digested with one or more appropriate restriction enzymes, such as Sall and XbaI, and the digested DNAs are then ligated together. Insertion of the *E. coli* J96 PAI DNA into the restricted pQE60 vector places the *E. coli* J96 PAI protein coding region, including its associated stop codon, downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook *et al.*, *Molecular Cloning: a Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing an *E. coli* J96 PAI protein, is available commercially from QIAGEN, Inc., *supra*. Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from

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resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lac repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH8. The cell debris is removed by centrifugation, and the supernatant containing the *E. coli* J96 PAI protein is dialyzed against 50 mM Na-acetate buffer pH6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. coli* J96 PAI protein. The purified protein is stored at 4°C or frozen at -80°C.

Example 5

Cloning and Expression of an E. coli J96 PAI protein in a Baculovirus

Expression System

A *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified as above. The plasmid is digested with appropriate restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1%

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agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.). This vector DNA is designated herein "V1".

Fragment F1 and the dephosphorylated plasmid V1 are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria are identified that contain the plasmid with the *E. coli* J96 PAI gene by digesting DNA from individual colonies using appropriate restriction enzymes and then analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing. This plasmid is designated herein pBac *E. coli* J96.

Five µg of the plasmid pBac *E. coli* J96 is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA.), using the lipofection method described by Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). 1 µg of BaculoGold™ virus DNA and 5 µg of the plasmid pBac *E. coli* J96 are mixed in a sterile well of a microliter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27°C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation is continued at 27°C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc.) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies

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Inc., page 9-10). After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4°C. The recombinant virus is called V-*E. coli* J96.

To verify the expression of the *E. coli* gene Sf9 cells are grown in Grace's medium supplemented with 10% heat inactivated FBS. The cells are infected with the recombinant baculovirus V-*E. coli* J96 at a multiplicity of infection ("MOI") of about 2. Six hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc.). If radiolabeled proteins are desired, 42 hours later, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then they are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled). Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the mature protein and thus the cleavage point and length of the secretory signal peptide.

Example 6

Cloning and Expression in Mammalian Cells

Most of the vectors used for the transient expression of an *E. coli* J96 PAI gene in mammalian cells should carry the SV40 origin of replication. This allows the replication of the vector to high copy numbers in cells (e.g., COS cells) which express the T antigen required for the initiation of viral DNA synthesis. Any other mammalian cell line can also be utilized for this purpose.

A typical mammalian expression vector contains the promoter element, which mediates the initiation of transcription of mRNA, the protein coding

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sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription can be achieved with the early and late promoters from SV40, the long terminal repeats (LTRS) from Retroviruses, e.g., RSV, 1HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter). Suitable expression vectors for use in practicing the present invention include, for example, vectors such as PSVL and PMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146) and pBC12MI (ATCC 67109). Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV 1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the gene can be expressed in stable cell lines that contain the gene integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful to develop cell lines that carry several hundred or even several thousand copies of the gene of interest. Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy *et al.*, *Biochem J.* 227:277-279 (1991); Bebbington *et al.*, *Bio/Technology* 10:169-175 (1992)). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

The expression vectors pC1 and pC4 contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen *et al.*, *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart *et al.*, *Cell* 41:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme

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cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors contain in addition the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene.

Example 6(a): Cloning and Expression in COS Cells

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The expression plasmid, p *E. coli* J96HA, is made by cloning a cDNA encoding *E. coli* J96 PAI protein into the expression vector pcDNAI/Amp or pcDNAIII (which can be obtained from Invitrogen, Inc.).

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The expression vector pcDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a cDNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson *et al.*, *Cell* 37:767 (1984). The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pcDNAIII contains, in addition, the selectable neomycin marker.

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A DNA fragment encoding the *E. coli* J96 PAI protein is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The *E. coli* cDNA of the deposited clone is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. coli* J96 PAI protein in *E. coli*.

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The PCR amplified DNA fragment and the vector, pcDNAI/Amp, are digested with appropriate restriction enzymes for the chosen primer sequences

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and then ligated. The ligation mixture is transformed into *E. coli* strain SURE (available from Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the *E. coli* J96 PAI protein-encoding fragment.

For expression of recombinant *E. coli* J96 PAI protein, COS cells are transfected with an expression vector, as described above, using DEAE-DEXTRAN, as described, for instance, in Sambrook *et al.*, *Molecular Cloning: a Laboratory Manual*, Cold Spring Laboratory Press, Cold Spring Harbor, New York (1989). Cells are incubated under conditions for expression of *E. coli* J96 PAI protein by the vector.

Expression of the *E. coli* J96 PAI - HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow *et al.*, *Antibodies: A Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988). To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson *et al.* cited above. Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 6(b): Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of an *E. coli* J96 PAI protein. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Acc. No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early

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promoter. Chinese hamster ovary- or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies, Inc.) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented (see, e.g., Alt, F. W. *et al.*, 1978, *J. Biol. Chem.* 253:1357-1370, Hamlin, J. L. and Ma, C. 1990, *Biochim. et Biophys. Acta*, 1097:107-143, Page, M. J. and Sydenham, M.A. 1991, *Biotechnology* 9:64-68). Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains for expressing the gene of interest the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus (Cullen, *et al.*, *Molecular and Cellular Biology*, March 1985:438-447) plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV) (Boshart *et al.*, *Cell* 41:521-530 (1985)). Downstream of the promoter is BamHI restriction enzyme site that allows the integration of the gene. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. coli* protein in a regulated way in mammalian cells (Gossen, M., & Bujard, H. 1992, *Proc. Natl. Acad. Sci. USA* 89: 5547-5551). For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the

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chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

5 The plasmid pC4 is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

The DNA sequence encoding the complete *E. coli* J96 PAI protein including its leader sequence is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene.

10 The amplified fragment is digested with appropriate endonucleases for the chosen primers and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction
15 enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. 5 µg of the expression plasmid pC4 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner *et al.*, *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an
20 enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methothrexate plus 1 mg/ml G418. After about 10-14 days single clones are
25 trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until
30 clones are obtained which grow at a concentration of 100 - 200 µM. Expression

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of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 7

Production of an Antibody to an E. coli J96 Pathogenicity Island Protein

5 Substantially pure *E. coli* J96 PAI protein or polypeptide is isolated from the transfected or transformed cells described above using an art-known method. The protein can also be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody
10 to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler and Milstein, *Nature* 256:495 (1975) or modifications
15 of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective
20 media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth.*
25 *Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis,

L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

Polyclonal Antibody Production by Immunization

5 Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other molecules and may
10 require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).
15

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall (See Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973)). Plateau
20 concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2nd ed., Rose and Friedman, (eds.), Amer. Soc. For Microbio., Washington, D.C. (1980).
25

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample.

TABLE 1 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
65	2	1902	1042	gi11655838	ORF8; putative transposase [Yersinia pestis]	100	100	861
65	3	2096	1821	gi1467612	ORF1 [Yersinia pestis]	100	100	276
63	11	7856	9238	gi1154262	transporter protein pgp [Salmonella typhimurium]	98	93	1383
65	4	2889	1915	gi11655837	ORF4; putative transposase [Yersinia pestis]	97	96	975
138	1	2	172	gi11208992	unknown [Escherichia coli]	97	78	171
64	6	4075	4338	gi11143207	Description: IS630 insertion element; ORF5 protein; Method: conceptual translation supplied by author [Shigella sonnei]	92	92	264
67	1	1	273	gi1809648	ExeF gene product [Aeromonas hydrophila]	92	71	273
73	4	3029	2511	gi1799234	glucose-1-phosphate thymidyltransferase [Escherichia coli]	92	86	515
73	5	3139	2996	gi1454900	rfBC gene product [Shigella flexneri]	92	92	144
64	5	3741	4088	gi147542	ORP (343 AA) [Shigella sonnei]	91	85	348
73	3	2613	2242	gi146985	glucose-1-phosphate thymidyltransferase [Salmonella enterica]	91	82	372
90	1	1	366	gi138826	ExeE gene product [Aeromonas hydrophila]	91	77	366
91	2	604	248	gi1609625	putative [Vibrio cholerae]	91	67	357
63	9	6301	5234	gi1858753	regulatory protein pgtb [Salmonella typhimurium]	89	84	1068
73	2	2179	1811	gi1294899	dTDP-6-deoxy-L-mannose-dehydrogenase [Shigella flexneri]	89	84	369
90	2	201	689	gi138826	ExeE gene product [Aeromonas hydrophila]	89	80	489
95	2	1519	413	gi1581654	dTDP-glucose 4,6-dehydratase [Salmonella enterica]	88	81	1107
96	1	729	457	pir154348315434	Orf104 homolog - Escherichia coli	88	72	273
63	6	4281	3019	gi1154255	phosphoglycerate transport system activator protein [Salmonella typhimurium]	87	79	1263
67	2	251	745	gi1609628	putative [Vibrio cholerae]	87	72	495
82	12	5254	4406	gi11208992	unknown [Escherichia coli]	87	74	849
60	1	693	4	gi1609625	putative [Vibrio cholerae]	86	57	690
95	1	428	3	gi1508238	dTDP-6-deoxy-L-mannose-dehydrogenase [Escherichia coli]	85	74	426
64	7	4336	4731	gi147542	ORP (343 AA) [Shigella sonnei]	84	81	396
80	8	2800	2582	gi138832	ExeK gene product [Aeromonas hydrophila]	84	53	219
82	10	4380	3829	gi1103137	ORP-0152 [Escherichia coli]	84	72	552

TABLE 1 (PAI IV)(CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
63	8	5199	4830	sp P37433 PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-)	83	75	570
63	10	7572	6259	gi 154258	regulatory protein pgtc (Salmonella typhimurium)	83	78	1314
65	7	3351	3100	gi 1196999	unknown protein (transposon Tn3411)	82	80	252
100	1	337	2	gi 41004	URF 2 (Escherichia coli)	82	64	336
138	2	109	429	gi 1033128	ORF_0273 (Escherichia coli)	80	62	321
74	4	1331	831	gi 38826	ExeE gene product (Aeromonas hydrophila)	79	62	501
63	7	4873	4256	sp P37433 PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-)	78	72	618
70	13	5759	5529	gi 1773143	lha protein (Escherichia coli)	78	58	231
91	3	1154	534	gi 609625	putative (Vibrio cholerae)	77	65	621
75	5	3524	3255	gi 463911	heat resistant agglutinin 1 (Escherichia coli)	76	62	270
63	1	2	667	gi 1574313	H. influenzae predicted coding region H11472 (Haemophilus influenzae)	75	56	666
104	2	485	315	gi 530438	arabinose transport protein (Mycoplasma capricolum)	72	41	171
63	3	2180	1629	gi 622948	transposase (Escherichia coli)	71	60	552
63	12	9688	10005	sp P39213 Y191_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	71	57	318
61	3	1283	876	gi 581535	ORF140 gene product (Rhizobium sp.)	70	54	409
84	3	2361	3437	gi 1772623	HecA (Erwinia chrysanthemi)	70	60	1077
91	1	300	4	gi 295430	epsE (Vibrio cholerae)	70	49	297
74	1	541	2	gi 609627	putative (Vibrio cholerae)	69	54	540
67	4	1297	1581	gi 151469	PIID-dependent protein (Pseudomonas aeruginosa)	68	50	285
84	1	578	1741	gi 1772622	HecB (Erwinia chrysanthemi)	68	54	1164
84	2	1698	2363	gi 1772622	HecB (Erwinia chrysanthemi)	67	48	666
63	2	1734	1393	gi 1323798	transposase (Plasmid pRL1063a)	65	46	342
71	1	1134	4	gi 397405	lpsE gene product (Escherichia coli)	65	36	1131
64	2	2828	1839	gi 310632	hydrophobic membrane protein (Streptococcus gordonii)	64	38	990
74	2	861	355	gi 148436	secretory component (Erwinia chrysanthemi)	64	54	507
66	1	556	2	gi 1235662	HLBC (Mycobacterium xanthus)	62	39	555
70	6	3017	2814	gi 1657478	similar to E. coli ORF_0308 (Escherichia coli)	62	41	204

TABLE 1 (PAI IV)(CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
85	1	278	56	pir A45253 A452	activator 1 37K chain - human	62	56	213
126	1	3	323	gi 1778562	hypothetical protein [Escherichia coli]	62	45	321
73	1	773	3	pir S32879 S328	lipA protein - Neisseria meningitidis	61	46	771
96	2	796	644	gnl PID e276217	T03P6.f [Caenorhabditis elegans]	61	46	153
67	3	743	1312	gi 609629	putative [Vibrio cholerae]	60	43	570
70	10	4666	4292	gi 1657478	similar to E. coli ORF 0208 [Escherichia coli]	60	45	375
81	1	1	1179	gi 1591717	spore coat polysaccharide biosynthesis protein E [Methanococcus jannaschii]	60	44	1179
80	5	2563	1790	gi 609632	putative [Vibrio cholerae]	59	41	774
137	1	73	528	gi 1736670	Adhesin AIDA-I precursor. [Escherichia coli]	59	45	456
61	1	773	3	gi 1196968	unknown protein [insertion sequence IS66]	58	41	771
63	5	2831	2178	gi 622948	transposase [Escherichia coli]	58	41	654
64	3	3568	2690	gi 1335913	unknown [Erysipelothrix rhusiopathiae]	57	36	879
64	1	1819	917	gi 153826	adhesin B [Streptococcus sanguis]	55	30	903
64	9	7008	6685	gi 152259	lcrB gene product [Rhizobium sp.]	55	42	324
70	14	6481	6753	pir G42465 G424	hypothetical protein 88 - phage phi-R73	53	30	273
85	5	9317	1530	gi 144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	7788
64	8	5063	4806	gnl PID e264304	P53C11.6 [Caenorhabditis elegans]	51	27	258
80	9	3411	2761	gi 149309	pulJ [Klebsiella pneumoniae]	50	40	651
88	1	98	388	gi 156087	[Brugia malayi] myosin heavy chain gene, complete cds., gene product [Brugia malayi]	50	32	291
96	3	1127	687	gi 1196964	unknown protein [Plasmid Ti]	50	38	441
89	1	981	4	gi 57633	neuronal myosin heavy chain (Rattus rattus)	48	22	978
113	1	657	199	gi 147899	extragenic suppressor [Escherichia coli]	48	25	459
118	1	654	145	pir S27564 S275	polysaccharide translocation-related protein - Escherichia coli	48	25	510
58	2	2101	4245	gi 1235662	Rfbc [Myxococcus xanthus]	47	35	2145
87	1	595	134	gi 1235662	Rfbc [Myxococcus xanthus]	42	28	462
85	2	1018	515	bbs 117606	glycine-rich protein, atGRP (clone atGRP-1) (Arabidopsis thaliana, C24, Peptide Partial, 210 aa) [Arabidopsis thaliana]	36	36	504
85	3	1779	973	bbs 157676	silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 633 aa] [Bombyx mori]	34	29	807

TABLE 2 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
58	1	1176	2120
61	2	54	560
63	4	1875	2639
64	4	3911	3627
65	6	3009	3239
65	12	6027	6683
66	2	1289	978
70	2	1418	861
70	3	1886	1476
70	4	2124	1900
70	5	2795	2220
70	7	3645	3259
70	8	4078	3680
70	9	4220	4513
70	11	4950	4498
70	12	4594	4866
70	15	6805	7449
70	16	9520	10806
73	7	3247	3666
74	3	720	1301
75	1	1	165
79	1	719	354
80	6	2108	2575
80	7	2831	2469
80	10	3223	3387
80	11	3541	3362
82	8	3313	4260

Contig ID	ORF ID	Start (nt)	Stop (nt)
82	11	4340	5218
82	13	6090	5614
84	4	3487	3281
85	4	1485	2285
85	6	8373	9320
104	1	358	2
112	1	677	105
142	1	3	143
142	2	119	328

TABLE 3 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	3	2826	3686	gi 1655838	ORF8, putative transposase [Yersinia pestis]	100	100	861
14	2	1837	2907	gi 1655837	ORF4, putative transposase [Yersinia pestis]	99	99	1071
3	9	7927	7995	gi 1657499	putative transposase for insertion sequence IS3 [Escherichia coli]	89	85	333
20	6	3462	4304	gi 1208992	unknown [Escherichia coli]	87	73	843
6	6	3541	3263	pir S43483 S434	Orf104 homolog - Escherichia coli	81	62	279
20	3	1616	2332	gi 1033129	ORF_0233 [Escherichia coli]	80	61	717
9	1	1	681	gi 537112	ORF_0396 [Escherichia coli]	77	55	681
15	3	1899	1672	pir S43483 S434	Orf104 homolog - Escherichia coli	75	55	228
20	9	4302	4880	gi 1552816	similar to E. coli ORF_0152 [Escherichia coli]	74	60	579
14	13	12972	15359	gi 1772623	HecA [Erwinia chrysanthemi]	70	60	2388
5	3	1112	1570	gi 1001717	regulatory components of sensory transduction system [Synechocystis sp.]	68	45	459
3	1	2572	1373	gi 849022	Lactate oxidase [Aerococcus viridans]	66	46	1200
3	8	6869	6498	gi 581535	ORF140 gene product [Rhizobium sp.]	66	45	372
6	5	3265	2951	gi 642184	FI9C6.1 [Caenorhabditis elegans]	66	44	315
14	12	11775	12974	gi 1772622	HecB [Erwinia chrysanthemi]	66	50	1200
20	1	545	1450	gi 1033127	ORF_0289 [Escherichia coli]	66	45	906
57	1	696	124	gi 1772622	HecB [Erwinia chrysanthemi]	66	47	573
3	3	3320	3700	gi 431950	similar to a B. subtilis gene (GB: BACHEMY_5) [Clostridium pasteurianum]	65	34	381
5	7	4565	4239	sp P39213 YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	65	38	327
22	2	1651	557	gi 290430	adhesin [Escherichia coli]	64	48	1095
5	4	1455	1841	gi 1575577	DNA-binding response regulator [Thermotoga maritima]	61	47	387
14	11	11161	11937	gi 1772622	HecB [Erwinia chrysanthemi]	60	39	777
14	1	930	1700	gi 1657478	similar to E. coli ORF_0208 [Escherichia coli]	58	47	771
5	6	3834	3391	gi 185032	ORF B (Plasmid pBa34)	56	36	444
3	5	6500	5982	gi 1633572	Herpesvirus saimiri ORF73 homolog (Kaposi's sarcoma-associated herpes-like virus)	54	25	519
14	7	8429	8809	gi 1196729	unknown protein [Bacteriophage P4]	54	41	381

TABLE 3 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	14	15191	21793	gi1144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	6603
14	16	21427	22671	bbs117613	glycine-rich protein, atGRP (clone atGRP-4) [Arabidopsis thaliana, C24, Peptide Partial, 112 aa] [Arabidopsis thaliana]	52	39	1245
5	2	1004	381	gi148518	HydC [Wolinella succinogenes]	51	34	624
5	5	1941	3311	gi1143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	51	21	1371
14	4	3968	5431	gi11033120	ORF_0469 [Escherichia coli]	51	29	1464
32	1	481	227	gi11673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from E. coli [Mycoplasma pneumoniae]	50	41	255
20	17	7039	7284	gi11123054	coded for by C. elegans cDNA CCE5N537; similar to protein kinases including CDC15 in yeast [Caenorhabditis elegans]	48	28	246

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TABLE 4 (PAI V)

Putative coding regions of novel *E. coli* PAI V proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	809	1165
3	2	3275	2640
3	6	6006	6425
3	7	6423	6833
4	1	3	455
5	1	501	4
6	1	2168	1749
6	2	2527	2114
6	3	2648	2331
6	4	3099	2626
14	5	7112	7699
14	6	7800	8507
14	8	9040	9624
14	10	10586	10846
14	15	21721	20921
15	1	575	826
15	2	850	1365
20	2	904	605
20	4	2330	3157
20	5	3139	3396
20	7	3812	3492
20	8	4373	3828
20	18	7282	7950
22	1	356	3
24	1	492	4

TABLE 5 (PAI IV)

Putative coding regions of novel *E. coli* PAI IV containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
59	1	968	54	emb X61239 ECPA	<i>E. coli</i> papABCFGHJK genes for P13 P-pili proteins	99	790	915
59	2	1551	805	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	99	518	747
59	3	1742	1494	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	99	182	249
61	4	1975	1220	emb X61239 ECPA	<i>E. coli</i> papABCFGHJK genes for P13 P-pili proteins	100	69	756
63	13	10097	10480	gb AE000133	<i>Escherichia coli</i> from bases 263572 to 274477 (section 23 of 400) of the complete genome	91	216	384
65	1	886	671	gb U06468	<i>Escherichia coli</i> O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	93	164	216
65	5	3218	2868	gb U06468	<i>Escherichia coli</i> O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	85	285	351
65	8	4064	3216	gb U06468	<i>Escherichia coli</i> O111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	86	145	849
65	9	4939	4337	emb Y00976 ECHN	<i>E. coli</i> hns gene for DNA-binding protein H-NS (5'-region)	96	53	603
65	10	4919	5266	emb Y00976 ECHN	<i>E. coli</i> hns gene for DNA-binding protein H-NS (5'-region)	98	310	348
65	11	5206	5781	gb AE000133	<i>Escherichia coli</i> from bases 263572 to 274477 (section 23 of 400) of the complete genome	89	431	576
68	1	1575	1315	emb X61239 ECPA	<i>E. coli</i> papABCFGHJK genes for P13 P-pili proteins	100	186	261
68	2	2468	1848	emb X51704 ECPA	<i>Escherichia coli</i> papJ gene for PapJ protein	99	621	621
68	3	2232	2594	emb X61239 ECPA	<i>E. coli</i> papABCFGHJK genes for P13 P-pili proteins	99	363	363
68	4	3212	2466	emb X61239 ECPA	<i>E. coli</i> papABCFGHJK genes for P13 P-pili proteins	100	747	747
69	1	300	4	gb M14040	<i>E. coli</i> apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	98	225	297
69	2	383	117	gb M14040	<i>E. coli</i> apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	95	162	267
70	1	832	149	gb U09857	<i>Escherichia coli</i> 4787 o115:v165:f165 fimbrial regulatory f16521, f16528 and f1652 A genes, complete cds	89	225	684
70	17	10799	11767	gb AE000291	<i>Escherichia coli</i> , anV, erfK, cobT, cobs, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	95	553	969
70	18	11809	11045	gb AE000291	<i>Escherichia coli</i> , anV, erfK, cobT, cobs, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	94	595	765
70	19	12022	15222	dbj D90836 D908	<i>E. coli</i> genomic DNA, Kohara clone #348(44.5-44.9 min.)	89	2667	3201

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
70	20	15316	16836	gb AE000292	<i>Escherichia coli</i> , yeaA, sbmC, yaeC, sbcB, yaeD, yaeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	1488	1521
70	21	16722	17711	gb AE000292	<i>Escherichia coli</i> , yeaA, sbmC, yaeC, sbcB, yaeD, yaeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	82	990
70	22	17426	16776	gb AE000292	<i>Escherichia coli</i> , yeaA, sbmC, yaeC, sbcB, yaeD, yaeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	63	651
72	1	12	1061	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1024	1050
72	2	947	1285	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	96	261	339
73	6	4437	3205	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	392	1233
73	8	6177	4555	gb U28377	<i>Escherichia coli</i> K-12 genome; approximately 65 to 68 minutes	90	1133	1623
73	9	6835	6128	gb AE000380	<i>Escherichia coli</i> , glcB, glcD, glcE genes from bases 3112500 to 3126189 (section 270 of 400) of the complete genome	93	703	708
75	2	1553	1059	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	90	385	495
75	3	2579	1566	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	464	1014
75	4	3297	2743	gb U07174	<i>Escherichia coli</i> O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	81	283	555
76	1	698	3	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	693	696
78	1	382	59	gb AE000360	<i>Escherichia coli</i> from bases 2885166 to 2897277 (section 250 of 400) of the complete genome	99	315	324
79	2	2620	1529	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1084	1092
79	3	2925	2587	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	97	322	339
79	4	3576	2923	gb H10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	654	654
80	1	376	83	gb U05251	<i>Escherichia coli</i> polysialic acid gene cluster region 3, promoter region	93	210	294
80	2	638	210	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	347	429
80	3	1246	710	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	96	388	537

TABLE 5 (PAIV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
80	4	1796	1182	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	397	615
82	1	1	567	emb x74567 ECKP	E.coli K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	87	551	567
82	2	549	1157	emb x74567 ECKP	E.coli K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	88	554	609
82	3	1500	1180	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	90	62	321
82	4	2163	1519	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	143	645
82	5	2594	2139	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	97	456	456
82	6	3000	2605	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	98	396	396
82	7	3463	3047	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	283	417
82	9	3831	3337	gb AE000292	Escherichia coli, yeaA, sbmC, yeaC, sbcB, yeaD, yeeZ genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	495
83	1	3	311	gb AE000151	Escherichia coli, ybaE, cof, mdIA, mdIB, glnK, amtB, tesB, ffa genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	99	207	309
83	2	176	433	gb AE000151	Escherichia coli, ybaE, cof, mdIA, mdIB, glnK, amtB, tesB, ffa genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	100	223	258
86	1	529	2	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	93	398	528
93	1	440	3	gb M10133	E.coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	95	351	438
94	1	368	72	emb x14180 ECOL	Escherichia coli glutamine permease glnHPQ operon	100	229	297
99	1	161	586	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	98	426	426
99	2	643	476	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	168	168
99	3	532	1092	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	537	561
99	4	1094	1396	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	274	303

TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
102	1	527	3	emb Y00529 ECPA	E. coli papC gene involved in formation of pap pilli	100	427	525
102	2	762	373	emb Y00529 ECPA	E. coli papC gene involved in formation of pap pilli	99	333	390
105	1	377	3	gb AE000480	Escherichia coli from bases 4277211 to 4288813 (section 370 of 400) of the complete genome	100	343	375
107	1	2	397	gb H10133	E. coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	390	396
107	2	406	966	gb H10133	E. coli (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	549	561
110	1	148	2	emb X56175 ECS8	Escherichia coli secD and secE genes for membrane proteins involved in protein export	99	143	147
110	2	312	40	gb H63939	E. coli tRNA-guanine-transglycosylase (tgt) gene, complete cds	100	125	273
115	1	501	325	gb AE000459	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	98	177	177
117	1	3	302	gb AE000506	Escherichia coli from bases 4584059 to 4594314 (section 396 of 400) of the complete genome	100	263	300
121	1	2	250	gb H16202	E. coli papH gene encoding a pilin-like protein	98	148	249
123	1	361	2	gb AE000379	Escherichia coli from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	113	360
127	1	2	229	gb AE000233	Escherichia coli, racC, ydaD, slsB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	100	200	228
127	2	227	382	gb AE000233	Escherichia coli, racC, ydaD, slsB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	97	113	156
130	1	337	2	emb X60200 ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	335	336
131	1	510	79	gb H30198	E. coli recQ gene complete cds, and pldA gene, 3' end	98	304	432
131	2	743	270	gb H30198	E. coli recQ gene complete cds, and pldA gene, 3' end	99	314	474
133	1	1	258	gb AE000115	Escherichia coli, yabP, ksfC, folA, apaH, apaG, kspA, pdaA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	98	237	258
133	2	192	350	gb AE000115	Escherichia coli, yabP, ksfC, folA, apaH, apaG, kspA, pdaA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	99	115	159
135	1	103	327	emb X02143 ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	97	178	225
135	2	152	409	emb X02143 ECPL	Escherichia coli K-12 pldA gene for DR-phospholipase A	98	157	258

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TABLE 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
136	1	122	532	gb AE000459	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	97	237	411
140	1	576	244	gb AE000291	Escherichia coli, asv, erfK, cobT, cobs, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	89	329	333
141	1	445	2	gb AE000291	Escherichia coli, asv, erfK, cobT, cobs, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	77	432	444

TABLE 6 (PAI V)
Putative coding regions of novel *E. coli* PAI V containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3	4	6150	4855	gb AE000292	<i>Escherichia coli</i> , yeaB, sbmC, yeaC, sbmB, yeaD, yeaE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	91	129	1296
3	10	8214	7723	emb X02311 ECIS	<i>E. coli</i> insertion sequence IS3	76	274	492
3	11	7867	8319	emb Z11606 ECIS	<i>E. coli</i> DNA for insertion sequence IS3	80	378	453
3	12	8462	8157	emb Z11606 ECIS	<i>E. coli</i> DNA for insertion sequence IS3	90	267	306
3	13	8487	8663	gb L19084	<i>Escherichia coli</i> RhaD genetic element; core protein (rhaD) gene, complete cds; complete ORF-D2; complete ORF-D3	96	112	177
4	2	1441	815	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	91	577	627
4	3	923	1372	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	448	450
4	4	2343	1324	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	244	1020
7	1	3	743	emb X61239 ECPA	<i>E. coli</i> papABCDPFGHIJK genes for F13 P-pili proteins	100	741	741
7	2	977	615	emb X61239 ECPA	<i>E. coli</i> papABCDPFGHIJK genes for F13 P-pili proteins	99	363	363
7	3	741	1214	emb X61704 ECPA	<i>Escherichia coli</i> papJ gene for PapJ protein	98	459	474
8	1	438	4	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	435	435
10	1	1932	2426	emb X61238 ECPR	<i>E. coli</i> prsEFG genes for F13 pili tip proteins	97	462	495
11	1	903	1550	gb H10133	<i>E. coli</i> (396) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	452	648
12	1	2559	1531	gb U82598	<i>Escherichia coli</i> genomic sequence of minutes 9 to 12	100	1029	1029
12	2	1594	1860	emb X13668 ECIS	<i>E. coli</i> insertion element 5 (IS5) DNA	100	267	267
12	3	1858	2235	gb U95365	<i>Escherichia coli</i> transposon IS5, transposase (ts5B) gene, complete cds	99	354	378
13	1	93	1424	emb X61239 ECPA	<i>E. coli</i> papABCDPFGHIJK genes for F13 P-pili proteins	99	885	1332
14	9	9832	10515	gb U09857	<i>Escherichia coli</i> 4787 o15:H16:165 fimbrial regulatory f16521, f1652B and f1652 A genes, complete cds	92	225	684
16	1	1	375	gb U07174	<i>Escherichia coli</i> O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	94	320	375
16	2	263	616	gb U07174	<i>Escherichia coli</i> O9:H10:K99 heat resistant agglutinin 1 gene, complete cds	98	283	354
17	1	282	4	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	98	240	279
17	2	410	174	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	100	168	237

TABLE 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
19	1	1	369	gb AE000418	Escherichia coli from bases 3550279 to 3561054 (section 308 of 400) of the complete genome	99	347	369
20	10	5401	4829	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	468	573
20	11	4874	5371	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	498
20	12	5245	5679	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	235	435
20	13	5732	6139	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	93	329	408
20	14	6316	5822	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	95	239	495
20	15	6048	6590	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	406	543
20	16	6569	7075	gb AE0000292	Escherichia coli, yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	136	507
20	19	8686	9915	gb H67452	Escherichia coli lysine decarboxylase (cadB, and cadC, complete cds, and cadA, 5' end) genes	98	1205	1230
20	20	10604	11938	gb U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	1308	1335
20	21	11940	12368	gb H76411	E. coli cadA gene, 5' cds and cadB and cadC genes, complete cds	100	363	429
21	1	369	4	emb X03391 ECPA	E. coli major pilu subunit genes pepI, papB, papA and papH 5'-region	98	201	366
23	1	1	879	gb U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	879	879
23	2	900	16	gb U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes	98	885	885
23	3	953	1186	emb X77707 ECCY	E. coli ORF112, DIPZ and ORF191 genes	99	225	234
23	4	1223	2677	emb X77707 ECCY	E. coli ORF112, DIPZ and ORF191 genes	97	1454	1455
25	1	536	171	emb X60200 ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	164	366
25	2	1128	562	emb X60200 ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	459	567
27	1	708	436	emb X61339 ECPA	E. coli papABCEGHJX genes for P13 P-pili proteins	100	252	273
28	1	309	4	emb X77707 ECCY	E. coli ORF112, DIPZ and ORF191 genes	98	278	306
28	2	431	213	emb X77707 ECCY	E. coli ORF112, DIPZ and ORF191 genes	96	150	219

TABLE 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
30	1	399	4	gb M26893	E.coli amidophosphoribosyltransferase (purF) gene, complete cds	98	295	396
31	1	706	170	emb X56780 ECRR	E.coli terminator sequence of RNA G operon gene	99	513	537
37	1	2	400	gb M63703	E.coli pyruvate kinase type II (pykA) gene, complete cds	98	399	399
38	1	463	2	emb X13463 ECGU	Escherichia coli guthM gene and guthR gene for activator and repressor proteins	99	363	462
42	1	413	3	gb M64367	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	97	316	411
42	2	115	591	gb M64367	Escherichia coli DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	98	266	477
46	1	2	277	emb X77707 ECY	E.coli ORF112, DIP2 and ORF191 genes	98	187	276
48	1	1	171	gb AE000491	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	162	171
48	2	105	464	gb AE000491	Escherichia coli from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	144	360
49	1	2	172	gb U00800	Escherichia coli cloning vector PK184, complete sequence, kanamycin phosphotransferase (kan) and (lacZalpha) genes, complete cds	98	167	171
50	1	414	4	gb AE000341	Escherichia coli, glyA, hmpA, glnB, yfha, yfhG genes from bases 2677406 to 2687636 (section 231 of 400) of the complete genome	99	411	411
52	1	2	307	emb X60200 ECTN	E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	284	306
53	1	280	41	gb M36536	E.coli htrA gene, complete cds	100	131	240
53	2	558	214	gb M36536	E.coli htrA gene, complete cds	99	315	345
54	1	9	263	gb AE000381	Escherichia coli from bases 3125914 to 3136425 (section 271 of 400) of the complete genome	94	111	255
55	1	1	675	gb AE000179	Escherichia coli, modA, modB, modC, ybha, ybhE, ybhD genes from bases 794199 to 805132 (section 69 of 400) of the complete genome	98	332	675

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While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

5 All patents, patent applications and publications recited herein are hereby incorporated by reference.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Nucleotide Sequence of *Escherichia coli*
Pathogenicity Islands

(iii) NUMBER OF SEQUENCES: 142

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
(B) FILING DATE: 22-NOV-1996 AND 14-OCT-1997

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CNTANATTAG GCCTGCTNAA TGTATTTATA TCTAAAAAAA TTCGCATCCA AAAGGAATCC	60
AATCTGTACT GTTTTTTCTT GTGCTGACAT CTTCTTTTCC CTGGCTGGTA TGGCAAGTGA	120
CGGAGACAAG AGAAACGTTT TAAGCTCAGT TATCTCCGCC ATCACTTTCC ACGAATGACA	180
AGTAATTTTG CCTATTTTAA AACCATGCAA AAGGCAGGGT AAAAGGAGAA AATTCGATCG	240
AATCGATCGA CAAAATCGAT CATACTGAT GAAGATTTCT TATCGAATCC ATAAAAATAG	300
TGACAGCTAA CCGGCGTTGC AGGAACAGTC AGAAATGGGC GTTTGGGAAA GAGCCATAGC	360
ATACGTCGTC GCTGACATAG AGGAACTGTG CTTTGTGTGAT AAGATCCTTT ATACGGCAAC	420
CAATCCACTG GACAAAAGAT GAACTACGTA ATCACCAGGT TCTACTGAC GAAATACAGA	480
AGTTAATGAC ACAACTGTGC CATGCACCTT GTACAACAGC GGTGGAAAGC TCTCAGAACA	540
ATGGAATTGC AGAAAGGTGT TAAAACGATG AAAGCCTTCA TACCCAAATC GAATGTAAGA	600
ACGGCAGTAA AGACTGAATT GCGTAACCTT GCAGTAGCTC GAGTATTACA CTGCATAGTG	660
TGCAGGGTTA TCTCCCATCG AGAAAATATC GGCGCCAGCG AATAACGTCA CCTTAGATGT	720
AGCAGTTGCC AAATAGTGAC TCAAGGGCGG GCTTACCGCA TACTACTGACA CTTAGCGGAT	780
CGACAGAATA TTATTAGCAG ATCATCACTG AACGCTACGT AATTATCGTA ATAAAGGCTT	840
TTTCTGGCTA CCAGGAAGAC CTGACATGGC TCTGCTCTGG AACCAGGCCG CAGGAAGCAT	900
CAATCTGGAG TTTATCAGCT ACTGGAATTC CGGTGTATTG GCAGCCCCTG ATAATCACCT	960
GACCCACGAA GAGCGCTCTG CTTTGCAGAA ACTCTGGGGC GGTTCGAGAG CAGGAGATGT	1020
AACGATTATA GGACGTTCTG ATGAAGTCCA TGATTTTACC TCCGCCTTAA TTAATGTTT	1080
TCTTTCTGAA GAAGAAATTG TCTGGTGGCA ATCAGGTGGC ATTTTCCCGG ATCCTTGGCC	1140
CGCTAATATA TCCCGGCTGA ACTGACGATT AACGCGAT	1178

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCCTATTCA TTTTGCCATG ACGGGCGAAC TCCAGATAAA GGTTTTGAAA GTAATGAGAA	60
ATTATTAATT CATCCATGTT ACTGGCTTGG TTTGAATCTA AATCGTAATG CACTTGCTCC	120
AGAGGAAGCA GAGGAGATAA ATGACGAATA TGATATTAAT ATTATTTTCTAG ATAATTCAGC	180

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CATTAGAAAT AAAACAATAG GTCAAATAAC TACTCATCTA GATCAGATAC CGATAGGAAA	240
TGAAGGTGCC ACTGAATTTG AACAAATGGTG TTTAGACGCA CTAAGAATAG TATTTGCATC	300
CCACCTAACA GACATCAAGT CCCATCCAAA TGGTAACGCA GTTCAGAGAC GAGATATTAT	360
AGGCACCAAT GGTGGCAAAT CTGAWTTTTG GRAACGAGTA TTGGAGGACT ATAA	414

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGGATCTG GTACANTCCA CCCAGCGGCA TTATCCNGAA GGCAATATTT TTAAGGATTA	60
TTCGTCCACA AAATCAGTAC TGGAAACCAGG CTCAAAAAG GCTTTAACGT GACCTGCTNC	120
CATCTACAGT AGATGTACAA CCTGTTAAGT TAATTGAAAA TGGTGTTAAT CCGGTTGTTT	180
CTCCAGGGGT AGCAAGGGCC TTATTCGATA CAGTGGGTAA TGTTACTGTA AAATTACCAT	240
CATTCCCTGT GGTACATTG CAGGTCTGAG CTACAAC TTT GCCTGTAAAC GTAATTGTTC	300
CGTCATAGGC CATAGCTGAA CCAACAAACA CAGCAGAAAC AAATGTAGCC AATGCTATAA	360
CTTTTATTTT CATAAAATGA ATTCTGT TTT AATTCCGGTA TTGATCATTT GTTCAGCAAT	420
CATCCCCAAC AAAACAATCA TTTTCAAAAT GTTTTTACCG ATCGATAACC AGCACATGAT	480
AGATTGCACC TATCATGATT GCTAAAACGA TCGGGAAAAG CGATCAAAAA CCATATTTAT	540
TGTGTTGGTA ATGACAAAAG ATATGCTTTA CCCTGAAATG AGCGACCTAT TCATGAAAAT	600
ATGTAGGTCT GTATTTGATT ACTATCATTG CTATATTTCC ACTATCCAAT TTATATTTCA	660
TGATTAAAAT ATACCTTTTT AACTATTAT TTATTTGTTG CAGCTTGCCT GGCTTTATCT	720
TATTCCGACT ATTTTATGGT AGATACAGAA TACAATTAAT TAACTTATT TAAAGATTTT	780
ATAAATACCA TATTGGAGTT GACCGATAGA TACCTACTAA CAAGAGCAAT CACCACCACC	840
CCATGAGGTG TTTAGGAATA CAATCAATAA ACAACATCCA TGCCCGGCGA CGTACATACC	900
TGTTTGCTAT GATATCTGTT ACGCTACGCT TGCTAATTTA CTGAAACTCA GCATCTGTCTG	960
ACGGAGATTC GTCCGGGCCC TGATACAACA AGGGCAAGAA AACCACCCGA AATACAGATA	1020
TTCTTATAAA AATGGATCAT ATTTCCATGT GCAAGTTCAG CTGGCATCGT CCAGAATGCG	1080
TGTCCAAGAA ATGAAGCAAA CACGGTATAC AGGCACAGAA TAATGCTCAC TGGCCGGGTG	1140
AAAAAGCCRA AAACAATCAT TAATGCTCCA ACGATTTCTGA CAAGGACCAC TATTGCTGCA	1200
GTAATCGCCG GAAATATAAG CCCAAGAGAG GCCATTTTAT CGATAGTGCC AGTGAATGAT	1260
AGCAGCTTGG GAACGCCGGA TATCATATAA AGGCATGCCA GCATCAGACG GGCAAGGAGC	1320

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AACAATGCCG ACGTGTAATT TCCCATATTA AAATACCTGA TTTTATCCAC TATCAATGCT	1380
CAGTCTCCTT GTTTCTGATA AAGCCCTGAG CCAAATCCTT AAGTGTACGA GCACCACTCA	1440
GTAACATTGC CGTCCTCAGC TCCGTCTTCA GGTGCTCAAT GACACTGGCA ACGCCCCCGA	1500
CACCACCTGC TGCATGCCA TAAAGAACAG GACGTCCGAC CGCAACAGCC GTTGCCCCAA	1560
GAGAGATAGC CTTTACAACA TCAACCCCCC TCGAATACC GCTGTCAAAA ATGACCGGAA	1620
CTTTGTGCCC GACTCTTGCA GCAACTTCCT GCAACTGGCT GATGGCAGAA GGAACACCAT	1680
CAATCTGGCG ACCACCATGA TTAGACACCT GGATGGCATC TGCTCCTGCA TCAATGGCGA	1740
CCACTGCATC CTCACCTCTG AGGATGCCCT TGACAATGAC TGGCAGCCCG GTGATTTTTT	1800
TTACAAACTC AATATCAGCC GGGGTCAGCT CAACTTTTTG GTTAAAAAA TCACCTTTGC	1860
CACCGTAACG GGGGTCATGA TTACCGAACG TCGCTCCTGC AGGGAAAGGC GAGCTCATGC	1920
TGAGAAAAGC ATCACTTGTC CCGGGACCAA GCGCATCCGC TGTGATAATA ATGGCTGAAT	1980
AGCCTGCCGC TTTTGCACGC TCCAGTAAAC TTCGSGTCAC ACCAGCATCC GCGTTAAAAT	2040
ACAGCTGGAA CCATTTAGGT CCTTTACTGG CTTTTGCAAT ATCCTCCAGA GAGCGGTTGG	2100
ATGCCCCCTGA TGATTCATAA AGTGCCCCGG CTTTTCTGC ACCCGCTGCA GCAATCACCT	2160
CCCCTTCCGG ATGGACGAAC ATATGCGCGC CCATAGGTGC TATCAGCAGG GGATGTTCCA	2220
GATGATGGCC CAAAAGGTCA GTCCGGATAT CAATGCTGTG GGCAGCAACT CCACTGAGTC	2280
GGTGAGGTAA CAAAGGATAA TCACTGAANT GCCTGCGGTT CTCATGATAC GTCCACTCAT	2340
CTCCAGCACC ATGAGCAATA TATGCATACG CAGCTTCCGT CATCACATCT TTTGCTGAAG	2400
TCTYCACTCT GTCCAGACTG ATGATATGAA GAGATTTGCT GGTGATGTA TCAGCATGTC	2460
CAGACGTTTT ACTGATGATA TGTGCCGTTG AAGATGAGAT ATTTTTGGCA AGGGCCGGCG	2520
CAGTTGACAG CCTGCGGCAG ATATTCCTAA AACGGCATTC TGAATAAAAT TACGTCGGGA	2580
AAGAGGCATA ATAAGCTCCA TATATTATAA ATAAGCCAGG TCTCCCTGGC TTATAATGAT	2640
CATGCCACGC CCTGAAGCGG GTTGGTGTTG AAGGTATAAA GGAAAATTTT CCATTCACCA	2700
TTAATTTTAC TGAGGACAAA AACTTCACGG TTCAGGTCAA TAATGGTTTT CTGCTCTTTA	2760
AAGTTCGTTA CAACAGAACC CACATGGTGG TGAGTGCGGA CAACCGCGGT ATCTCCGTTG	2820
ATCCAGATAG AGTCAAACGC AAAATCGGTC TCAAACTTTT CACGCTTGAA CAGATCATCG	2880
TACTGCCCCCT GCGTTTTTTC TGTATTGTCA GCCGTCAACT TATCATTCCT CTGGGAATAA	2940
CTTTCATCAG CAAACAGGCC CAGGATGGTT TTTGTATCCC CGGCATTCAG TGCCTTCTGA	3000
TACTTGATTA TCGTGTCATA CACGTTCTTC TGCTCAGTAG CAATCTTACT GTCTGTGGAG	3060
TATTTGAATG TACCGCCGGA TTGTTCAGGT GAGCTTTCCT TCTGTGCTGT CGACGATGAG	3120
GCAGCCAGAG CATTAGAGCC GAAAAGAAGG GATGATGCCA TGAATGCTGT TGCTATAAAA	3180
TGTTTCATAT ATTCTCCATC AGTTCTTCTG GGGATCTGTG GGCAGCATAT AGCGCTCATA	3240

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CTATGCTGCT	GTTTCAATAT	TAGCGGCAGA	CGTCAGCCTT	ACCGCACTAC	TTATTGGATA	3300
AGAATATCAA	AAGTGACCGT	GAAGTCAATT	TTATCACAAC	ACAGAAGGCC	ACTATTTATG	3360
CCCAGAAAAT	ATGAATCGTC	CTCATCATGC	ACGAAAGACT	CGTAGTTGCA	GCCCCGAAAA	3420
AACTGCCAGG	ACACGACAGC	AGATAGCCCG	GGCAGCACTT	GAGGAGTTCT	CTGCACAAGG	3480
GTTGCTCTGC	GCCACATNCA	GCAATATCAG	CAAGCGCGCA	GGAGTAGCTA	AAGGCACGGT	3540
ATATAACTAC	TTCCCAACAA	AGGAATTATT	GTTTGAAGCG	GTTCTGAAGG	AGTTCATTGC	3600
TACCGTCCGT	ACTGAACTGG	AATCTTCCCC	CCGCCGCAAC	GGGGNAAACC	GTAAAAGCCT	3660
ATCTGTTGAG	AGTGATGTTA	CCTGCCGTCA	GGAAAATTGA	CGACGCATCA	ACAGGCAGAG	3720
CCAGAATAGC	CCACCTGGTT	ATGACAGAAG	GGAGCCGGTT	CCCGGTAATC	GCTCAGGCTT	3780
ATTTACGGGA	AATACATCAG	CCACTACAGC	AAGCCATGAC	CCAACTGATT	CAGGAAGCAG	3840
CATCAGCCGG	AGAGTTAAAA	GCAGAGCAAC	TGCTCTGCKT	CCCCTGTTTA	TTGCTGGCTC	3900
CAAACCTGGT	TGGCATGGTG	TATAACGAAT	TCTGAACCCG	GCAGCACCCG	TCAGTACAGG	3960
CGATCTTTTT	GAAGCCGGAA	TTGGTGCTTT	TTTCCGATAG	ACACATAACT	GTCAGTATTA	4020
TGACCATGCC	GTCAGGAGGA	GGTATACCAG	TGATACCCTG	CCATGACCCG	GTAACGTCTC	4080
CTGGCTGCCT	TAAACCTGAA	AGACCTGGCC	CCACCACACT	GCCGGTTACG	CATCAAGATG	4140
CAGCAACCCT	TGCATAAGGC	TGTTTTGTGC	AGAGGGCTAC	CGGAAAGATA	ATAACGTCAC	4200
AGCCCGTATG	CATCAGATAA	AACAGTGTAT	TTTATCTGTC	AGCAGTCACT	GGAGCGGATT	4260
GTGGGGCGAG	ATTGAGGTGC	TGATACTGTA	ACGACTCTGC	GCCGCTGCTG	CGGTAAAAGC	4320
GGCTGCCACC	AGGCACGGTT	ATCAGAGGAG	GATGACCGTG	TCCGCCCCTG	GTGGTGATGA	4380
ACTCTCCATC	ACAATCAATA	ATGCCGCCGG	GTGGATGAAG	CAGACAGGGA	TGGCAAGTCC	4440
CACTATCCCG	GATAAAATGG	GCTCTGGGCG	CTCAGAAGAC	CTGTGTGTCA	GGCAGGGGTG	4500
AGAACGGTGA	TGTTTTTTGT	TGTCTGAAAG	TCCAGCTCCA	GCATTGCCTG	CCAGCCTCAA	4560
GACTTCCGCT	TTCTGCCCTT	TCCGGCATT	TCTTCCGTTA	CCATCATTCT	GTTAATTCAG	4620
AGGCGTAGTA	GTAGTAAACG	TAATACATAT	CCGGGAGGAT	GAAGTCATCT	AATCCTGCTC	4680
CCCGAATATC	ATACAGCCAT	TCCTGAGTGT	GACTGCACCA	TTTCCAATTA	TGCAGTCTGT	4740
CCTCATCACA	AAAATGTTGC	AAGCAGTGCG	GAGTCACGTT	CCGTATTTCAT	GCCCTCTGCC	4800
AGATATTGAG	CGGGGGAGAA	ATGTGTAAGC	GTCAACAGAG	CGCCGTATTG	ACACTTATTT	4860
ATCGGTGAAA	ACTACGTTCC	ATGGCAGCAG	TTCGTCAACA	CGGTTGGAGG	GCCATTCCGG	4920
CAGTACGCTC	AGGATATGGC	GCAGATACGC	TTCTGGATCG	ATACCGTTCA	ACCGACAGCT	4980
CCCGATTAGT	CCGTACAGCA	GAGCTCCGCG	CTCGCCTCCA	TGATCGTTGC	CGAAGAACAT	5040
GTAATTCTTT	TTCCCGAGAC	AGACGGCAGC	AAGCGCTCTT	TCTGCTGTGT	TATTGTCCGC	5100
CTCCGCCAGA	CCGTATCAC	TGTAATAACA	GAGGGCGTCC	CACTGATTCA	GGACATAGCT	5160

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GAACGCTTSR CCCAGTCTGG ATTTTTTCGA CAACGTGCCA TTCTTCTCCA CCATCCATTC	5220
ATGCAGCGAC GTCAGTAACG CTTTGCTTCG CTGCTGCCTG GCTGCAAGAC GTTCAGACTC	5280
CGGTAAAGCCC CGTATTTTCAT CMTCAATGGC GTACAGTTCA CTGATGCGCT TCAGAGCTTC	5340
TTCTGCCGTC GTACTTTTGC TGCTGATGTA TACATCGTGG ATTTTTTCGCC GGGCATGGGC	5400
CCAGCACGCA ACTTCTGTCA GTGCACCACC TTCACGTTCC GCACTGAACA GCCGATCGTA	5460
ACCGCTGAAT GCATCCGCCT GCAGGATACC CCGGAAGGGA CGAAGGTGTT GTACCGGATG	5520
TTTTCCCTGC CTGTCTGGTG AGTAGGCGAA CCAGACCSCT GGTGGCTCTG ATGAGCCCGC	5580
ATTCCGGTCA TCCCSGACAT ACGTCCAGAT GCGTCTGTGTT TTTGCCTTTT TTCTGCCCCG	5640
TGCCAGCACT TTTACTGGTA TGTCCTCAGT GTGAACCTTG CGGGTGTTCA TCACGTAACG	5700
GTACAGGGCA TCATTACGCG GAGTCATTAA CTGGCAGCAC GCGTCAACCC AGTTGGAGAG	5760
TAATGCACGG CTCAGTTCGG CACCCTGTCC GGCAAAGATT TCACTCTGAC GATACAGTGG	5820
CAGGTGTTCC CAGTATTTTC CCGTTAACAC GCGGGCAAST AATCCGGAGC CCGCGATGCC	5880
GCGCTCTATC GGGCGGGACG GCGCTGGCGC TTCAACTATA CAGTCACATT TTGTACAGGC	5940
TTTTTTTTACC CGAACAGTGC GGATCACTTT CAGGGCGCTA CTCACCAGTT CCAGCTGCTC	6000
AGCACTAACT TCACCCAGAT AATCCAGCTC ACTGCCACAC TCCGGGCAAC AACTTTCTTC	6060
AGGCTCCAGG CGGTGTATTT CACGGGGAAG ATGTGCTGGT AACGGACGAC GATGACGTGA	6120
TTGTCGCAAC TGGCGGGGAA CTGCGGGTCA TCCTCACGCC CACTGTAACG ATCGCTTTCC	6180
TGTTCCGCGTT GTTTCAGTTG GGCCTCAGCC TGTTCAACCT CACGCTGCAG TTTTTCAGAA	6240
CGGGTACCGA ACAGCATCCG GCGCAGTTTT TCTATCTGGG CCCTCAGATG TTCTATTTCC	6300
CGCTCCTCCT CTTCGATCTT TTCTTCGGCA CGTGCCARTG CAGAGCGCAG GAAGGCCTCC	6360
GTCTCTTCAA CCAGACTCAG TTGCTGATCT TTCTGACGGA GGGCTTCAGC CTGCTCAGAG	6420
AGTAGCCTTT CCAGCTCAGT GATACGAATG AGGTATTTCC GACTCATGAC CGTTTTTATA	6480
ATCCGGCCAT GACATTTTTA CAACATTGTC AGTGCATTAA GCGGGATGT TTTGGGTTGA	6540
CGCCAGTCCA GTTTATCGAG GAGCATTGCC AGCTGCGAGC GGGTAATGGA TACCTTACCG	6600
TCACGCACCG CAGNCCAGAT AAACCTGGCT TCCTCCAGAC GTTTGGTGAA CAGGCACAGA	6660
CCATCAGCAT CAGCCCACAG GATTTTAATC GTGTCACCCC GTCGGCCGCG AAAGATAAAC	6720
AGGTGACCGG AGAAGGGGTT CTCATCCAGC ACATGTTGTA CCTGTTACC CAGACCGTTG	6780
AAGGATTTAC GCATATCAGT AACGCCGGCA ACCAGCCAGA TTCGAGTGTG TGATGGGAGC	6840
GAGATCATCG TCCTCTCCCG GTCAGTTCAC GGATCAACAC CGTGAGCAGC TCTGGTGAAG	6900
GATTTTCCAG CGTCATGTTA CCGTGGCGGA ACTCAACTTT ACAGGAACTG GCACTGACTG	6960
TGCTTTGTGA AGGAGTGGAT AAAAGCGGAG TAAGAGCCGC CATAGGCTCT TTCTGCTCAT	7020
CAGGCGTTAT CTCAACAGGT AATAATTCAA CGCCACCGCC AGAAGAGGTT GTTACCGGAA	7080

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GACGCCGCGA	TATACGCCCT	TCGTTCTGCC	AGAGCCTGAG	CCATTTGAAC	AGGAGGTTAT	7140
CATTGATATC	GTGTTCCCTG	GCAATACGGG	CAACAGAGGC	TCCTGGTTGT	GAAGCCAGTT	7200
TAACCATTTG	AAGTTTAAAC	TCATTTGAAA	ATGTTCTGCA	GGTTCTGCG	GATAATATTT	7260
TCTGTTCCAT	AACAGGTGTC	CACTAGTTGA	AAAAGTGGGC	ACCTACGTTA	CCAATACTGG	7320
CTTAATGGCT	ACATACGGCG	GTCAGTTTAC	GCTTACAGAA	ATGTAATGAA	CACGTCTTAC	7380
CATTAAGTGA	AGAGCATGGT	GACGGATGAA	GGAAAAAGCA	GGAGTGTGTG	GTGCCTCACA	7440
GATTTCCGAC	ATCATAGCTG	TCAACGACGG	ATGAAAAGCG	GCTCTTCCGC	AACTTGGGTG	7500
GAAGAAAATG	GATGAAACTT	TCTGGTGTGA	GAACCTTAAG	GAAACAACAT	GTTGGGTGGA	7560
GCGGACAATC	CAAATGGTGA	ATTACCGTCT	TATATCACTG	GCCTGACAT	TCCGGGCGTC	7620
TTCTCCGCCA	CAACGCCATT	TGCAGTGCAT	CACAGGCCAG	TTGTGCTGTC	ATTCGCGGTG	7680
ACATCGACCA	GCCAATAACG	GCGCGTGACC	ACAGGTCGAT	GACTACTGCG	AGATACAACC	7740
AGCCCTCATC	GGTACGCAAG	TAMGTGATGT	CACCCGCCCA	MTTCTGGTTC	GGAGCCTGGC	7800
GCTGAAGTTC	CTGCTCCAGC	AGATTCTCCA	ATACGGGCAG	GCCATGTGCA	CGGTAGCTGA	7860
CCGGGCTGAA	CTTCCGGCTG	CTTTCGCCCC	CAGCCCCTGA	CGACGCAGGC	TGGCGGCAAT	7920
GGTTTTAATA	TTGAACTCCG	GCATTTCTGC	AGCAAGGCGG	GGAGCACCGT	ATCGCTGCTT	7980
TGCCTCAATG	AATGCCTTAT	GGACAGCGGC	ATCGCAGGTG	AGCCGAAACT	GTTGGCGCAG	8040
GCTCATCTGG	TGACGACGCC	TGAGCCAGAC	ATACCAGCCG	CTGCGGGCAA	CCCGAAGTAC	8100
ACGACACATC	GCTTTGATGC	TGAACTCTGC	CCGATGATTT	TCGATGAAGA	CATACTTCAT	8160
TTCAGGCGCT	TCGCGAAGTA	TGTCGCGGCC	TTTTGGAGGA	TGGCCAGTTC	CTCAGCCTGC	8220
TCCGCCAGTT	GTCGTTTAAG	GCGGACATTT	TCAGCGGCCA	GTTGCTTTTC	GCGCTCTGAC	8280
GAACTCATTT	GTTGCTGCTG	TTTACTGCGC	CAGGCATAAA	GCTGAGATTC	ATACAGGCTG	8340
AGTTCACGGG	CTGCGGCGGC	CACACCGATG	CGTTCAGCGA	GTTTCAGGGC	TTCGTTACGA	8400
AATTCAGGCG	TATGTTGTTT	ACGGGGCTTC	TTGCTGATTG	ATACTGGTTT	TGTCATGAGT	8460
CACCTCTGGT	TGAGAGTTTA	CTCACTTAGT	CCTGTGTCCA	CTATTGGTGG	GTAAGATCAC	8520
TCAGCAACGT	ATCAAAAGTC	TGTAAATCA	TGGGCGTTTC	GCGTGATACA	TTTTATCGTT	8580
ACCGCGAACT	GGTCGATGAA	GGCGGTGTGG	ATGCGCTGAT	TAATCGTAGT	GCCGCGCTCC	8640
TAACCTTAAG	AACGTACCGA	TGAGGCAACT	GAACAGGCTG	TTGTTGATTA	CGCCGTCGCT	8700
TTCCCGGCAC	ACGGTCAGCA	CCGGACCAGC	AAACAAGCTG	CGTAAACAGG	GC	8752

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TGGTCAAAGA TGCAACTGCA TTTCGTCGCG GCTTTGCGGC AAATACTTAC ATCGCAGAAA	60
TACTGTGCGG AAATCTGCAT CCATTTCCAC TTGCTGTATG GCATAACTTT TCAGGCGGTC	120
CGGATACTGC CGAAGATTAT TATGCCACAT ACCACCCGTT ATGGGGGCAA TATCCGGAAG	180
CATTGCTGTT TGTAAGTGG CTCTATAATC ATTCTCTGT GCTGCATGAA CGGGCAGAAA	240
TCATTAAATG CGCCGAAATG CTGATGCAGG AAGATGATTT CGAAATATGC GAAAGTATTT	300
TAAGACAGCA GGAGAAGTTG CGTGAAAGAA TTGATGAGAC GCTTCTGAG AAAATTGTAC	360
AGAAATGCAG AAATATGAAT GGTGAATATG TCTGGCCCTG GATATTGCCG TTTTCAGCGG	420
CAGGCATGAA ACATACTGGC ATACAGTATC AGTAGATATT GCATTAGTGT ATCCTGCACA	480
CAAGTAATAA TTTATCCACC AATAATAACA CTGTAAATGT CCCCTTCCCC TGGTTGTCAG	540
CCAGGGGTTA TCTTCTGAAT ATTTCTTTTG AAAAGGATAA CACAATAAAT TATTTTATG	600
AATTATCCCA TGGACTCATT AACACCCTTT CATAATGTTT TATTGTCAA CACGTTATGG	660
CTGACATCAA AAAAAACCGG ATTTCTCTG CCAGCGGGTA ATCACCTCCC CGGTGTTTTT	720
GGTTGGTCTG GTTACTCCTG TCTGGTTATT AGCAAGATAA TTGCTATAAA CAGTGAAAA	780
CTCATCGTAC ATAATCTGGT GATGAACATT ACGCTTATTT TCCCTTGACC GGAAGAATCA	840
GAGGCTGCGG TTTCACTG TCTGCCGGTA CATTCTCTC TCCGTTAAAA ACCATAATGG	900
GTTTATTATC TTCGTCTGTC AGTAGATTGA ATGGCGGTAT ATTTTCAGTA CGAATGCCGG	960
TCAGCCACTG AAAAATACCT GCGAAATGAC GGGCACTGAT TTTTCTGCTG ACGGACTGAT	1020
GAGACGTGAT GTCCTGGCG GTAATAATCA GGGGAACGCT GTAGCCTCCC TGCACATGAC	1080
CATCATGATG AACAGGATTA GCACTGTGCG TGACCGACAG CCCATGGTCA GAAAAGTAAA	1140
GCAATGACGAA ATGACGGGAA TGCCGGCGAN GGATACCATC AAGCTGACCG AGAAAGTTAT	1200
CCAGTTTACT GATGCTGGCG AGGTAACAGG CAACCTTTG GGGATACTGC TCCAGGTAAT	1260
GATTCGGCCA GGAGTGAAGC CGGTCACAG GGTTCGGATG AGACCCATC ATGTGCAGGA	1320
ATATCACCTT CGGAGAGGAT TTATCCGCCA GCGCACGTTT TGTTTCCTGT AACAACAACA	1380
TGTCATCCGT TTTACGGGAA GCGAATGCSC TTTCTTGAGG AAAACGGTAT GCTCCGCATC	1440
AGAAGCAATA ACAGAGATGC GTGTGTCATG CTCTCCCACT TTTCCCTGAT TGGATATCCA	1500
CCATGTGCTG TATCCTGCTT TTGCTGCCAG CGCCACCACG TTGTTGCCGG AATCAGGGTT	1560
CTGCTCATAG TCATAAATCA GTGTCCSGCT CAGGGAAGST ACGGTACTGG CTGCTGCCGA	1620
TGTATAGCCG TCAATAAATA AACCGGGAGC TGTCATTCCA GCCACGGCGT GGTGCGCCAC	1680
GGGATAACCA TATACCGACA TATAATCCCT GCGCACACTC TCACCACTGA CAATCACAAT	1740
CGTGTCATAT AACGGTGTTT CCCGGCCAGG ATTTTCCCAG TTGTCAGCCC CGTGCTGACT	1800

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CAGTTGTTTTA TAATGCTGCA TTTCACGCAA TGTGTEAGTT GTCCCCACAA CAGTTCCTTT	1860
AACCATCCGC AACGGCCAGC TGTTTACTGA GCATAATACG AACAGCAGCA GTGCCAGCCA	1920
GTTACGGTGA CCACGGCGGT GTGTCGCCA GAAATCACC ATGAATACCT GAATCGCGGC	1980
ACTGACCAGA AAATGATAAA CAGGAATCAT CCCGGTAAAC TCCGCTGCCT CATCASTTGT	2040
GGTCTGCAGC AACGCGACAA TAAAACTGTT GTTGATTTTA CCGTACGTCA TACCGGCAGG	2100
CGCATACAGT GCACAACAGA ACAGAAATAA CAGCGCTGTA ATGGATGTGA GGGTATTTCT	2160
GTGTGCAAGG AGCAGAAGGA GAAACAGAAG CAGCACATTT CCTGTTGCAT TCCTCTCAGT	2220
GTATCCGCAT GCAATTGTGG TTATTGCAGA CACAACAAA AAGAATAAAA ACAATAAAAT	2280
CCGGGGGGGG TTGCCCCGAC AAAACAGTTT TCTGATATTC ATCGGAGTAT ATCGACAACA	2340
TTATTATGAA GAGAACAGGA TAATAAAAT CAGAAATTAT TGTAAAACAG ATAAAAGCAN	2400
CNATGCAGTA ATAGACT	2417

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGACAAAAAC CAGTTACGGT TATCACGTAC CAGCCCCGT ATTTCCAATT TATAATCCTG	60
GCCATCAATT ACTGGGATCT CTTCTTCTCC ATAGAAGGCA TTAAAAGGGA ATGGAGTGGT	120
AATGTCCTCT GGAAGATATT CTGGTGCCAC ACTGTTTTTG CTGAACAGAA AACTTTGAAT	180
CCGGTCATTA AATCTGGATA TACGGAACAA TGCTTTTTCA ATATCATCAT TATTGCTTAT	240
ATCACAGCCA GTCAGCATCA TAATCCCCC AAGCGTCAGT CCCTGTTGGA GTAAACGACG	300
TCTGTCCGGC GCAAGGATTT TTTCTGCATC TTTCACCACG TAATGGGCAT CACTGTCAGA	360
CAAAAAACGT TTTTCTTCA TTAGTGACCC CGTATCATAG ATAACAATGC ACGCGGAACC	420
AATAACACCA TAACCAGGTG AATAATAATG AACAGTACCA TAATGTTTAT GCACAGAAAG	480
TGGATATAAC GCGCTGTATC ATAACCACCG RATAGTATAG TCAGAAGGGA AAAGTGAACG	540
GGTTTCCATA AAACCAGACC AGACAATAGA AGAGCAGCGC CATCTAAAAT AATCAGAATA	600
TAGGCGACTT TTTGCACCAT ATTGTATTCC TGCATATTCG TATGATGCAG CTTTCCATAC	660
AGTGCCTGCG TAAGGGATTT TTTAGTGTAG GTCCATGACA GCGGGAAAAA CTTGCTCCGG	720
AAACGTCCGC TACAAATTCC CAGAGTAAGA TAGATCGTGG CATTAATCAG CAGAATCCAC	780
ATCAGGGCGA AGTGCCACAG TAACGCACCG CCAAGCCAGC CACCGAGAGT TAATGCTGCC	840
GGATAGTTAA AAGAAAACAA AGGAGAAGCA TTATAAATGC GCCATCCACT ACATATCATG	900

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CCTGCGACAG TAACAGCATT AATCCAGTGG CAACAGCGTA ACCACAGAGG RTGTATTTGT	960
TTTAACGGTA ATGGCTGCAT TATGTGATCT CTGTCTGTAA ACTAAGTATA TTATGGAAAG	1020
GAATGTTTCAT CACATCCTCA CAAGAGTTTA AAAAAAATGT GACAANTCAT CGTCAAATGC	1080
TGGGGTAAAA TTCAGATAAA GAATATGTGG ATAACTTTTG ATGAATAACG TAAAAAAAT	1140
ACTGCTGATG GAAGATGATT ATGATATTGC AGCTCTGTTG CGGCTTAATC TGCAGGATGA	1200
AGGGTATCAG ATAGTTCATG AAGCGGATGG CGCCAGAGCT CGTTTATTAC TAGACAAGCA	1260
GACCTGGGAT GCCGTAATAC TTGATCTTAT GCTGCCTAAT GTTAATGGGC TGGAGATTTG	1320
CCGTTATATC CGTCAGATGA CCCGTTATCT GCCTGTGATT ATCATCAGTG CCCGTACCAG	1380
CGAAACCCAC CGCGTCTGG GACTGGAAAT GGGGGCTGAT GACTATCTAC CGAAACCCTT	1440
TTCCATTTCCT GAGCTGATTG NCCCGCATCA AAGCGTTGTT TCGTCGTCAG GAAGCCATGG	1500
GGCAAATAT TCTCCTGGCA GGTGGACTGA TTTGCTGTCA CGGTCTGTGC ATCAATCCAT	1560
TTTCACGTGA AGTTCATTTG CATAATAAAC AGGTTGATCT TACCCACGC GAGTTTGATC	1620
TGCTGCTCTG GTTTGCACGT CATCCTGGCG AAGTTTTTTC CCGTCTTTCA CTGCTGGATA	1680
ATGTCTGGGG GTATCAGCAT GAAGGATATG AGCATACAGT CAACACGCAT ATCAACCGTC	1740
TTCGTGCCAA AATTGAACAG GATGCAGCAG AGCCAAAGAT GATCCAGACC GTCTGGGGAA	1800
AAGGGTATAG GTTTTCAGTT GACAATGCAG GAATGCGATA AATGAATTGT AGCCTGACAT	1860
TAAGCCAGAG GTTAAGCCTA GTATTTACAG TCGTTTTGCT GTTTTGCGCC GTGGACATGT	1920
GGCGTTCATA TTTACAGCAG TAATCTGTAT GGCAATGCAA TGGTACAGCG TTTATCTGCA	1980
GGCTGGCGCA ACAGATTGTC ATCACGGAGT CTCTGCTGGA TAATCGTGGG CAGGTGAATC	2040
ACCGGACATT AAAGAGTCTG TTTGAGCGTC TGATGACGCT TAATCCCAGT GTGGAGCTGT	2100
ATATTGTCTC GCCGGAAGGT CGGCTGCTTG TGGAGGCCGC CCCTCCAGGT CATATCAAAC	2160
GTCGGTATAT CAATATAGCG CCCTTGAAAA AATTTCTCTC CGGTGCTGTC TGGCCCGTAT	2220
ATGGTGATGA TCCCCGAAGT GTAAATAAGA AAAAAGTTTT CAGTACCGCA CCGCTTTACC	2280
TGAGGGATGA TCTGAAAGGA TATCTGTATA TTATTTTACA GGGAGAGGAA CTTAATGCTC	2340
TTACTGATGC AGCCTGGACA AAGGCACTAT GGAATGCACT GTACTGGTCG CTGTTTCTGG	2400
TAGTGATATG TGGTCTGCTG TCGGGTATGC TGGTCTGGTA CTGGGTAACC CGTCCCATAC	2460
AGCAACTAAC TGAAATGTC AGCGGGATAG AGCAGGACAG TATTAGTGCC ATTAACAAC	2520
TGGCAATTCA GCGCCCTGCC ACCCCCCCTA GCAACGAGGT CGAGATATTA CACAATGCCT	2580
TCATTGAACT GGCCCGTAAA ATATCCTGTC AGTGGGATCA ACTTTCAGAA AGTGATCAAC	2640
AGCGCCGTGA ATTTATTGCC AATATCTCCC ATGATTACG GACGCCATTA ACATCACTTC	2700
TGGGATATCT GGAAACCCTG TCAATGAAGT CGGATTCGCT ATCATCAGAG GACTGTCATA	2760
AATATCTGAC AACAGCTCTC CGGCAGGGAC ACAAGGTGAG GCATCTGTCC TGTCAGCTTT	2820

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TTGAGCTGGC	ACGTCTTGAG	CATGGTGCTA	TAAAACCTCA	ACTGGAGCAA	TTTTCTGTCT	2880
GTGAACTTAT	TCAGGATGTA	GCTCAAAAAT	TTGAGCTCAG	CATAGAAACC	CGTCGATTGC	2940
AACTAAGAAT	TATGATGTCA	CATTCCCTGC	CTCTTATCAG	GGCAGATATT	TCAATGATAG	3000
AGCGTGTGAT	AACAAATTTA	CTGGATAATG	CTGTACGCCA	CACACCTCCG	GAAGGCTCGA	3060
TCAGGCTGAA	AGTCTGGCAG	GAAGATAATC	GGTTGCACGT	CGAAGTGGCT	GACAGCGGCC	3120
CTGGACTAAC	TGAAGATATG	CGAACTCATC	TTTTCCGGCG	GGCATCAGTG	TTATGTCATG	3180
AACCGTCAGA	AGAGCCCCGG	GGAGGACTGG	GATTGCTGAT	TGTACGCAGG	ATGCTGGTAC	3240
TACACGGTGG	TGATATCAGG	TTGACTGATT	CAACGACTGG	AGCCTGCTTT	CGTTTTTTTC	3300
TTCCATTATA	ACATCAGGCG	GCATATTTTG	GGGTGGTTAT	GTGTATCTGC	CTTTGTAAAA	3360
GGGATACAAG	TTCTGTAGTG	GAGCACAAAA	TCAGGACACC	GGAATAACCT	GTTTCCACTT	3420
TTCTTCATGT	AAGCAAGGCG	GTAAACCATC	GTTGTTCGTG	TGAGGTCGAT	AAACGTTGTA	3480
ATAACCATTA	ATCCACTGGT	TTATATCACG	TACCGCATGG	ATAAAATCAC	CATAACCACC	3540
TTTCGGAAGC	CATTCATTTT	TAAGGCTGCG	AAAGACTCTT	TCCATCGGCG	AATTATCCAG	3600
GCCATTCCCT	CTGCAACTCA	TACTTTGCAT	TACCCCATAA	CGCCAGAGTA	ACTTTCTGTA	3660
TTTATTGCTT	TTATACTGAA	CACCTTGATC	TGAATGAAAC	AGCAGGCGGC	CATCACGCGG	3720
TCGAGTTTCC	AGTCCGTTAC	GCAAAGCCCT	ACACACCAAC	TCAGCATCAG	CGGTTAATGA	3780
GAGGGCTGAA	CCGATAATCC	GCCGTGAATA	TAAATCAACA	ACGAGCGCGA	GCTAACACCA	3840
TTTGTCTGCG	AGGCGAATAA	AACTGATGTC	GCGCACCAGA	CGCAGTTTGG	TGCGGCGGGG	3900
TGAAATTGCC	GGTTCAGTAA	ATTTGGCAAT	GGCGGACTTT	TGTCTTCGTT	TACCCGGTTG	3960
TGATGTTTTAA	CCGGCTGTGCG	ACTTGTGAGC	CCTCATTTCC	GCATCAGTCG	TCATGCCAGC	4020
CACCGGCCTG	CATCAACGCC	ACTCTGGCGC	AACATCTGAC	TGATTGCCCCG	GCTACCCGGC	4080
TGCGCCACGA	CTGAGAGCAT	GGAAAGCCCT	CACCCGGCTT	CGTAATTCAA	TTCTTTGCAC	4140
ATTAACAGGA	CGCTTCACCT	GCGCGTAATA	AACGCTACGG	TTAATACCGA	ATAAATGACA	4200
AATAACCCAC	ACTGGCCACT	TTGCTTTTCA	CTGTGTGATT	AGCGCGACAG	CTTCCCGGGG	4260
ATTTGCTGCTA	TCAGCACGGC	AGCCTGCTTT	AGTATTTCTT	TTTCCATCTC	AACGCGCTTT	4320
ATCTGCGCTT	TAAGCTGCTG	AATTTGCGGT	TGTTGAGGGG	TAATAGCATT	ACCAGCTGGC	4380
TCAATACCCT	GAAGTTCCTG	CTTATACAAC	CGTATCCATT	TACGCAAATG	GTCAGGGTTG	4440
AGCTCGAGTG	CCTGCGCGAC	TTCTCTGACA	TCACGCTGGT	ATTTAACCAC	CACCTGCTCG	4500
AAAGCTTCAA	GCTTGAAGTC	CGGGGAAAAG	GTACGTTTAG	TCCGACGAGT	TTTGATCATG	4560
CATCACCTCA	TTTTCACTGT	TTTAACATTA	ACAGGATTTT	GAGGTGTCCT	GAATTACCGA	4620
TCCACTACAA	AGTACGACAG	GTAAGTGGA	GGTACTCCCG	TAAAGACGGC	CATCAAGCTC	4680
CCGCTCCGAC	ATACCTGCGG	GCAGAGGCCA	TGAAAAGCCA	GCTTTGCGAA	AGCGCACGAA	4740

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CATACCACAA GCTGTTGATT TTGGTACGCC CAGGCGACGC CCGACCACAA CCTGGGGTAA	4800
ATGTTCTTCA AAGTGAAGAC GTAAAGCTTC AGTGATCCAA GTCCGGTGTT TCATACGATA	4860
GTGTCCATTA AAAATGATGG ACATTATTTT TGTA AAAACCG GAGGAAACAG ACCAGACGGT	4920
TTAAATGAGC CGSTTACATG TAATCCATAC TCATCCAAGG TTTAATTCTG ACACAATAAG	4980
AAAATATGSA AAGTCTCGCT CTAGAGATGG GGAGAGGGAT ATTGAAGTGT ATGATATTCC	5040
AAGAACTGCC GGAGATATCC TCGTAAATGG ATTTTCCAGT GCAAACTGAT AACAAATTCG	5100
AAGTCATTAT CTGCAACAAG ATTGATTGAT GTAGGGGATA TGTTAGAGCA TTATAATGCT	5160
CAAGGATTTG GCGTGATGAC ATCTGCGCCA ATTGATGCGA CACTATATGA TAAACTGGAT	5220
GCTATTTGCA GTAAGTGTA AATAGAACAA ATAAATTTTT CAGTATTAGA GTCAGAACGC	5280
GCACTATATT ATGACGATAT ATTAAGATGC CGTTACTTTG GTAAATAMCA TAAAATTAAT	5340
CAATATGGTA ATATATCAGT TGTAATTGAT CGAAACAAAG CACATAAATG CCATCTTATA	5400
AAGATGGTGT TTKTTAAGCA TATAAAATAT ATTTTCTATA AGATATAGGG CAAACTAAAT	5460
TTCTTGA CTATGATGGA CTAAGTAGAT ATACATGCCG CCAGTTTTTA TAAAACGACG	5520
GCATATATAA TCATTTATAT ATCTTTTGAT TTTATTCGTA ACCACTCATG TTGATCTAAA	5580
CCTATTCTTG ACAGATTAGC AACAAATATCA GTTGTTATTT TTTGCGCGTA CGTTGTTTTT	5640
ATTTCCCGA TCCATTTCAA TACTTTTGGA GTAGATATTT TTTCAACGAG TAAAGGAACG	5700
AATGAGATAT AGTCAGTATT AACTAGATTG TTCTTTTCC CTATGATGAC ACCGTTTCCA	5760
TTTTCGACTC CAAATGAAAA TGAAATAATA TTAGAAGCTT TTGCCGGCAT TTTAATTTTA	5820
TAAAACCGC CATATTCATC TTCGATTAAC AAATTGTAAT TATTATCGTC CAGTGTTCCC	5880
CTGAGGAATA AAAAATCGGC TTTTTCATGC AATCTGACGC TATCACATAA TGGTTGTATG	5940
CATAGATAGA CAAAATTATA TGCATCTAAA AGTAAAGTTC CTTGTTTTAA GGACACATTA	6000
TCTATATGAG AATGATATCT TAAACTCCTG CGCGTGATTT CCAGAGAGCA TAATTGCATT	6060
AACTTTTTAT CTTCTTCACC ATCTTGCTT AAGTATTCCT TTTTACCTAA AGATGCGTGT	6120
TCAATAGCGT GTTGAATTTT TTCTAAAGAA TCAGCAGAGA GTATATTCCT TAGATGTTCT	6180
ACTGATAAGT CTTTTTGTTT TTTTCCAGTT AATAGAAAAT TCTTACAACC ATTTTTTGCA	6240
TAGTGAAAAA TAGGCCAATG GGATAAGGAG TTTTGTCTTA GAGATTTCTG GGGG	6294

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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TATTCCTTTT	TCTCCCATGA	TAGGGCGAAA	GGCTTTATTA	CTATCCACTG	CTGGTTTATT	60
AATTGCATCA	TCGTCGATTA	ATTTGCTGGA	GSTTCCAATA	GTCAACCACC	TCTCTTCAAA	120
TTCATCGGTT	GTCATACCTA	ATCCATCATC	TCTCAAGATA	AGAAGATTTT	CTTTCCTAAA	180
AAAATCAACT	TCGACATTAT	CAGCATAGGC	ATCATGAGCA	TTTTTAAATA	ACTCACTCAA	240
GGCAGTAGGT	ATACCTGCAA	TTTGTTGTCT	GCCAAGCATG	TCCAAAGCTC	GAGCCTTTGT	300
TCTTATTTTA	GCCATATATC	TATGAATCCT	TATTAGTACA	ATTTTCTATG	AGATGTAGCC	360
CAAATAGTCT	AGCGAGTTCT	CAAGGTACAG	CATTGCCGAT	TTGCTTTGCC	ATTGAATTCA	420
GCGAACCTTT	AAAAACATAG	CTTAAAGGAA	ATGTTTGTA	TCTTGATGCT	TCTCTTATGC	480
TAATTGCTCT	ATGTTGAGTG	GGGTCAGGAT	GCCCAAACG	ACCATTGGAG	TAATATTAC	540
ATTTGCTCGT	AAGGTAGGC	GCAGGCTTAT	CCCAACTCAT	TCTTCCATAA	GTATCTGTGT	600
GGCCATCATA	ATTTTTATGG	CATTTATTAA	CTAACTCTTC	TGGCCAATTT	CTTCTATCCC	660
CTCCTTCTGG	AGTGTGCATA	AKTCTTTTTA	GGTTAAGAGG	GCTCAGTGTT	CCAGCCCTAT	720
GTAAGGATC	TTTGGGGTCG	GTTTCTCCTG	AACATAACTT	TGTGAAGTCC	TGGATATAAT	780
CTCGTACAGT	TTGAATGGG	ATTTTATTTT	TACCATGGGT	TATCTCTGGT	AGGGTAACTT	840
TACCTACTCG	ACTAGCTAAG	AGCACGAGTC	TTTTTCTTCT	TTGGGGAATC	CCATAGTTCT	900
CAGCATTGGC	TATAAAAGAT	ATATAGTTAT	ACTCTAACTC	TTTAAGTAGC	TTAATAAACT	960
CCTGAAATGG	GCCTTCTTTT	TCTTCATCAA	TTTTTTGCAT	TCCAGGAACA	TTTTCAAGCA	1020
TAATATATTC	AGGAAGAAGT	TCTCTAATAA	AACGATGAGT	TTCATTTAGT	AGATTTCTCC	1080
TTGAGTCGTC	ACTAGTTTTA	TTTTTATTCT	GTTGCGAAAA	TGGTTGACAT	GGTGCACATG	1140
CACTCAGTAA	CAAAGGCCGT	TTAGCTTTAA	TATCAATGAT	GTCGGAGATA	TCTTGAGGTT	1200
CGATTTTCCT	AATATCATCT	TGGATGAATT	TTGCATCAGG	GAAATTAGCT	TTAAATGTTT	1260
CTGATGCTTG	TTGGTCAATA	TCTAATCCAA	GCTCGATATC	AAAGCCAGCC	TGACGTAGCC	1320
CTTCACTGGC	TCCACCACAG	CCACAAAAAA	AATCTATAAC	TATCAATTTG	ATACCTTCTT	1380
TGAACTAAAT	AAAACAACCT	GAATAAGTTG	ATATTTTAAA	TAAAAATAAT	TGGTATGGAT	1440
ATGAACTTTG	GTCACGCTAC	CGCCCTGAGK	TCATGGCCAT	CCCCAGACCT	TTTAAAGGGA	1500
TTATGAACAA	CACCCAGCCG	ACGTTCAACG	GTGTTACCCA	TACATATCAC	AAAGTTAGTT	1560
AATTGGTTGG	TCGTAAATTG	ACCTAAAATG	GATTGAGGGC	AATGCAAAAA	TCATTGGGAA	1620
ATCCAGGCGA	CACAGATGTT	CGGAAGAGAC	TGAATGTTAA	AAATATAGAA	TGTATATTCT	1680
CAAAAAAGAG	ATATTTTATT	ACATTTTATA	TGTGTATAGG	AAAGTGAGAT	TGGCGAATCA	1740
CCTCCCAATC	ATCCCGCCAG	CGCTCCATTC	AACGCCACGC	CAACCCCTCAC	TCCAGCCAC	1800
GTCATCGCCC	CCAGCCAGAA	TGTCGSCAAC	ACCAGAAACA	TCAACCTCAT	CACCAGATTG	1860
ATAATCACGT	CATCCTGCGT	ATTCTGGATC	CCGGCTAAAT	TCCAGCTACT	GTGGGTATCG	1920

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CTGTTGTAGA GCACATCCAG CAGCCAGCTA TCAAGCCACC GTGCCAGTTC CCACCAAAAG	1980
GTGAGGAAAA ATAGTGCAAA CTGCACAAAC GTCAGCGTCA TCACTACTTT CACATCCCAC	2040
GCCGAACAGA GUGTTATCAG CGGAATACAG ATCACCAGCG CTATTTGCAG TGCGCCTGTA	2100
CCATCGGTAG TSCCTAACGC ACGCTGTGCA ATGCCGTACA TGCCGCTATG CTGCCGAGGA	2160
TATTTCTAGC GCCGGATGCC AACCGBGTGG CGGCATTGGC GACGGTGCCA TCAACGTTAC	2220
CGCCATAGCT TGGATAAACG CGCCCATTCT GCGATACCTG CATATTTCTG TCACTGACCC	2280
GCGAGCGCAG CACGGCCTCT TCATACACTA CCTGCGACTG GTCGATTTTT TTAAACGCCG	2340
TCCAGATATC TAGGGCAGGA AGTTGCAGTA GACGGGCTTT CAGCCCAAGC GGTGTCGTCG	2400
GCCCACCGCT GTTTACAAGT GGGATAGCCG CCCGCGCCCG TATCGGCCAG CCCGGCATCG	2460
CGCGATGCAC TGTACGGCCA AGCACTGTGT GGTGAAAGCG CATGGTCGGA AAAGGCCTGT	2520
TCAGCTAACG AAGCACATCC CACCATCACA AGAATCGCCA GAAAACCAAA CTCAGTCAGA	2580
ATAACTCTTC CTGATTCAGG CTTTGCTCCT GCATTATGSC TACCACTATT GTTTGCCTGC	2640
ACGTATCATC TGATAACGGT TAATTAAGTG ATTTAGCGCC ATTTGAGCCT GTTTTTGCTG	2700
CTGTTCACTG CCATTCTGGT TACGGACTTC ACCGTAGCGA CGTAACTGCT CTTCCGCCGG	2760
GATATGCCGG TTAAAGCCT GCATGATGCC AAACACCTCC GTTTTCAGTT CACTGACCGT	2820
CATGTATTTT CCCCCTGTGTT CATCCTGACG GTTCAGGCGC TCAGCCAAGT GCTGTAAGCG	2880
GATCATGCCT TCGTTCCAGC CCGTCATCGC CTCTTCCGGG AGCGCACGAC TCCTTACACT	2940
CTTCTGCCAG TTATCCACCA TTTCTGAAC ACGGGGATTG CCGGGGACAA GAACCCTCAG	3000
TTGCTGCAGC AGCTGCGCAC TGCACCGCAG GTTGTATGCT GGAGGTAATT CTGCCAGTCG	3060
CGTTATCTGC TGACCGGAAA GGGTTATCCA GTGCACTCAG GGCAGATACC GGATTCAGGT	3120
TAATTTTTTT AAACAGGGAA GCATATACGC TGTCGCCGGT ATCCGTTTCA GATACCACAC	3180
TCTCTGCGAC GTTCTTTTCT TTCTGTACAG ACATCAGCAT TTTCTGTAAG CGTACAGCGA	3240
GGGCCGTATT GACGGGGATG TGTATTTCAG CTGGCAGTGC TATGCGCCAC GGAAGCAGTT	3300
CGCTGACCCG GTTGACCGGC CAGTCTGCTA TGACGGCAAG CACATGGCGA AGGTAGCTTT	3360
CTGGATCCAC GTCATTTCAGT TTGCACGTCC CGATCAGGCT GTACAGTAGC GCTCCCCGCT	3420
CACCACCATG GTCAGAGCCG AAGAACAGGA AGTTTTTACG ACCCAGACTG ACCGCCGCGA	3480
GGNCATNTTT CAGCGATGTT GTTGTGATT TCCACCCAGC CATCGTTTCG ATAGTACGTC	3540
ATGCCGGCCA CTGGTTAAGT GCGTACGCGA ACGCCTTCGC CACCATCAGG CTGGACAGGG	3600
GACTTTCACC CCCAAGCTGC TGAACATGCC CGGCACACAA AGAAGATCTC GGCTCAGTGG	3660
CCGGGATTAG TTATACAATT ATCTGATTGA TTTTAAATAT ATCTTTTCTT AAATCATCGT	3720
TAATATCTGA CGGTTCTAGC TGGTTTATAA GTTGCCCTTAT TTGGGTAAAG GTACTTTTCT	3780
GATCTTTTAG ATCTTCTCCT TTTATCGTTG ATAAAGCTGC AATTAGTTCA CCATCGTAAT	3840

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ATTCACCCGC TAACGGCTCT TTAGTTAGAA CTTCCAACAC TCTTGGCATC AACTGATCAA	3900
TACATAAATT TTGTCGGATA GCGCGGCAAA GATCTTCCAC TGTAACTTT TCAAGAGGCA	3960
CATCTATGAT ACGTTCGAAC CAGASTTCAA GCGGTGATTG TTGCTCAGGC TCTTTTGTCA	4020
TATTGATGTT TCCAATCAAT TTACSTAAGG TAATCATATT CCATATCCTT TCAAGGCTGA	4080
TTCTATTTTA TTAATAGCAT CTGTTGCTCT GCCATACGCA GCCTGAGCTT CAGGATTGTT	4140
GACGTTTTTC AACGTATCCG CATGATTCTT TAATCCTCTG AGCGTATTTT GCATTTCTTG	4200
CATATGATCC CAATATCCTC CATTCTCTTT AGGAACTGGC TTACCATCCA TATCCTTGAG	4260
AGTTCCAATT AATATCATGA ATCTTTTCAG ANCATTTTTT TAATAGTGGT TAATCGANTC	4320
TTCTTTAANT CGGCAACTTT TCTTGGCCTT CCTGGAATTA AAGGCTTTAA TCCTAACAAG	4380
TTTTTTTCTC AATTTTTGGC TGGCTTTAGG GAATCAATTT TTCCCGGATT GGGTGGGTGG	4440
GTGGTAACCC GGGTTTCCCT TGAAGCCCGG GAAACCCGGC CCCAAGTTCT TACTTTTTTT	4500
CCCGCAATCG GGTCAAGAT	4519

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATTACAGAAT GTGGAAATTA AGTAIGATTC GAAAAAAGAT TCTGATGGCT GCCATCCCCC	60
TGTTTGTTAT ATCCGGGGCA GACGCTGCTG TTTCGCTGGA CAGAACCCGC GCGGTGTTTG	120
ACGGGAGTGA GAAGTCAATG ACGCTTGATA TCTCCAATGA TAACAAACAA CTGCCCTATC	180
TTGCTCAGGC ATGGATAGAA AATGAAAATC AGGAAAAAAT TATTACAGGG CCGGTTATTG	240
CCCCCCCTCC GGTTCAGCGC CTTGAGCCGG GTGCGAAAAG CATGGTCAGG CTGAGTACCA	300
CACCGGATAT CAGTAAACTT CCTCAGGACA GGGAATCACT GTTTTATTTT AATCTCAGGG	360
AAATACCGCC GAGGAGTGAA AAGGCCAATG TACTGCAGAT AGCCTTACAG ACCAAAATAA	420
AGCTTTTTTTA TCGCCCGGCA GCAATTAAAA CCAGACCAAA TGAAGTATGG CAGGACCACT	480
TAATTCTGAA CAAAGTCAGC GGTGGGTATC GTATTGAAAA CCCAACGCCC TATTATGTCA	540
CTGTTATTGG TCTGGGAGGA AGTGAAAAGC AGGCAGAGGA AGGTGAGTTT GAAACCGTGA	600
TGCTGTCTCC CCGTTCAGAG CAGACAGTAA AATCGGCAAA TTATAATACC CCTTATCTGT	660
CTTATATTAA TGACTATGGT GGTGCCCCGG TACTGTCGTT TATCTGTAAT GGTAGCCGTT	720
GCTCTGTGAA AAAAGAGAAA TAATGTACCG CAATAACGGT TAAATGCGGG TGGGATATTA	780
TGGTTGTGAA TAAAACAACA GCAGTACTGT ATCTTATTGC ACTGTCGCTG AGTGGTTTCA	840

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TCCATACTTT CCTGCGGGCT GAAGAGCGGG GTATATACGA TGACGTCTTT ACTGCAGATG	900
AGTTGCGTCA TTACCGGATA AATGAACGGG GGGGACGCAC CGGAAGCCTG ACCGTCAGTG	960
GTGCACTGCT GTCCTCACCC TGCACGCTGG TGAGTAATGA GGTGCCGTTA ARCCTCCGGC	1020
CGGAAAATCA CTCTGCGGCA GCCGGAGCAC CTCTGATGCT GAGGCTGGCA GGATGTGGGG	1080
ACGGTGGTGC ACTTCAGCCC GGAAAACGGG GCGTTGCCAT GACAGTCTCC GGCTCACTGG	1140
TAACCGGTCC CGGAAGCGGA AGTGCTTTAC TTCCTGACCG TAASCTATCC GGCTGTGACA	1200
TCTTGTTATA CAC	1213

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACGCTCTAGT ATTCTCTGTC GTTCTGCCTG GGCCACTGCA GATAGAATAG TGACAACCAT	60
TTTACCCATC TCCCCATCGG TACTGATTCC GTCATCAATA AACCGAATGG ATACACCTTG	120
GGCGTCAAAC TCTTTTATTA ACTGGATCAT GTCAGCAGTA TCGCGCCCAA GGGGTTCAAG	180
TTTCTTCACC AAGATGACGT CACCTTCCTC CACCTTCATC CTCAGCAAGT CCAGCCCTTT	240
CCGATCGCTT GAACTGCCCC ATGCCTTGTC AGTAAAGATG CGATTTGCTT TCACGCCTGC	300
GTCTTTGAGT GCCCGAACCT GAATATCGAG AGATTGCTGG CTGGTTGATA CCCGTGCGTA	360
ACCAAAAAAGT CGCATAAAAA TGTATCCYAA ATCAAATATC GGACAAGCAG TGTCTGTTAT	420
AACAAAAAAT CGATTTNAAT TAGACACCNT T	451

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACAAGGCTT ATAACTCAC TGACGGGGCT GGCATGTTCC TGCTGGTACA TCCTAATGGT	60
TCCCGTTACT GCGCTCTCCG TTATCGTATT CTGGGTAAGG AGAAGACTCT GGCACTTGGT	120
GTGTATCCAG AAGTTTCTCT CTCCGAAGCT CGTACAAAAC GGGATGAGGC CCGAAAAC TG	180
ATTTCGGAGG GGATTGACCC TTGCGAACAG AAAAGAGCTA AAAAAGTAGT CCCTGATTTA	240
CAGCTCTCTT TTGAACATAT TGCACGAGGC TGGCATGCCA GTAATAAACA ATGGGCACAA	300

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TCACACAGCG ATAAAGTACT CAAAAGCCTC GAAACACACG TTTTCCCCTT TATCGGCAAC	360
CGGGATATCA CAACACTCAA TACCCCGGAT CTGCTTATCC CTGTTCGTGC TGCAGAAGCT	420
AAACAAATTT ATGAAATCGC CAGTCGTCTG CAGCAAAGAA TATCTGCCGT AATGCGTTAT	480
GCCGTACAGT CTGGCATCAT CAGATATAAT CCTGCTCTGG ATATGGCTGG CGCATTGACT	540
ACGGTAA AAC GCCAGCATCG CCCCGCTCTT GATCTTTCAC GTCTGCCTGA ACTTCTGTCTG	600
CGTATTAACA GTTATAAAGG NCAGCCTGTC ACCCGGCTTG CGTTGATGCT GAATTTACTG	660
GGTTTTTATT CGTTCAGTG AACTCAGATA CGCCCGCTGG TTCTGAAAAAT TGATATTGGA	720

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

NCNTTAATTT TATATCTCGT AAAATAAAAT GTTTTCTGTA CCGCTCTCCG GAGGGGGGAA	60
TGATTTCGTTT ATCATTATTT ATATCGTTGC TTCTGACATC GGTGCTGTGA CTGGCTGATG	120
TGCAGATTAA CATCAGGGGA AATGTTTATA TCCCCCATG CACCATTAAAT AACGGGCAGA	180
ATATTGTTGT TGATTTTGGG AATATTAATC CTGAGCATGT GGACAACTCA CGTGGTGAAG	240
TCACAAAAAC CATAAGCATA TCCTGTCCGT ATAAGAGTGG CTCTCTCTGG ATAAAAGTTA	300
CGGGAAATAC TATGGGAGGA GGTCAGAATA ATGTACTGGC AACAAATATA ACTCATTTTG	360
GTATAGCGCT GTATCAGGGA AAAGGAATGT CAACACCTCT TACATTAGGT AATGGTTCAG	420
GAAATGGTTA CAGAGTTACA GCAGGTCTGG ACACAGCACG TTCAACGTTT ACCTTTACTT	480
CAGTGCCCTT TCGTAATGGC AGCGGGATAC TGAATGGCGG GGATTTCCGG ACCACGGCCA	540
GTATGAGCAT GATTTATAAC TGAGTCATAC CCAAATGAAT AACTGTAATT ACGGAAGTGA	600
TTTCTGATGA AAAAATGGCK CCCTGCTTTT TTATTTTAT CCCTGTCAGG CTGTAATGAT	660
GCTCTGGCTG CAAACCAGAG TACAATGTTT TACTCGTTTA ATGATAACAT TTATCGTCST	720
CAACTTAGTG TTAAAGTAAC CGATATTGTT CAATTCATAG TGGATATAAA CTCCGCATCA	780
AGTACGGCAA CTTTAAGCTA TGTGGCCTGC AATGGATTTA CCTGGACTCA TGRCTTTTAC	840
TGGTCTGAGT ATTTTGCATG GCTGGTTGTT CCTAAACATG TTTCTATAA TGGATATAAT	900
ATATATCTTG AACTTCAGTC CAGAGGAAGT TTTTCACTTG ATGCAGAAGA TAATGATAAT	960
TACTATCTTA CCAAGGGATT TGCATGGGAT GAAGCAAACA CATCTGGACA GACATGTTTC	1020
AATATCGGAG AAAAAAGAAG TCTGGCATGG TCATTTGGTG GTGTTACCCT GAACGCCAGA	1080
TTGCCTGTTG ACCTTCCTAA GGGGGATTAT ACGTTTCCAG TTAAGTTCTT ACGTGGCATT	1140

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CAGCGTAATA ATTATGATTA TATTGGTGGA CGGTACAAAA TCCCTTCTTC GTTAATGAAA	1200
ACATTTTCCTT TTAATGGTAC ATTGAATTTT TCAATTAAAA ATACCGGAGN ATGCCGTCCT	1260
TCTGCACAGT CTCTGGAAAT AAATCATGGT GATCTGTCGA TTAATAGCGC TAATAATCAT	1320
TATGCGGCTC AGACTCTTTC TGTGTCTTGC GATGTGCCTA CAAATATTCG TTTTTTCCTG	1380
TTAAGCAATA CAAATCCGGC ATACAGCCAT GGTCAGCAAT TTTCGGTTGG TCTGGGTCAT	1440
GGCTGGGACT CCATTATTTT GATTAATGGC GTGGACACAG GAGAGACAAC GATGAGATGG	1500
TACAGAGCAG GTACACAAAA CCTGACCATC GCAGTCGCCT CTATGGTGAA TCTTCAAAGA	1560
TACAACCAGG AGTACTATCT GGTTCAGCAA CGCTGCTCAT GATATTGCCA TAAATGGTTT	1620
ATCCGGAGCC GGATAGTGTG TTGTGGATAT CTGGCATGCC CCGGGAAGTC ACCTTTCAGA	1680
CGGGCGGAGG GCTGGTGAAT TATCCGCGAT TACTGAGCAG TATGGATAAT CCTTTTTTAC	1740
AGACTTGTCA GCAGCCAGCA TTTATGTTCT TTTATCTGAG GGAATTTATC TGTACGCTGT	1800
GCCGGGATAT CTCAGTTATA CAGAAATCAG GCAGGAATAA ATTGTAGTGG AAAGTCGATG	1860
TTTACCGGAT GACTGATGCG CGCTTGTAACA CAGACAGTGT GTTTCAGTAA TATGGAGAAT	1920
AATGAAATGA ATAACACAGA CACATTAGAA AAAATAATCA GACACCAAAA AAACAAAGAC	1980
CCCGCATATC CTTTCGGGAA CATTTGTTGA TGCAGCTCTG TATTCGCACA AATAAAAGAA	2040
TGCAGGATAA TATATCTGAA TTTCTGGGGG CGTATGGAAT AAATCACTCA GCATATATGG	2100
TCCTCACCAC ATTATTCGCA GCGGAGAACC ATTGTCTGTC ACCTTCAGAG ATAAGCCAGA	2160
AACTTCAGTT TACCAGAACT AATATTACCC GCATTACAGA TTTTTTAGAA AAAGCCGGAT	2220
ATGTAAAAAG GACGGATAGC AGGGAGGATC GCCGTGCTAA AAAAATCAGT CTGACATCTG	2280
AAGGTATGTT TTTTATTCAG AGGCTCACTC TTGCACAAAG CATGTATCTG AAAGAAATCT	2340
GGGATTATCT GACCCATGAT GAACAGGAAC TGTTTGAAGT CATTAAATAA AAATTACTGG	2400
CACATTTTTT TGATGCCAGC TCATAAAGTG CGAAATATCT GAGGATGCCG GATAGCTTCA	2460
GGCAAAATAA TAATGATTCT TGCAGATGTG TTTTCCGGA TACAAAAACA AATGATAAAA	2520
ATTGCAGCGC CAGGCACCTT TCAAAGCAGG GAGACCTGTA CCGCGTCGAA AATTCAGCC	2580
AGTTAATATC ATTGTCTGAA CCAGGCACTT TGCCCGGGCA GGAGAAGGAG TTGTGGCGGT	2640
CTCAGCCCGG AACAAATTTGA AAACCATAAT CTCGCTTAGG GCCGTGTCCA CATTACGTGG	2700
GTAGGATCAC TCCTGGATTT TCTCTTTTTC GACATTGACG TCTCCATTGG TTAAACACG	2760
GCAATGGAGA CTGCGGTGAA AAGAGTTAAT TCCCGGAGTG ACTGGCTGGA TGCCAATCAA	2820
TGATCGGAAG CATGCCAAAC TGTGAACGGA GATGGATGCC GCCAAATCAT GATCGATTCA	2880
GATGCCATAT TTGCAATATC GCGTTAATCG TCAGTTCAGC	2920

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGTAAGGAAG TTATATATAT GAGCAACTAT ACATCTTAGA TGTATGATAA AGAAAAAGAT	60
AACAGTTCTT TAGAATATGT ATATTGAAGA GAATGCAATA GCATGGTTTA TATAAATTAC	120
GCATAAAAT AAGCATATGT AAGCATTTTG GTTTGCTTTT TTTAACCTGC CACCGCAATG	180
AATGCTTTTT TTATGTTAAT GTGCGTTATG AAATAAATG CAAGAAACAT ATTTAAAGGA	240
TTAATATCGT TCTCTCACAG ACTCCGTTTA CTTATTCAAG AATATAATTT AATTTATAGT	300
GAGCTTATTA TGAATATGAA CAATCCATTA GAGGKTCTTG GGCATGTATC CTGGCTCKGG	360
GGCCAGTTCC CCATTACACA GAAACYGGCC AGTTTCTTTG TTTGCAATAA ATGTATTACC	420
TGCAATACGG GGCTAACCAA TATGCTTTAT TAACCCGGGG ATAATTACCC TGTTGCATAT	480
TGTAGTTGGG GCTAATTTAA GTTTAGAAAA TGAAATTAAA TATCCTAATG ATGTTACCTC	540
ATTAGTCGCA GAAGACTGGA CTTCAGGTGA TCGTAAAKGG TYCATTGACT GGATTGCTCC	600
TTTCGGGGAT AACGGTGCCC TGTACAAATA TATGGGAAAA AAATTCCCTG ATGAACTATT	660
CCGAGCCATC AGGGTGGATY CCAAACTCA TGTTGGTAAA GTATCAGAAT TTCACGGAGG	720
TAAATTGAT AAACAGTTAG CGAATAAAAT TTTTAAACAA TATCACCACG AGTTAATAAC	780
TGAAGTAAA AACAAGACAG ATTTCAATTT TTCATTAACA GGTTAAGAGG TAATTAAATG	840
CCAACAATAA CCACTGCACA AATTAAAAGC AACTACAGT CTGCAAAGCA ATCCGCTGCA	900
AATAAATTGC ACTCAGCAGG ACAAAGCACG AAAGATGCAT TAAAAAAGC AGCAGAGCAA	960
ACCCGCAATG GGGGAAAACA GACTCATTTT TACTTATCCC TAAAGATTAT AAAGGACAGG	1020
GTTCAAGCCT TAATGACCTT GTCAGGACGG CAGATGAACT GGGAATTGAA GTCCAGTATG	1080
ATGAAAAGAA TGGCACGGCG ATTACTAAAC AGGTATTCGG CACAGCAGAG AAATCATTTG	1140
GCCTCACCGA ACGGGGAGTG ACTATCTTTG CACCACAATT AGACAAATTA CTGCAAAGT	1200
ATCAAAAAGC GGGTAATAAA TTAGGCGGCA GTGCTGAAAA TATAGGTGAT AACTTAGGAA	1260
AGGCAGGCAG TGTACTGTCA ACGTTTCAA ATTTTCTGGG TACTGCACTT TCCTCAATGA	1320
AAATAGACGA ACTGATAAAG AAACAAAAAT CTGGTAGCAA TGTCAGTTCT TCTGAACTGG	1380
CAAAAGCGAG TATTGAGCTA ATCAACCAAC TCGTGGACAC AGCTGCCAGC ATTAATAATA	1440
ATGTTAACTC ATTTTCTCAA CAACTCAATA AGCTGGGAAG TGTATTATCC AATACAAAGC	1500
ACCTGAACGG TGTTGGTAAT AAGTTACAGA ATTTACCTAA CCTTGGATAA TATCGGTGCA	1560
GGGTTAGATA CTGTATCGGG KATTTTATCT GCGRTTTCAG CAAGCTTCAT TCTGAGSCAT	1620

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GCAGATGCAG ATACCGGRAC TAAAGCTGCC AGCAGGTGTT GGATTNACCA ACGGAANT 1678

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGGATTACT TTGGAATCTG ACAACAAAGT TACTATGAAA AAGAACTAAC AAAGTTATAT	60
AATGACGCTA AAAATGCTTT GAAAGATGTG CAATCTAAAG CAAATAGGTT AATTTCTGAT	120
AATAAGANAA AACATAAGAG TGAACATAAA AACATTTCTT ATGAATTCCA ATCAACTAAT	180
CTCAATGGCA AAGATACTGC GTATATATTG GATGTARAAA GAAATCTAGA AAGTAAAATT	240
GAGAATACTT CAAACGAATG AGTSTAATGA AATAAGAAAA CTAACCGACC AGATTGCAAT	300
AATTAGTGAT AGTACCACTT CTGAAAATTT ATCATCGGCT CAAGTAACTG AAGCAATCGA	360
AACTGAACTT GAACATTTAC GAGACCAACA AGCAAATAAC GCAGAGTTAA TACTACTTGG	420
CATGGCTCTT TCTGTAGTAC ATCATGNATT TAATGGTAAT ATTAGGGCAA TTAGAAGTGC	480
GCTAAGGGAA TTAAAAGCAT GGGCTGACAG AAATCCTAAG CTTGATATTA TATACCAAAA	540
AATCAGAACT AGTTTTGATC ACTTAGATGG TTATTTAAAA ACCTTTACAC CATTGACAAG	600
ACGTTTAAGT CGCTCTMAAA CCAATATAAC TGGAAGTACC ATTTTAGAAT TTATCAGAGA	660
TGTATTGATG GATCGTCTTG AGAAAGAAGG AATTGAATTA TTCACTACCT CAAAGTTTGT	720
TAATCAAGAA ATTGTAAGTT ACACATCAAC CATTTACCCT GTCTTTATAA ATCTAATTGA	780
TAACGCAATA TACTGGCTTG GGAACAAC TGGAGAAAAA AGACTTATAC TTGATGCKAC	840
TGAAACAGGA TTTGTTATTG GTGATACTGG TCCCGGTGTT TCAACTAGAG ATCGAGATAT	900
AATATTTGAT ATGGGATTTA CACGAAAAAC AGGAGGGCGT GGAATGGGAT TATTCATTTT	960
CAAAGAGTGT TTATCTCGAG ATGGATTTAC TATAAGATTG GATGATTACA CTCCTGAACA	1020
GGGTGCTTTC TTTATTATTG AGCCATCAGA AGAAACAAGT GAATAGCGGA TATAAATAAA	1080
TGACAAGCTC TACTGATTTN CATAAACTTT CTGAAGACTG CGTTCGCCGT TTTTACATT	1140
CTGTAGTTGC TGTAGATGAC AATATGTCTT TTGGAGCTGG TAGTGATACT TTCCCTACAG	1200
ACGAAGATAT TAATGCTTTA GTTGATCCCG ACGATGATCC TACACCAATA ATAACAGCAT	1260
CAGCATCCCC AAGGATAGAA TCAACTAAAT CAAAAGCAAA GGTAAAAAAC CATCCTTTTG	1320
ATTACCAAGC TCTAGCAGAA GCTTTC3CCA AAGATGGTAT TGCTTGTTGC GGATTATTAG	1380
CTAAGGAAGG TSCGAATAAG CGGGGAAATT CTTCTCGGCT GACTCAGTCA TTTCAATTTCT	1440
TCATGTTTGA GCCGATTTTT TCTCCGTAAT ATGCCTTGAA TCAGCCTATT TAGACCGTTT	1500

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CTTCGCCATT TAAGGCGTTA TCCCCAGTTT TTAGTGAGAT CTCTCCCACT GACSTATCAT      1560
TTGGTCCGCC CGAAACAGGT TGGCCAGCGT GAATAACATC GCCAGTTGGT TATCGTTTTT      1620
CAGCAACCCC TTGTATCTGG CTTTCACGAA GCCGAAGTGT CGCTTGATGA TGGGAAATGG      1680
GTGCTCCACC CTGGCCCCGA TGCTGGCTTT CATGATTTCG ATGTTGATGG CCGTTTTGTT      1740
CTTGCGTGA TGCTGTTTCA AGGTTCTTAC CTTGCCGGGG CGCTCGGCGA TCAGCCAGTC      1800
CACATCCACC TCGGCCAGCT CCTCGCGCTG TGGCGCCCGT TGGTAGCCGG CATCGGCTGA      1860
GACAAATTGC TCCTCTCCAT GCAGCAGATT ACCCAGCTGA TTGAGGTCAT GCTCGTTGGC      1920
CGCGGTGGTG ACCAGGCTGT GGGTCAGGCC ACTCTTGGCA TCGACACCAA TGTGGGCCTT      1980
CATGCCAAAG TGCCACTGAT TGCCTTTCTT GGTCTGATGC ATCTCCGGAT CGCGTTGCTG      2040
CTCTTTGTTC TTGGTCGAGC TGGGTGCCTC AATGATGGTG GCATCGACCA AGGTGCCTTG      2100
AGTCATCATG ACGCCTGCTT CGGCCAGCCA GCGATTGATG GTCTTGAACA ATTGGCGGGC      2160
CAGTTGATGC TGCTCCAGCA GGTGGCGGAA ATTCATGATG GTGGTGCGGT CCGGCAAGGC      2220
GCTATCCAGG GATAACCGGG CAAACAGACG CATGGAGGCG ATTTGGTACA GAGCATCTTC      2280
CATCGCGCCA TCGCTCAGGT TGTACCAATG CTGCATGCAG TGAATGCGTA GCATGGTTTC      2340
CAGCGGATAA GGTGCGCCGC CATTACCAGC CTTGGGGTAA AACGGCTCGA TGAATTCCAC      2400
CATGTTTTGC CATGGCAGAA TCTGCTCCAT GCGGGACAAG AAAATCTCTT TTCTGGTCTG      2460
ACGGCGCTTA CTGCTGAATT CACTGTCGGC GAAGGTAAGT TGATGACTCA TGATGAACCC      2520
TGTTCTATGG CTCCAGATGA CAAACATGAT CTCATATCAG GGACTTGTTT GCACCTTCCC      2580
TAAGAGTTTT AATGTTTGAA GAAAGAGATA TAATTACAGC ATCATCCAC AAAGCAGATA      2640
TTACAATACC TTGACTGGGN TATTGCCAAG CGGATA      2676

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(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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AAATTTGTCC TCCGNTCTT TTCCCGTGGA TACGGGCATT GAGACCCGAA AGGSCCTGTA      60
TTTGCGACCG GAGAGGCATC CTGGGGGCTC AGTAAACCAG TGGTCGCTGT ATGGCGGGGC      120
TGTGCTTGCC GGTGATTATA ATGNDACTGG SAGCCGGTGC CGGCTGGGAC CTGGSTGTGC      180
CGGGGACCCT TTCCGCTGAT ATCAGCGAGT CAGTAGCCCG TATTGAGGGA GAGAGAACGT      240
TTCAGGGAAA ATCCTGGCGT CTGAGCTACT CCAAACGGTT TGATAATGCG GATGCCGACA      300
TTACGTTTCG CGGGTATCGT TTCTCAGAGC GAAACTATAT GACCATGGAG CAGTACCTGA      360

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ACGCCCCGCTA CCGTAATGAT TACAGCAGTC GGGAAAAAGA GATGTATACC GTTACGCTGA	420
ATAAAAACGT GCGGACTGG AACACCTCTT TTAACCTGCA GTACAGCCGT CAGACATACT	480
GGGACATACG GAAAACGGAC TATTATACGG TGAGCGTCAA CCGCTACTTT AATGTTTTCG	540
GACTGCAGGG TGTGGCGGTT GGATTGTCA GCTCAAGGTC TAAATATCTG GGGCGTGATA	600
ACRRTTCTGC TTACCTGCGT ATATCGTGC CGCTGGGGAC GGGGACAGCG AGCTACAGTG	660
GCAGTATGAG TAATGACCGT TATGTGAATA TGGCCGGCTA CACTGACACG TTCAATGACG	720
GTCTGGACAG CTACAGCCTG AACGCCGGCC TTAACAGTGG CGGTGGACTG ACATCGCAAC	780
GTCAGATTAA TGCCATTAC AGTCATCGTA GTCCGCTGGC AAATTTGTCC GCGAATATTG	840
CATCCCTGCA GAAAGGATAT ACGTCTTTCC GCGTCAGTGC TTCCGGTGGG GCAACAATTA	900
CCGGAAAAGG TGCGGCGTTA CATGCAGGGG GAATGTCCGG TGGAACACGT CTTCTTGTTG	960
ACACGGATGG TGTGGGAGGT GTACCGGTTG ATGGCGGGCA GGTGGTGACA AATCGCTGGG	1020
GAACGGGCGT GGTGACTGAC ATCAGCAGTT ATTACCGGAA TACAACCTCT GTTGACCTGA	1080
AGCGCTTACC GGATGATGTG GAAGCAACCC GTTCTGTTGT GGAATCGGCG CTGACAGAAG	1140
GTGCCATTGG TTACCGGAAA TTCAGCGTGC TTAAAGGGAA ACGTCTGTTT GCAATACTGC	1200
GTCTTGCTGA TGGCTCTCAG CCCCCGTTTG GTGCCAGTGT AACCAGTGAA AAAGGCCGGG	1260
AACTGGGCAT GGTGGCCGAC GAAGGCCTTG CCTGGCTGAG TGGCGTGACG CCGGGGGAAA	1320
CCCTGTCGGT AAATGGGAT GGAAAAATAC AGTGTGAGGT AAATGTACCG GAGACAGCAA	1380
TATCTGACCA GCAGTTATTG CTTCCCTGTA CGCCTCAGAA ATAAATGAAA GTCCGGAATA	1440
TTAACGGCTG ATTGAATTGC GGTTTATGCC ATTTTCCCGG ACCAA	1485

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTACCAATTT CATCGTCCGG TACATCCTCC AGAACATCTC GCAATAAACT CTCGTCTGCC	60
TCATTCCATG CCACACCAGC ATTTGGGAAA CGAGGATCGA TCTCTCTTTC CTTCTTCTCC	120
TTCTTACTTT GCTCTTTTCC GGATGATACA GATACGACAG AACGTTCTTT TACCGCTGTA	180
ATTGCCATAA CTGCATTGAG CAGAGATCTG CGCTCCACAT CSTTCAGCAT TTTTCCTTCA	240
CAGATCAAAT CATTGAGGAT GTCAATGACT AGATTGAGAC TTTCTTCTGT TAGCTTCATA	300
TTTCAGACCT TGAAGTATGT AGATAATCAG CACAATTACT AATGTGATAA ATATCAGAAG	360
ATAATTTACA GGTAAACCGG AAAATACATC TGAAGAATAA AGGCCTCAGC TTAACGTTTC	420

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AGCCAGTTTG	TGAGCTGATT	GAGGTACGGC	GATGACATTA	ACGGGAATTA	CTCCCCATA	480
GCTCTGAGCT	TATTTTTTAC	CCTGGCAACA	TATGCTGGCT	ACTGCGCATG	GTTTTGAGT	540
AGATATCTTA	CTACTCGTAG	AATTGTGCTT	ACTGCTCAGG	CCAGCGCACA	GGCATTCCGT	600
GCAATCAATA	GAACACTGGT	TTTTTAGTCT	TCCGTTACCC	ATCAGGATGT	TAGTGAGAT	660
TCCGGTGTAT	TCGATCAGTT	GTTCCGGCGAA	TCAGCGATCG	ATCACGATGC	GATTTCTGTAT	720
GTTAGGGATG	CTGGTATGAT	TACTCGCTGA	AAAATAATGT	GAAAAGGCAG	TTTTTCTTTA	780
GACATTTAGC	TCATTCATGC	TGTTGTTTTA	CGTTTTGCTG	TCGTGTGCAG	GATTATCTTT	840
TCGTTACGGG	ACGATTCATT	CCGTTTTAAT	CAGGAGCTAT	TGGCGTTGCT	CATTGGTGGG	900
ATGCCGTAAA	GTTTTACCGC	GGCGATTAAT	GATGTGAAGT	CAATCCAAAT	CAACGGAGAT	960
CTCTCATCAT	GAATCAACCA	ATACACAATG	ATTACTGGTT	ATCCCGTTTT	GAAAGTATTC	1020
TCAACAGTGC	CCTGGTGCAA	CACCGTGCCG	TCTCGTTAAT	CTGGGTGGAT	TTACGTTTCC	1080
CTGAGCATAT	GCCTGTCACC	ATCATGGATC	CCGATCCGGA	TTCAGCGGTG	ATTTCTCGTT	1140
TTTTCGAATC	CCTGAAAGCC	AAAATTCAGG	CTTACCAGCG	GAAAAAACGA	CGTACCAACA	1200
AGCGTGTGCG	TGCAACCACC	CTGCATTATT	TCTGGTGTG	GGAGTTTGGC	AAGGAAAAAG	1260
GCAGGAAACA	TTATCACGTG	ATATTACTGC	TCAACAAAGA	TACCTGGTGC	TCGCCAGGGG	1320
ATTTACCCGT	TCCTTCTTCG	CTGGCGACGC	TGATCCAACT	GGCATGGTGT	AGCGCTCTGC	1380
ATCTTGAGCC	CTGGCAGGGT	AATGGACTGG	TTCATTTTTT	CAGGCGGACG	CYTTTCCGTA	1440
AACCGGTATC	ATCTGATGCT	CGCCCTTCTT	CCGATGATAC	GCCTTTGTG	GGTGGATGTT	1500
CTGAAACCAG	GAAGGCTTCA	GACAAAAAGC	CGGGTGAAGC	CGCTGTTCTC	TGGATCAAGC	1560
GTGGTGTATG	GGAAGCGATG	CAGAAAGCCA	TGGAGAGAGC	CCGTTATCTC	GTGAAGTATG	1620
AGACGAAGCA	GCATGACGGT	TCTGGTCAAC	GTAATTATGG	TTGCAGCCGT	GGAGCGGGGC	1680
GTCTACTGGA	TGGCAGGTGA	ACCCTGTAAA	ACGGCATCCG	GTGCCAGAGT	ATATGTCACA	1740
GTAAGGGCGT	GGTTGATGCC	CTTAGCTCGT	TTTCTGAAAA	AGTCGTCCTG	AAGTCATGTG	1800
TCACGAACGG	TGCAATAGTG	ATCCACACCC	AACGCCTGAA	ATCAGATCCA	GGGGGTAATC	1860
TGCTCTCCTG	ATTCAGGAGA	GYTTATGGTC	ACTTTTGAGA	CAGTTATGGA	AATTAAAATC	1920
CTGCACAAGC	AGGGAATGAG	TAGCCGGGCG	ATTGCCAGAG	AACTGGGGAT	CTCCCGCAAT	1980
ACGGTTAAAC	GTTATTTGCA	GGCAAAATCT	GAGCCGCCAA	AATATACGCC	GCGACCTGCT	2040
GTTGCTTCAC	TCCTGGATGA	ATACCGGGAT	TATATTCGTC	AACGCATCGC	CGATGCTCAT	2100
CCTTACAAAA	TCCCGGCAAC	GGTAATCGCT	CGAGAGATCA	GAGACCAGGG	ATATCTTGCC	2160
GGAATGACCA	TTCTCAGGGC	ATTCATTGCT	TCTCTCTCGG	TTCCTCAGGA	GCAGGAGCCT	2220
GCCGTTCCGT	TCGAAACTGA	ACCCGGACGA	CAGATGCAGG	TTGACTGSGG	CACTATGCGT	2280
AATGGTCGCT	CACCGCTTCA	CGTGTTCTGT	GCTGTTCTCG	GATACAGCCG	AATGCTGTAC	2340

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ATCGAATTCA CTGACAATAT GCGTTATGAC ACGCTGGAGA CCTGCCATCG TAATGCGTTC	2400
CGCTTCTTTG GTGGTGTGCC GCGCGAAGTG TTGTATGACA ATATGAAAAC TGTGGTTCTG	2460
CAACGTGACG CATATCAGAC CGGTGAGCAC CGGTTCCATC CTTCGTTGTG GCAGTTCGGC	2520
AAGGAGATGG GCTTCTCTCC CCGACTGTGT CGCCCTTCA GGGCACAGAC TAAAGGTAAG	2580
GTGGAACGGA TGGTGCAGTA CACCCGTAAC AGTTTTTACA TCCCACTAAT GACTCGCCTG	2640
CGACCGATGG GGATCACTGT CGATGTTGAA ACAGCCAGCC GCCACGGTCT GCGCTGGCTG	2700
CACGATGTGG CTAACCAACG AAAGCATGAA ACAATCCAGG CCGGTCCCTG CGATCGCTGG	2760
CTCGAAGAGC AGCAGTCCAT GCTGGCACTG CCTCCGGAGA AAAAAGAGTA TGACGTGCAT	2820
CCTGGTGAAA ATCTGGTGAA CTTCGACAAA CACCCCTGC ATCATCCACT CTCCATTTAC	2880
GACTCATTCT GCAGAGGAGT GGC GTGATGA TGGAAGTGCA ACATCAACGA CTGATGGCGC	2940
TCGCCGGGCA GTTGCAACTG GAAAGCCTTA TAAGCGCAGC GCCTGCGCTG TCACAACAGG	3000
CAGTAGACCA GGAATGGAGT TATATGGACT TCCTGGAGCA TCTGCTTCAT GAAGAAAAAC	3060
TGGCAGTCA TCAACGTAAA CAGGCGATGT ATACCCGAAT GGCAGCCTTC CCGCGGTGA	3120
AAACGTTTCA AGAGTATGAC TTCACATTCG CCACCGGAGC ACCGCAGAAG CAACTCCAGT	3180
CGTTACGCTC ACTCAGCTTC ATAGAACGTA ATGAAAATAT CGTATTACTG GGACCATCAG	3240
GTGTGGGGAA AACCACCTG GCAATAGCGA TGGGCTATGA AGCAGTCCGT GCAGGTATCA	3300
AAGTTCGCTT CACAACAGCA GCAGATCTGT TACTTCAGTT ATCTACGGCA CAACGTCAGG	3360
GCCGTTATAA AACGACGCTT CAGCGTGGAG TAATGGCCCC CCGCTGCTC ATCATTGATG	3420
AAATAGGCTA TCTGCCGTTT AGTCAGGAAG AAGCAAACT GTTCTTCCAG GTCATTGCTA	3480
AACGTTACGA AAAGAGCGCA ATGATCCTGA CATCCAATCT GCCGTTCTGGG CAGTGGGATC	3540
AAACGTTCCG CGGTGATGCA GCCCTGACCT CAGCGATGCT GGACCGTATC TTACACCACT	3600
CACATGTCGT TCAAATCAAA GGAGAAAGCT ATCGACTCAG ACAGAAACGA AAGGCCGGGG	3660
TTATAGCAGA AGCTAATCCT GAGTAAACG GTGGATCAAT ATTGGGCCGT TGGTGGAGAT	3720
ATAAGTGGAT CACTTTTCAT CCGTCGTTGA CATCATGCAA TCTTTCCTGG TTTTCATGCA	3780
TCCATCATTT GTCGCTGCGA TGCCAGACTT CTGGATGCAC ACATGTTGTT TTACTTTTGT	3840
CAGCATCATA AATGCGCCGG GACTGGTGAA TGGAGATAAG CCATTTTATT ATCGACGTCA	3900
GCGAACATAC TCACCATGCC GGTATGTTCC TGAAGTGAAC AATAAGTTT GCGCTGATTA	3960
CAGTATGTGA AGGAGGTCCG TTACAATGAA TTCCGCTTAT ATGCAATCCT TGCAGACATC	4020
CCACCACTTC CCAGCTGATT TAACCTACAG ATTATTTCTT AGTGAGCTTG CATATCTCAT	4080
TGACGACTTA TATGAAAGTA CCCAACTTCC GCTGAGCTC ATTTTAAATA CTGTACTGGC	4140
AACGCTCTCA CTCTCCTGTC AGTCACTGGT TGACGTTGTT CATCCTCACA CCAACATGCC	4200
GGAACCTTGC TCACTTTATC TGTTGGCAAT CGCAGAGCAA GGCGCGGGAA AAACAACGAT	4260

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AAACAGACTG	GTGATGAACC	CCTGTTACGA	ATTTGCCGAT	CGACTCATTC	AACAATACGA	4320
AGAGAGAAAC	AAAGATTATA	AGACTGAACT	ACAGATCTGG	AATACCCGGC	AGAAAGCGCT	4380
TGCTGCCAAT	TTAAGAAAGG	CTGTTAACCG	GGGSTATCCG	GGGGAACAGG	AAGAAGAGGC	4440
GCTGCGTAAT	CACGAAAGAA	ATAAACCGAC	ACGTCCGGTT	CGAOCGAATT	TTATCTATGA	4500
AGATGTTTCG	CTTAAAGCGC	TTGTGGAAGG	GCTCAATGAA	CATCCTGAGG	CAGGGGTTAT	4560
TTCTGACGAG	GCGGTCACCT	TTTTCAGAAG	CTATCTGAAA	AATTATCCGG	GCCTGTTGAA	4620
TAAAGCATGG	AGTGGACAAC	CGTTTGATTT	TGGACGGGCT	GACGAGAAAT	ACCATATCAC	4680
GCCACGTCTG	ACATTTTCGT	TAATGTCCCA	GCCGGATGTC	TTTACGAATT	ATATAAATAA	4740
AAATGACGTA	CTGGCGTGGG	GAAGCGGATT	TCTTTCCCGG	TTTCTGTTCA	GTCAGACCGG	4800
AAGTCCTTCC	CGGGTACGGG	ATTATACGAG	AGGCGAGTTC	AGAACAAAAC	CAACCCTGGA	4860
GAAGTTTCAT	AAAAAGATTA	ACGGATTTCT	GTTAAGCCAT	AACATTAATT	CCCCCGGTAT	4920
GAGCACCGAA	AGGAAAACAT	TAAAACTTGC	AAAGAAAGCG	TTGGGGGAGT	GGCAAGAAAA	4980
CCAGATTAAG	ATTGAAAGAA	AAGCGCTTGC	AGGAGGGGAG	TGGGAACACA	TCAGAGATAT	5040
TGTTCTGAAA	GCAGGTTCTA	ATATACTGAG	GATAGCTGGA	ATATTCACCT	GCTATTGCTA	5100
TAAAGATGCT	GAGGAAATTG	AATCAATTGC	GCTTTTTTAA	GCTATGCATC	TCATGGGCTG	5160
GTATCTGGAG	GAGGCGAGCA	CAATATTTTA	TCCCATGTCT	GCACGATGCC	AGTTTGAACA	5220
GGATGCCTGT	GAAGTGTATG	CATGGATTAT	GACCCGAATA	AGGCAGAATA	ATTGGCGTGC	5280
TATCAGGAAA	ACAGACATTG	AAAGATATGG	TCCCAATCGT	CTGAGAAGAG	CAGAAAAACT	5340
TACACCTGTA	CTCAATCAGT	TAATCGYTCA	GAATTATTTT	CGTATCATCM	AAGATGCGAT	5400
CGCATCAGGC	ACTTTATGTT	TCTGCTCTTG	ATAATAATGG	TTACATCCTT	CCTTTTCGGC	5460
CAATGTCTTA	CGAACCGTTT	GATATTGTTT	CACCCAGTA	TAACCATAAT	GCGAAAACAT	5520
ATTCCGTTGT	TATTCCACCG	GCATTAATTC	AGTCATTTAC	ACCTGATTCC	TCAGCTTACA	5580
CCTTATTTTA	AAACAATTTT	GTGAGTAGAA	AACGAAAATC	ATAATCCTTC	GAATGAAGGT	5640
TAATGATAAG	GTGTGTTGCA	TATCCTGCAC	CTGTGCAAAT	ATTCACCAAT	CATTGGGTGT	5700
GAATGAAAAT	TTCTCTGAAA	AAATCGCTAT	GGTAGCAACA	GTAGCAGCAC	ATACACTACA	5760
TCTGTGATTT	GGTTTTGTTT	TCATAATGAC	CTGCTGTCAG	AGCTGATTGA	ATGCTGGGAT	5820
GTGCGCACTG	GTGGAAGAGT	GGTTTTCGTT	TCAGATATAA	CGAAAGGTAA	TCGAAAGATT	5880
GTTTTAAACA	TGGATTAAAG	CTAATAATTA	ACCATATTGT	GTGAGTTTTT	ATATATAAGT	5940
TTGTTTGATT	CTTGCCGTGA	TGAGTGCTGG	GGTATATGAC	GATGTCGCTC	TCTTTCTGAA	6000
TAACAAATTA	TTATTCGTCT	GTTACTGATA	AGGGATGCGA	TTCATGTTTT	AATAGAGGGT	6060
TGAAGAAAAT	TAATTTGATA	TTTTTTTGTA	AGGGAATGGA	ACTGTCCGGA	ATATGTTTAC	6120
AACGGCGGAT	TTCTCATTTT	CATTCATTAA	ACATGGATAA	TTTTAATTTA	GGTTTATTAC	6180

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TATTATTATA CTCACCTCCCT TTTTCATACA ATCTCTATTG TTATTTACTT CCTGTCTTTA	6240
CTCACTCTCT ATCTTTACGA TTATATTCAC TCTATCGTTA CACATTCCAT TAGTATTACT	6300
CTTGTTATCG TATTCATTCC ATCCCTCAAT CATATTTACT GTAACTCATA TGATGTTTCTAG	6360
GTAAGTTATT CTCTACCATT CTACTGATGA TATCCATCTG TTCTCATTCTT CAGTGAAACA	6420
GCAATTGATT TTAATCTTAT CCATCATGAA CTGTATTTGC TTAACAATGA TTGTTTATCT	6480
GAAGTGTTTT AACTATTCTG GTTGGAAACA ATTTCTCTGT CATCACAGAT TAACTGAATG	6540
TTTACTCTTT GATAAGGTAT CCATGATTCC GTCATGTTTA ACAGCGCAGG ATAAACAACA	6600
GAATTAACAG AGTGAATTC TGATTATATT TGTTGCCGGT TGTATTGTTT AAGGTACTGG	6660
GTGAAAATTA TTCATCCATG GTATGTTGTC TTATGCTATC GTGTGTCGTT AACGTTTATA	6720
TCCTGGAGAA CAGATTGAAT GAGCGCATAT AAGTTTATTG CATTGGCCTT GTACACGGTT	6780
TTTACAACCA CTGAGAGCAA GTTTGTAGTT TATGATGTGA TTGGTCGCAA TATGTTTCTT	6840
AACCTTCTGG TCGTGGTGTT TTATCGCGTA TTTTGCAGTA TTTCGTGATG TTTTATTGAG	6900
TCTGTATTTT CTTTACTCCT CGTTTATCTC ATCTCTTTAG CTAATACCAT CAGATAATCC	6960
ATTTCTTTCT GCATAATGCT GCGTATCGTT AATAACCCGT CGTATCCATT CTGCTACAGC	7020
ATGCCTGATA AATACCATCT GTAAGTTATT ACCGTTTTAG ATCTGATTAT GAGCGAAAGC	7080
ATTAATTCGT TCACAGAGCT TAAACATCA TTAACCTTCA GGAGTCATCA ACATGCCTAA	7140
ATCTTACACA CCAAACCTGGT TTTTACCAGC TTTACTTGAC AATCACATCA ATCAAATGAT	7200
GGCAGCTAT TCCTGCCTGC GGGCCTTACG CATGGATTTC TTCTACAGGA AAGATACGCC	7260
CGATTTCTTA CAACCTGATC ATCGCTGGCT TGAATTGCAG TTGCGTATGA TGCTGGAGCA	7320
GGTGGAAACA TTTGAAAATA TCGTTGGCTT CTTCTGGGTG ATTGAATGGA CGGCTGATCA	7380
TGGTTTTTAT GCGCATGCGG TTTTCTGGAT CGATCGTCAG AGGTTAAAAA AAATATATCC	7440
CTTTGCGGAG CGGATTACGG AATGCTGGCG GTCTATTACG CATAACAGCG GTTCGGCACA	7500
CCGCTGCACA TATCAGCCGC ATTATACATA CAACATCAAC ATTCCTGTGC GCCACAACGA	7560
TCCTGAAAGC ATCGATAATA TTCGCGGTGC CCTGCATTAT CTGSCGAAAG AAGAGCAAAA	7620
AGACGGGCTG TGTGCTTACG GCTGCAATGA AGTTCCTGAA CGTCCTGCTG CAGGGCGTCC	7680
TCGTAAGCCT CACTTCTGAA GCTTAAGGCC TGAGCCTTCG CTCCTGGAAA CACTCCGTCTG	7740
GTAAAACTT ACCGCCTTGA TTAATGATGT GAACTGAAGT CAACGGAGAT CATTATCCTT	7800
GAACCTGCAT CCGGTGTTTT GTTCCTTGTC TTCCCGTTCT GCTTCGGTTT TTAATTATT	7860
CCATCAATCT CATTCCGCAA GCCATAACAC GTCAGCTCAT TCACGGGCAG GACGCTATTGT	7920
GGGCTGCGCA TAACGGAACA TATCTTATGA ATGCTATTCC TTATTTGAGT TATAGCCTGG	7980
CACCCTTCTG GCCATCTTAT CAGAACAAAG TCATCGGCGT CCTTGAGCGT GCGCTGCGTG	8040
AGCAGTCCGG CTCACGGATA CGGCGGATCC TGCTTCGTCT GCCGTGGGAA CATGACAACG	8100

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CCTTCAGCAG	CAGAAAGATC	TGSTTCGGTA	TGGACTTTAT	CGAAACCGTC	ACTGCGCTGA	8160
TGAATGCGAA	ACCCGGACGC	GACCTTTGCT	GGCTCCTGAC	CGGTCATCCG	GAAAAGCCGG	8220
AATACCACGT	GGTGCTGTGC	GTCAGACAGG	AGTATTTTGA	CGGCCCCGAA	CTGGATCGGT	8280
TGATACTGGA	TGCCTGGAGT	AATGTGCTGG	GTTTCGCGTC	ACCAGGTGAA	GCAAAGCCGT	8340
ACCAGAAGCA	GATCACCCGG	GATGTGGTAC	TGGATCGCCG	GTCACCGGAC	TGCGAAGCCC	8400
TGTTTAAGGA	CCTTATCTGG	GCGTTCAGTG	ATTTTCGCCG	CGATCGCCGT	GGAGTGTGCG	8460
ATCCGGAAGC	CCGTTGCCCT	GCCGGCAATC	CCGGTTGGCA	GTGCTGAAAG	CAGCACGCCA	8520
TCCCATCCCC	CGTATTACCC	CATTCTTCAT	AAATCTCACT	GAGGACATTC	TGACCATGTT	8580
GACCACAACA	AGCCACGACA	GCGTATTGCT	GCGTGCCGAC	GATCCCCCTGA	TCGACATGAA	8640
CTACATCACC	AGTTTCACCG	GCATGACCGA	TAAATGGTTT	TACAGGCTGA	TCAGTGAAGG	8700
GCATTTTCCT	AAACCCATCA	AACTGGGGCG	CAGCAGCCGC	TGCTACAAAA	GTGAAGTGGA	8760
GCAGTGGATG	CAACAACGAA	TTGAGGAATC	ACGAGGAGCA	GCAGCATGAA	ACGTGTTGTG	8820
ATGCCAGTAC	GTTGGCAATG	TGCAAAATGC	CAGCGCTGGT	ATTGTGGAAA	TCAGCCCTGT	8880
CCCTGGTGCT	GGCGACATTC	CCGCTTATCT	TTCCGCTGAC	ACCTCCGGT	CAGCCAACTG	8940
TTAGTCATCA	TTTCCTGACT	GATTCGTCAT	TCCATTCTTA	TTGATTATAA	CTGGCATTAC	9000
ACCGGTGCTG	GCGTGCTTTC	CTGCGTGTCT	GCACCGGTTT	GACAAAATTC	AACAGGGTTT	9060
GAAAAGGAAC	ATTTTCGTGCA	AATAACCGAA	GCCTTAATTT	CAGAGCCGGG	AGACATCCGG	9120
CGTTTTATTC	AACATGCTGT	TGACCACTGG	CCGCGTCTGC	TGTCAGTCCA	CTTCATACTC	9180
CATTCGACAG	AAGGAAACAT	CTACGGGCAA	CAGATTCATG	CATTCTGCAC	TTCTTTTAT	9240
CGACAACTGC	ATGAACGTAT	TACTGAGAGC	AATCACACTG	CCAGTCCATC	ATCGTCGGTG	9300
GTATTACGCT	GGTTGCGGGA	ACAACATGGA	GGAGCAACAA	TTGATGCCT	GTTGCTGCTC	9360
AGCCAGACGA	GTATTTGTCA	CCGCGAGCC	AGTGTCACAG	TTGATGAACA	ATGTTGCGAA	9420
GTGGTGGATT	TACTGCAACA	TAGCTGGCAG	GTGATAAGTG	CTGGCGGACA	ATGCCGGGTG	9480
GAAAGGTGTT	TTCGGGTGTC	CCGGGGTGAT	ACATCCGGTC	AGTATGTTGC	GTTAAAAACA	9540
GTCGCATTGT	CTCTGGGGTT	ACCGGTTGTG	ACCGCCATTA	CCCATCGTCC	GGTACAGCGC	9600
TGTACATTGA	TTACAGCTCA	GTGAATCAGC	GCTTTCTGGC	TTTTCGTCGG	TCATTCTGTC	9660
AACGCCACGA	TGTTTGACCG	TTATGGGGAT	GCGGACGATT	CCCTGCACAG	CGTTGTTTCA	9720
CGGTGGTGGA	TGACGCAACA	CCGCTGTTAA	AAACAGTCGT	TCAGTCCTTT	GTGTTACCGG	9780
TTGTGACAAC	AATCAGTTGG	TAATGGACGT	GTGAACCATC	TGCGCTTCCG	TTGATTTTTA	9840
TGGACTGATA	AAGTTTTGCC	AGCTGAATCT	TTATACGGAA	TGCTCTTCAG	TATGCGTACA	9900
CGAATTGACT	ATCTGGCGGA	TAAATACTCT	TTTACCGAAC	GGAATGAATC	TCCACGCCTT	9960
CGCCGGCAGT	GGCAGGATGT	TCTGGAGGAG	TGTCGGCTGA	CAGAGCCCGG	ACCAGAAGAA	10020

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CGGCTGCGTA TTGCCCTGCT GAATGTGGAT TACGTCACCA GTTTTGAACT GCCTTTTTCGC	10080
TTGTTGCTTA CTCGTACACC ACAACTGATT GCCGCGCTTC GGAAGAATG GGGCCTCAGC	10140
CAGAAAAATG TGGTGTTCAG CGATAAACGG TTTGCTGCG TGTACAGCCT GAAGGCCAGT	10200
CTTTCTGGTG TACCGGATAC ATTCCGGTAT CATCTGTCTC ATCGTATTCC CCGGATGGTT	10260
GGGAATGAAA ATACATCATC GCCATATCAG CAGATTGCCC GGAAGTGAA AGTGCCCCGT	10320
GAACGGCTGA AGTATGCGCT GGAAGCCGGT TTAAGGTGA CTGCACTGGA CGGGCTGTTC	10380
TGGTCTGGTA GTCAGCGCAT TCGGCTGAT ATCCTGAGAC TGAGAAAGAG CGGAATGCCG	10440
GTGGTGACAA CGTCCGTGGA AGCGAGCGAT AACCTGACGG GAACAACCCG CAAAATACCG	10500
GCATACCATC TCTGACATTG CGATGAAGGG CAGATTTTAC CTTGACAGGG GCAGAGTGCC	10560
GCTTTTTATA CTTTATTCCC GTGTCTGAAA AAAATGTGCA AAGGAAACGG GAATGGCAAG	10620
GTCCGATTAC GATTTTATCA ATCTGTCTCT GGGACATGAA CTGAATGAGT GGCTGGCAGA	10680
GAGAGGTTAT GCCGGACAGG CGGATAACCG GAACCGACTG GCAGAGGTGG TTACCCGCAA	10740
ATTGCGGGAC AGTTTTTATG CGGACGTCTC CTGGGATGCG CTGAATGTGG CATAAGTGA	10800
ACACCCTGAG TGGTTTTTAC AGCTTGCCCTC CGGGGATGAG GATTAACAGG CAAATTATGC	10860
TGCTATCGGG CAGAGTGATT ACCTGCAGGG ATTTCCATTT ATAAGAATAC GCCGCTTCGG	10920
GAAAGCTCCG GTTCTCCGGA GAGTTACGAT TATTTTACT CAAATTCACA ACACCTGAAC	10980
TGGAACCTGC GTTGTGTCCC GGATTGTTAC TCCGCAGAAG CATCCTTTTT ACCATACGGA	11040
TGTTTGTTTT CCATTTCCCC TCCGAAAAAT ACAACTCCGA TCACATTTCT GATATTTTCC	11100
CCGGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTA ATTTAGCAC	11160
TGACATTCCG CTTACGTTAA TTTACACTGG ATACCCACG AGGAGAATAT GCAGCACCGG	11220
CAGGATAACT TACTGGCGAA CAGAAATTTG TTGCCTGGTA TGGTTTCCGG TCAGTACGCA	11280
TTCAGGATCC GTACCTTATC TCAGGTGGTA CGCTATTTTT CCCTCCTCCC CTGCCTTTGC	11340
ATTCTTTCAT TTTCGTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG TGCAATTCAG	11400
CAGCAACAGC AGCAGTTGTT GGATGAAAAC CAGCGCCAGC GTGATGCGCT GGAGCGCAGT	11460
GCGCCGCTGA CCATCACGCC GTCTCCGGA ACGTCTGCCG GACTGAAGG TCCCTGCTTT	11520
ACGGTGTAC GCATTGTTGT CAGTGGGGCC ACCCGACTGA CGTCTGCAGA AACCGACAGA	11580
CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCAGG GACTGACCGC GGTCACGGAT	11640
GCCGTGACGG ACGGCTATAT ACGCCGGGA TATATACCA GCCGGGCCTT TCTGACAGAG	11700
CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGTCTATG AAGGCAGGCT GCAGCAAATC	11760
CGGGCGGAAG GCGCTGACCT TCCTGCCCCG ACGTGAAGA TGGTTTTCCC GGAATGGAG	11820
GGGAAGGTTT TGAAGTGGG GATATTGAGC ACGGGATGGA GCAGATTAAT CGTCTGCGTA	11880
CGGAGCCGGT ACAGATTGAA ATATCGCCCG GTGACCGTGA GGGATGGTCG GTGGTGACAC	11940

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TGACGGCATT	GCCGGAATGG	CCTGTCACAG	GGAGCGTGGG	CATCGACAAC	AGCGGGCAGA	12000
AGAATACCGG	TACGGGGCAG	TTAATGAGTG	TCCTTTCCCT	TAATAATCCT	CTGGSGCTGG	12060
CTGACAACTG	GTTTGTGAGC	GGGGGACGGA	GCACTGACTT	TTGGGTGTCA	CATGATGCGA	12120
GGAATTTTGC	CGCCGGTGTG	AGTCTGCCGT	ATGGCTATAA	CCTGGTGGAT	TACACGTATT	12180
CATGGAGTGA	CTACCTCAGC	ACCATTGATA	ACCGGCGCTG	GCGGTGGCGT	TCCACGGGAG	12240
ACCTGCAGAC	TCACCGGCTG	GGACTGTGCG	ATGTCTGTGT	CCGTAACGGG	GACATGAAGA	12300
CAGCACTGAC	CGGAGGTCTG	CAGCACCGCA	TTATTCACAA	TTATCTGGAT	GATGTTCTGC	12360
TTCAGGGCAG	CAGCCGTAAA	CTCACTTCAT	TTTCTGTGCG	GCTGAATCAC	ACACACAAGT	12420
TTCTGGGTGG	TGTCGGAACA	CTGAATCCGG	TATTCACACG	GGGGATGCCC	TGGTTCGGCG	12480
CAGAAAGCGA	CCACGGGAAA	AGGGGAGACC	TGCCCCGAAA	TCAGTTCCGG	AAATGGTCGG	12540
TGAGTGCCAG	TTTTCAGCGC	CCCGTCACGG	ACAGGGTGTG	GTGGCTGACC	AGCGCTTATG	12600
CCCAGTGGTC	ACCGGACCGT	CTTCATGGTG	TGGAACAACG	GAGCCTCGGG	GGTGAGAGTT	12660
CAGTGCGTGG	CTTTAAGGAG	CAGTATATCT	CCGGTAATAA	CGGCGGTTAT	CTGCGAAATG	12720
AGCTGTCTTG	GTCTCTGTTC	TCCCTGCCAT	ATGTGGGGAC	AGTCCGTGCA	GTGACTGCAC	12780
TGGACGGCGG	CTGGCTGCAC	TCTGACAGAG	ATGACCCGTA	CTCGTCCGGC	ACGCTGTGGG	12840
GTGCTGCTGC	CGGGCTCAGC	ACCACCAGTG	GTCATGTTTC	CGGTTCGTTC	ACTGCCGGAC	12900
TGCCTCTGGT	TTACCCGGAC	TGGCTTGCCC	CTGACCATCT	CACGGTTTAC	TGGCGCGTTG	12960
CCGTGCGGTT	TTAAGGGATT	ATTACCATGC	ATCAGCCTCC	CGTTGCGTTT	ACTTACCGCC	13020
TGCTGAGTTA	CCTTATCAGT	ACGATTATCG	CCGGGCAGCC	GTTGTTACCG	GCTGTGGGGG	13080
CCGTCATCAC	CCCACAAAAC	GGGGCTGGAA	TGGATAAAGC	GGCAAATGGT	GTGCCGGTCG	13140
TGAACATTGC	CACGCCGAAC	GGGGCCGGGA	TTTCGCATAA	CCGGTTTACG	GATTACAACG	13200
TCGGGAAGGA	AGGGCTGATT	CTCAATAATG	CCACCGGTAA	GCTTAATCCG	ACGCAGCTTG	13260
GTGGACTGAT	ACAGAATAAC	CCGAACCTGA	AAGCGGGCGG	GGAAGCGAAG	GGTATCATCA	13320
ACGAAGTGAC	CGGCGGTAAC	CGTTCACTGT	TGCAGGGCTA	TACGGAAGTG	GCCGGCAAAG	13380
CGGCGAATGT	GATGGTTGCC	AACCCGTATG	GTATCACCTG	TGACGGCTGT	GGTTTTATCA	13440
ACACGCCGCA	CGCGACGCTC	ACCACAGGCA	AACCTGTGAT	GAATGCCGAC	GGCAGCCTGC	13500
AGGCGCTGGA	GGTGACTGAA	GGCAGTATCA	CCATCAATGG	CGCGGGCCTG	GACGGCACCC	13560
GGAGCGATGC	CGTATCCATT	ATTGCCCCGTG	CAACGGAAAT	GAATGCCGCG	CTTCATGCGA	13620
AGGATTTAAC	TGTCAGTGCA	GGCGCTAACC	GGATAACTGC	AGATGGTCGC	GTCAGTGCCC	13680
TGAAGGGCGA	AGGTGATGTG	CCGAAAGTTG	CGGTTGATAA	CGGCGCGCTC	GGTGGAAATGT	13740
ACGCCAGGCG	TATTCATCTG	ACCTCCACTG	AAAGTGGTGT	CGGGGTAAAT	CTGGGTAAAC	13800
TTTATGCCCG	CGAGGGCGAT	ATCATACTGA	GCAGTCCCGG	AAAAGTGGTC	CTGAAGAACA	13860

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GCCTTGCCGG	CGGCAATACC	ACCGTAACCG	GAACGGATGT	CTCACTTTCA	GGGATAACA	13920
AAGCCGGAGG	AAATCTCAGC	GTTACCGGGA	CAACGGGACT	GACACTGAAT	CAGCCCCGTC	13980
TGGTGACGGA	TAAAAATCTG	GTGCTGTCTT	CATCCGGGCA	GATTGTACAG	AACGGTGGTG	14040
AACTGACTGC	CGGACAGAAC	GCCATGCTCA	GTGCACAGCA	CCTGAACCAG	ACTTCCGGGA	14100
CCGTGAATGC	AGCTGAAAAT	GTCACCCTTA	CCACCACCAA	TGATACCACA	CTGAAAGGCC	14160
GCAGCGTTGC	CGGGAAAACA	CTCACTGTCA	GTTCCGGCAG	CCTGAACAAC	GGTGGGACAC	14220
TGGTTGCCGG	GCGCGATGCC	ACGGTGAAAA	CCGGGACATT	CAGTAATACC	GGTACCGTCC	14280
AGGGGAATGG	CCTGAAAGTT	ACCGCCACTG	ACCTGACCAG	CACCGGCAGT	ATTAAAAGTG	14340
GCAGCACACT	CGATATCAGC	GCCCCGAATG	CCACACTGTC	CGGTGATGCC	GGTGCAAAAG	14400
ACAGTGCCCG	CGTTACCGTC	AGCGGTACAC	TCGAAAACCG	CGGCAGACTT	GTCAGCGATG	14460
ACGTGCTGAC	GCTCAGTGCC	ACGCAGATAA	ACAACAGCGG	TACCCTCTCC	GGGGCAAAGG	14520
AACTTGTGGC	TTCTGCAGAC	AACTGACCA	CCACAGAAAA	ATCGGTCACA	AACAGTGACG	14580
GTAACCTCAT	GCTGGACAGC	GCGTCTTCCA	CACTGGCGGG	TGAAACCACT	GCGGGTGGCA	14640
CGGTGTCTGT	AAAAGGCAAC	AGTCTGAAGA	CCACGACCAC	TGCGCAGACG	CAGGGCAACA	14700
GTGTCAGCGT	GGATGTGCAG	AACGCACAGC	TTGACGGAAC	ACAGGCTGCC	AGAGACATCC	14760
TTACCCTGAA	CGCCAGTGAA	AAGCTCACCC	ACAGCGGGAA	AAGCAGTGCC	CCGTCGCTCA	14820
GCCTCAGTGC	GCCGGAAGTG	ACCAGCAGCG	GCGTACTTGT	TGGTTCCGCC	CTGAATACAC	14880
AGTCACAGAC	CCTGACCAAC	AGCGGTCTGT	TGCAGGGGGA	GGCCTCACTC	ACCGTTAACA	14940
CACAGAGGCT	TGATAATCAG	CAGAACGGCA	CGCTGTACAG	TGCTGCAGAC	CTGACGCTGG	15000
ATATACCGGA	CATCCGCAAC	AGCGGGCTTA	TCACCGGTGA	TAATGGTTTA	ATGTTAAATG	15060
CTGTCTCCCT	CAGCAATCCG	GGAAAAATCA	TCGCTGACAC	GCTGAGCGTC	AGGGCGACCA	15120
CGCTGGATGG	TGACGGCCTG	TTGCAGGGCG	CCGGTGCACT	GGCGCTTGCT	GGCGACACCC	15180
TCTCACAGGG	TAGTCACGGA	CGCTGGCTGA	CGGCGGACGA	CCTCTCCCTC	CGGGGCAAAA	15240
CACTGAATAC	CGCAGGACCA	CGCAGGGACA	GAATATCACC	GTGCAGGCGG	ACAGATGGGC	15300
GAACAGTGGT	TCCGTGCTGG	CAACCGGTAA	CCTTACTGCT	TCGGCAACCG	GTCAGTTGAC	15360
CAGTACCGGC	GATATCATGA	GCCAGGGTGA	CACCACGCTG	AAAGCAGCCA	CCACGGACAA	15420
CCGGGGCAGT	CTGCTTTCGG	CCGGCACGCT	CTCCCTTGAT	GGAAACTCAC	TGGATAACAG	15480
CGGCACTGTC	CAGGGTGACC	ATGTCACGAT	TCGCCAGAAC	AGTGTACCA	ACAGTGGCAC	15540
GCTCACCGGG	ATCGCCGCGC	TGACGCTTGC	CGCCCGTATG	GTATCCCTC	AACCTGCGCT	15600
GATGAATAAC	GGAGGTTTCAT	TGCTGACCAG	CGGCGATCTG	ACAATCACCG	CAGGCAGTCT	15660
GGTAAACAGC	GGGGCGATCC	AGGCGGCTGA	CAGCTGACT	GCACGTCTGA	CGGGTGAGCT	15720
CGTCAGCACA	GCGGGCAGCA	AAGTCACCTC	GAACGGTGAA	ATGGCGCTCA	GTGCCTGAA	15780

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TTTAAGCAAC	AGCGGACAAT	GGATTGCAAA	AAATCTGACC	CTGAAGGCGA	ACTCACTGAC	15840
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CAATCAGGCG	AACGGAAAAC	TGCTCAGTGC	AGGTGTGCTG	ACGCTGAAGG	CAGACAGTGT	15960
CACAAACGAC	GGGCAATTAC	AGGGAAATGC	CACCACCATC	ACGGCAGGAC	AACTCACAAA	16020
CGGCGGGCAT	CTGCAGGGCG	AAACGCTGAC	GCTGGCCGCC	TCCGGTGGCG	TGAACAACCG	16080
TTCCGGTGGT	GTTCTGATGA	GCCGGAATGC	ACTGAATGTC	AGTACTGCGA	CCCTGAGTAA	16140
CCAGGGCACG	ATACAGGGTG	GTGGCGGGGT	TTCCCTGAAC	GCCACTGACC	GTCTGCAGAA	16200
CGACGGCAAA	ATCCTCTCCG	GCAGTAACCT	CACGCTGACG	GCGCAGGTGC	TGGCGAACAC	16260
CGGCAGCGGA	CTGGTACAGG	CTGCCACCCT	GCTGCTGGAT	GTGGTGAATA	CTGTCAACGG	16320
CGGACGCGTA	CTTGCCACCG	GCAGTGCCGA	CGTTAAAGGA	ACCACGCTGA	ATAATACCGG	16380
TACGCTTCAG	GGTGCGGACC	TGCTGGTGAA	TTACCACACA	TTCAGCAACA	GCGGTACCCT	16440
GCTGGGAACC	TCCGGGCTTG	GCSTCAAGGG	CAGTTCAGTG	CTGCAAAATG	GTACAGGGCG	16500
GCTGTACAGT	GCAGGCAACC	TGCTGCTTGA	CGCTCAGGAC	TTCAGTGGTC	AGGGGCAGGT	16560
GGTGGCCACC	GGTGATGTCA	CACTGAAACT	GATTGCTGCC	CTCACGAATT	ACGGTACCCT	16620
GGCCGCAGGG	AAAACCCTTT	CCGTCACGTC	GCAAAATGCC	ATCACCAACG	GCGGTGTCAT	16680
GCAGGGTGAT	GCCATGGTGC	TCCGTGCCGG	AGAGGCATTG	ACCAACAATG	GAACGCTGAC	16740
TGCCGGTAAA	GGCAACAGTG	TTTTCAGCGC	ACAGCGTCTT	TTCCTTAACG	CACCGGGTTC	16800
ACTTCAGGCC	GGTGGCGATG	TGAGTCTGAA	CAGCCGGAGT	GATATCACCA	TCAGTGGTTT	16860
TACCGGCACG	GCAGGCAGTC	TGACAATGAA	TGTGGCCGGT	ACCCTGCTGA	ACAGTGCCT	16920
GATTTATGCG	GGGAATAACC	TGAAGCTGTT	TACAGACCGT	CTGCATAACC	AGCATGGTGA	16980
TATCCTGGCC	GGCAACAGTC	TGTGGGTACA	GAAGGATGCT	TCCGGCGGTG	CAAACACAGA	17040
GATTATCAAT	ACTTCCGGGA	ATATTGAGAC	GCATCAGGGC	GATATTGTTG	TAAGAACCGG	17100
GCATCTTCTG	AACCAGCGGG	AGGGATTTTC	TGCCACAACA	ACAACCCGGA	CTAACCCTC	17160
ATCCATTAG	GGAATGGGAA	ATGCTCTGGT	TGATATTCCC	CTTCCCTTC	TTCCTGACGG	17220
CAGCTATGGC	TATTTACCC	GTGAAGTTGA	AAATCAGCAC	GGTACGCCCT	GCAACGGGCA	17280
CGGGGCATGC	AATATCACAA	TGGATACGCT	TTATTATTAC	GCTCCGTTTG	CTGACAGTGC	17340
CACACAGCGC	TTTCTCAGCA	GCCAGAACAT	CACAACAGTA	ACCGGTGCTG	ATAATCCGGC	17400
AGGCCGCATT	GCGTCAGGGC	GTAATCTTTC	TGCTGAGGCT	GAACGACTGG	AAAACCGGGC	17460
GTCATTTATC	CTGGCGAATG	GGGATATCGC	ACTCTCGGGC	AGAGAGTTAA	GCAATCAGAG	17520
CTGGCAGACG	GGGACAGAGA	ATGAATATCT	GGTATACCGC	TACGACCCGA	AAACGTTTTA	17580
CGGTAGCTAT	GCAACAGGCT	CTCTGGATAA	ACTGCCCTTG	CTGTCACCGG	AATTTGAAAA	17640
CAATACCATC	AGATTTTCAC	TGGATGGCCG	GGAAAAAGAT	TACACGCCCG	GTAAGACGTA	17700

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TTATTCCGTT	ATTGAGGCGG	GCGGGGATGT	TAAGACCCGT	TTTACCAGCA	GTATCAATAA	17760
CGGAACAACC	ACTGCACATG	CAGGTAGTGT	CAGTCCGGTG	GTCTCTGCAC	CTGTACTGAA	17820
TACCTTAAGT	CAGCAGACCG	GCGGAGACAG	TCTGACACAG	ACAACGCTGC	AGCAGTATGA	17880
GCCGGTGGTG	GTTGGCTCTC	CGCAATGGCA	CGATGAACTG	GCAAGTGCCC	TGAAAAATAT	17940
TGCCGGAGGT	TGCCCCACTGA	CCGGTCAGAC	CGGTATCAGT	GATGACTGGC	CACTGCCTTC	18000
CGGCAACAAT	GGATACCTGG	TTCCGTCCAC	GGACCCGGAC	AGTCCGTATC	TGATTACGGT	18060
GAACCCGAAA	CTGGATGGTC	TCGGACAGGT	GGACAGCCAT	TTGTTTGCCG	GACTGTATGA	18120
GCTTCTTGGA	GCGAAACCGG	GTCAGGCGCC	ACGTGAAACG	GCTCCGTCGT	ATACCGATGA	18180
AAAACAGTTT	CTGGGCTCAT	CGTATTTTCT	TGACCGCCTC	GGGCTGAAAC	CGGAAAAAGA	18240
TTATCGTTTT	CTGGGGGATG	CGGTCTTTGA	TACCCGGTAT	GTCAGTAACG	CGGTGCTGAG	18300
CCGGACGGGT	TCACGTTATC	TCAACGGACT	GGGTTCAGAC	ACGGAACAGA	TGCGGTATCT	18360
GATGGATAAC	GCGGCCAGAC	AACAGAAAGG	ACTGGGATTA	GAGTTTGGTG	TGGCGCTGAC	18420
AGCTGAACAG	ATTGCTCAGC	TTGACGGCAG	CATGCTGTGG	TGGGAGTCAG	TCACCATCAA	18480
CGGACAGACA	GTCATGGTCC	CGAAACTGTA	TCTGTCGCCC	GAAGATATCA	CCCTGCATAA	18540
CGGCAGCGTT	ATCAGCGGGA	ACAACGTGCA	GCTTGCGGAC	GGCAATATCA	CCAACAGCGG	18600
CGGCAGCATC	AACGCACAGA	ACGACCTTTC	GCTCGACAGT	ACCGGCTATA	TCGACAACCT	18660
GAATGCAGGG	CTGATAAGCG	CGGGCGGTAG	CCTGGACCTG	AGCGCCATCG	GGGATATCAG	18720
CAATATCAGC	TCAGTCATCA	GCGGTAAAAC	CGTACAACTG	GAAAGCGTGA	GTGGCAACAT	18780
CAGCAATATC	ACCCGGCGTC	AGCAATGGAA	TGCGGGCAGT	GACAGCCGAT	ATGGTGGTGT	18840
GCATCTCAGC	GGTACGGACA	CCGGTCCGGT	TGCGACCATT	AAAGGCACTG	ATTCACTTTC	18900
ACTGGATGCA	GGGAAAAACA	TTGATATTAC	CGGGGCAACG	GTCTCGTCCG	GTGGAGACCT	18960
TGGAATGTCT	GCGGGTAATG	ACATCAACAT	TGCCGTAAAC	CTGATAAGCG	GGAGCAAAAG	19020
TCAGTCCGGT	TTCTGGCACA	CTGATGACAA	CAGTTCATCA	TCCACCACCT	CACAGGGCAG	19080
CAGCATCAGC	GCCGGCGGTA	ACCTGGCGAT	GGCTGCAGGC	CATAATCTGG	ATGTCACAGC	19140
ATCCTCTGTT	TCTGCCGGGC	ACAGCGCCCT	GCTTTCTGCA	GGTAACGACC	TGAGTCTGAA	19200
TGCAGTCAGG	GAAAGCAAAA	ACAGTCGCAA	CGGCAGGTCA	GAAAGTCATG	AAAGCCACGC	19260
AGCTGTGTCC	ACGGTGACGG	CGGGCGATAA	CCTCCTCCTT	GTTGCCGGTC	GTGATATTGC	19320
CAGTCAGGCT	GCCGGTATGG	CTGCGGAAAA	TAACGTGGTC	ATCCGGGGCG	GACGTGATGT	19380
GAACCTGGTG	GCAGAGTCTG	CCGGCGCAGG	CGACAGCTAT	ACGTCGAAGA	AAAAGAAAGA	19440
GATTAACGAG	ACAGTCCGTC	AGCAGGGAAC	GGAAATCGCC	AGCGGTGGTG	ACACCACCGT	19500
CACCGCAGGA	CGGGATATCA	CCGCTGTTGC	GTCATCCGTT	ACCGCAACCG	GCAATATCAG	19560
CGTGAATGCC	GSTCGTGATG	TTGCCCTGAC	CACGGCGACA	GAAAGTGAAT	ATCACTATCT	19620

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GGAAACGAAG	AAAAAAGCG	GAG3TTTTCT	CAGTAAGAAA	ACCACCCACA	CCATCAGTGA	19680
GGACAGTGCC	TCCCGTGAAG	CAG3TTCCCT	GCT3TCGGGG	AACCGCGTGA	CCGTTAACGC	19740
CGGTGATAAN	CTGACGGTAG	AGG3TTCGGA	TGT3GTGGCT	GACCGGGATG	TGTCAGTGGC	19800
GGCGGGTAAC	CATGTTGATG	TTCTTGCTGC	CACCAGTACA	GATACGTCCT	GGCGCTTTAA	19860
GGAAACGAAG	AAATCCGGTC	TGATGGGTAC	CGGCGGTATT	GTTTTCACCA	TTGGCAGCAG	19920
TAAGACAACG	CACGACCGCC	GCGAGGCSGG	GACAACGCAG	AGTCAGAGTG	CCAGTACCAT	19980
CGGCTCCACT	GCCGGTAATG	TCAGTATTAC	CGCGGGCAAA	CAGGCTCATA	TCAGCGGTTC	20040
GGATGTGATT	GCGAACCGGG	ATATCAGCAT	TACCGGTGAC	AGTGTGGTGG	TTGACCCGGG	20100
GCATGATCGT	CGTACTGTGG	ACGAAAAATT	TGAGCAGAAG	AAAAGCGGGC	TGACGGTTGC	20160
CCTTTCCGGC	ACGNTGGGCA	GTGCCATCAA	TAATGCGGTC	ACCAGTGCAC	AGGAGACGAA	20220
GGAGAGCAGT	GACAGCCGTC	TGAAAGCCCT	GCAGGCCACA	AAGACAGCGC	TGTCTGGTGT	20280
GCAGGCCGGA	CAGGCTGCGG	CAATGGCCAC	CGCAACCGGT	GACCCGAATG	CGACGGGAGT	20340
CAGCCTGTCT	CTTACCACCC	AGAAATCGAA	ATCACAACAA	CATTCTGAAA	GTGACACAGT	20400
ATCCGGCAGT	ACGCTGAATG	CCGGGAATAA	TCTGTCTGTT	GTCGCAACCG	GCAAAAACAG	20460
GGGAGATAAC	CGCGGAGATA	TTGTGATTGC	AGGAAGCCAG	CTTAAGGCCG	GTGGTAACAC	20520
AAGCCTGGAT	GCCGCGAATG	ATGTTCTGTT	GAGTGGCGCT	GCAAACACAC	AAAAACAAC	20580
GGGCAGGAAC	AGCAGCAGTG	GCGGTGGCGT	GGGTGTCAGT	ATCGGTGCCG	GTGGTAACGG	20640
TGCCGGTATC	AGCGTCTTTG	CCAGCGTTAA	TGCGGCAAAA	GGCAGCGAGA	AAGGTAACGG	20700
TACTGAGTGG	ACTGAAACCA	CAACAGACAG	CGGTAAACC	GTCACCATCA	ACAGTGGTCG	20760
GGATACGGTA	CTGAACGGTG	CTCAGGTCAA	CGGCAACAGG	ATTATCGCCG	ATGTGGGCCA	20820
CGACCTGCTG	ATAAGCAGCC	AGCAGGACAC	CAGTAAGTAC	GACAGTAAAC	AGACCAGCGT	20880
GGCTGCCGGC	GGCAGTTTTA	CCTTTGGCTC	CATGACCGGC	TCAGGTTACA	TCGCTGCCTC	20940
CCGGGATAAG	ATGAAGAGCC	GCTTTGACTC	CGTTGCTGAA	CAAACCGGGA	TGTTTTCCGG	21000
AGATGGCGGC	TTGATATCA	CGGTGCGCAA	CCACACCCAG	CTCGATGGTG	CGGTTATCGC	21060
TTCCACGGCG	ACGGCAGATA	AAAACAGCCT	CGATACCGGG	ACGCTCGGCT	TCAGCGATAT	21120
TCACAACGAA	GCGGATTATA	AAGTCAGTCA	CAGTGGAATC	AGTCTGAGCG	GTGGTGGCAG	21180
CTTCGGGGAT	AAATTTTCAGG	GTAACATGCC	GGGTGGCATG	ATATCCGCCG	GAGGTCACAG	21240
CGGACATGCG	GAAGGAACGA	CTCAGGCCGC	AGTGGCAGAT	GGCACAATCA	CCATCCGGGA	21300
CAGGGACAAT	CAGAAGCAGA	ATCTGGCGAA	CCTGAGCCGT	GACCCTGCGC	ACGCTAATGA	21360
CAGTATCAGC	CCGATATTTG	ACAAGGAGAA	AGAGCAGAGG	CGTCTGCAGA	CAGTGGGGCT	21420
TATCAGTGAC	ATTGGCAGTC	AGGTGGCGGA	TATCGCGCGG	ACGCAGGGGG	AACTGAATGC	21480
GTTGAAGCTG	CGCAGGATAA	ATATGGGCCT	GTTCCGGCGG	ATGCGACGGA	AGAACAGCGG	21540

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CAGGCATATC TGGCAAAACT GCGTGATACG CCGGAATACA AAAAGGAACA GGAAAAGTAT	21600
GGTACCGGCA GCGATATGCA GCGCGGTATC CAGGCTGCAA CGGCTGCACT TCAGGGCCTG	21660
GTGGGCGGCA ATATGGCAGG CCGGTGGCA GGTGCTTCAG CGCCGGAGCT GGCGAACATC	21720
ATCGGTCATC ACGCGGGTAT TGATGACAAT ACAGCGGCAA AAGCCATTGC CCATGCCATT	21780
CTCGGTGGTG TGACAGCAGC CCTTCAGGGC AACASTGCGG CAGCAGGCGC AATTGGTGCG	21840
GGTACTGGTG AAGTGATCGC GTCAGCCATT GCGAAAAGCC TCTACCCGGG CGTAGATCCG	21900
TCGAAACTGA CAGAAGATCA GAAGCAAACGT GTAAGCACGC TGGCAACGCT GTCAGCGGGT	21960
ATGGCCGGCG GCATTGCCAG TGGCGATGTG GCTGGCGCGG CTGCTGGAGC TGGTGCCGGG	22020
AAGAACGTTG TTGAGAATAA TGGCTGAGT CTGTTGCCA GAGGCTGTGC GGTCGCAGCA	22080
CCTTGCAGGA CTAAAGTTGC AGAGCAGTTG CTAGAAATCG GGGCGAAAGC GGGCATGGCC	22140
GGGCTTGCCG GGGCGGCAGT CAAGGATATG GCCGACAGGA TGACCTCCGA TGAAGTGGAG	22200
CATCTGATTA CCCTGCAAAT GATGGGTAAT GATGAGATCA CTACTAAGTA TCTCASTTCG	22260
TTGCATGATA AGTACGGTTC CGGGGCTGCC TCGAATCCGA ATATCGGTAA AGATCTGACC	22320
GATGCGGAAA AAGTAGAACT GGGCGGTTCC GGCTCAGGAA CCGGTACACC ACCACCATCG	22380
GAAAATGATC CTAAGCAGCA AAATGAAAAA ACTGTAGATA AGCTTAATCA GAAGCAAGAA	22440
AGTGCGATTA AGAAGATCGA TAACACTATA AAAAATGCTC TGAAAGATCA TGATATTATT	22500
GGAAGTCTCA AGGATATGGA TGGTAAGCCA GTTCCTAAAG AGAATGGAGG ATATTGGGAT	22560
CATATGCAGG AAATGCAAAA TACGCTCAGA GGATTAAGAA ATCATGCGGA TACGTTGAAA	22620
AACGTCAACA ATCCTGAAGC TCAGGCTGCG TATGGCAGAG CAACAGATGC T	22671

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT	60
ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGGCA ACTGAAACCC	120
GCTGACGGAT NANGTGTACA GTGGCATCAG TGGACGGM TT ACAGCATAAG TGCTTAAGGC	180
GCGTGACCAT ACAGMTACGG TCGGTGCAGA GAACAGGGAG AATATCATCC GGAACACGGT	240
GGCCATAAAC CGTAACAACA GGGGCTGCT TTCCCCGGA GAGGTGCTGG AGATGCATGC	300
GGACGTCTGA ACAGTCAGCA GGGCTGATTA ATGAGAATCA CGAGGAAATG AAGCGGGAGC	360
CGTACAGTGA GGATAAATTT AACGCCATAG CGGCTGTGGG CGGGTATAGT GCCAAGCAGA	420

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CTGCTTAAAG GCAGGTA	CTTTCAGTGG	CGGCTATGTT	TCCTGGAATG	TGGGTGTCAA	480
CTGGTAGTTC TGAACCCGG	CCTGAGTCAC	CGGGGAGGCA	GTTTTCGGTA	TGAAGTAATG	540
ATTCGCTGCC TGTTTTTCTC	CCTGATGGCA	TAACTGACTG	TTCCCGGGTA	TTCCTGAAGA	600
TCTGAGAGGA AGAGTGTATA	TGCTGAACTA	TCGCATAAGG	TCAGTGCAGC	TATTTATTGT	660
AAACGGTCGG GCTGACAGGG	CGCAGGTGCG	TCTGGAATGC	GACGATGAAG	CCGTTTTTGA	720
ATGTTATCTT CTTGCTGAAG	GGGAAGGGGA	ACTGAAAGAA	CTGAGCCTGT	CAGAGCTGGA	780
AGAGCGGGCG CTGATGTATG	CGGCAGACAG	TTTCCGTTAT	GAATGATAAG	TCAGTTATAC	840
CGGTAATGGT AAACGGAGCC	GGTATCCGGG	ATACAAGGGG	CAGAGAGTAT	GCTGATTATT	900
ATTATGACCC GGGACAGATA	TCTGGAATAT	GGCCTGATGC	GTATACTGAG	CGGATATCAG	960
GTCACGACAG GCAGAGAGCT	GTTTAATGCC	GGAAAGCAAC	GTCAGTCACT	TCCCGAAGAC	1020
AGTTATGTGA TTCTCTGTGA	CCGTAATCTG	GAAAGGCTTA	CATACTCTAT	GTTCTGTGGG	1080
CGTCGGTTTC TTGTCATTCC	TGTTTCCTCT	GTGAGATGCC	TGACAGATAT	CAGGCAAACC	1140
ATCCGCCGTG GAGCGTGGCT	GTTCCGACAT	ACGGCAAGGC	CACTGACCCG	GACAGAGATG	1200
GTGGTGGTCT TCGGGGTTGT	TTTCCATGAC	TACGGGTTTA	CCTTTCTGGC	AGACCGGCTG	1260
GGGATAACCA TGAAGACGGT	ATGTGCGCAT	CTTTACAATG	CGATGGAGAA	AAATGGTATG	1320
CGCGGCGTCA GTATTAAATA	TCTCTGCAAC	ACCATAGACC	GGTAAAAAGA	TGGTTTTCTG	1380
ATAAAGGCTG TTGCGACGGG	GATTTCTGTG	CATGCTGTGT	CACGGGCATC	CCAGCTCTCC	1440
GGATAATTAA TGTTATGTAG	TCAGGCGTGA	TAAATTTTAT	ATGGAACAGG	TATGCGTTTT	1500
ATTTGTGATA ACAGTTAATG	AGGTGTTTTCC	ATACACACTG	AAGTTACCTG	TAATATTAGC	1560
GGGGGATTTG AATGATGTTG	CGTGTCTGCG	ACCACTCGTT	TATTCATGCA	AATAAGTGGA	1620
CTGCTGGATC CACGGTAAGA	GTACAGCGAG	GGCCGTATTG	ACGGGGATGT	GTTATTTCAGC	1680
GGGCAGTGCT ATGCGCCACG	GAAGCAGTTC	GCTGACACGG	TTGACCGGCC	AGTCAGCTAT	1740
GACGCCAAAC ACATGGCGAA	GGTAGTTTTC	TGGATCCTCG	TCGTTCAATT	TGCACGTCCC	1800
GATCAGGCTG TACAGTAGCA	CTCCCCGCTC	ACCACCATGC	TCAGAGCTGC	GTATTACCGT	1860
GAAGGAGATC GGTGAGTAAC	CCTCTGTGTC	GGCACATTAT	AGCCGTCACA	TCGGATAACT	1920
GTTATCCTTC TGTTCTGATG	TATTCTGGGA	GGTGATGTTT	CACTCCTGAT	AAGAGCATTG	1980
CTAATTACAG CTGCTTTTTCG	GATAACATTC	GGGCAGTTTT	CTTTAATTCT	GAAGTCTGAA	2040
AGAGATATCA GTAATTGTAT	TGCTTTTAAA	CATTGTCAGT	ATTTATTTGT	CCAAATCGTT	2100
CACGTTTCTC ATAATCTTCC	CGACAGTCAC	CATCACAAAA	CAATCCAGTC	TTAACAGGTT	2160
CTCCGCAGTT ATAGCAGAAT	CCTGTTTCAG	GGAGTCTATT	CCGGATACGA	TTTTTTAGTC	2220
TGATGCTCAT GCTGAATTGT	TCATTTTTCAT	AAGCAATATC	TGCACTATCT	GCCATAAACG	2280
ATCCTCTGAG GAGACCACAT	CTTTATAACC	CACCACCGAA	ATATTACAAA	GTAATACTCA	2340

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TTGTATAATC TTTAACCRGG GGCAGGATAA TTGTATCCTG CCCCT

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(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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CTTTCAGACC AGCGTTTCCT GTCAGGAGAT GAGGAAGAAA CATCAAAGTA TAAAGGCGGC      60
GATGACCATG ATACGGTATT CAGTGGGGGT ATTGCGGGCG GTTATGATTT TTATCCGCAG      120
TTCAGTATTC CGGTTTCGTAC AGAACTGGAG TTTTACGCTC GTGGAAAAGC TGATTCGAAG      180
TATAACGTAG ATAAAGACAG CTGGTCAAGT GGTTACTGEC GTGATGACCT GAAGAATGAG      240
GTGTCAGTCA ACACACTAAT GCTGAATGCG TACTATGACT TCCGGAATGA CAGCGCATTC      300
ACACCATGGG TATCCGCAGG ATTGGCTACG CAGAATTCAC CAGAAAACAA CCGGTATCAG      360
TACCTGGGAT TATGAGTACG GAAGCAGTGG TCGCGAATCG TTGTCACGTT CAGGCTCTGC      420
TGACAACTTC GCATGGAGCC TTGGCGCGGG TGTCCGCTAT GACGTAACCC CGGATATCGC      480
TCTGGACCTC AGCTATCGCT ATCTTGATGC AGGTGACAGC AGTGTGAGTT ACAAGGACGA      540
GTGGGGCGAT AAATATAAGT CAGAAGTTGA TGTTAAAAGT CATGACATCA TGCTTGGTAT      600
GACTTATAAC TTCTGACGAC ACTGCTCCTG AACGATAATT GCGTATATTC TGTAATTAAG      660
ATAATTGCAT ATCTCTGCA ATTAACACAGA AATACCCTGC AGTCTATTAC TGCAGGGNTG      720
TCTTTTATCT GTTTTACAGA NAATTT      746

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(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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TCTGTTTGTC GTTTTTTCCC CGTTGTAGCG GYTCTGCTCC TGGCTTCCCT GATAGTCAGC      60
CCGCAGGCGC CAGGGCCCCA GATTCCCCC CACAGTCCCG TTATAACTGA ACTGATGAGA      120
GTCTCCTCCC TGATAATTAC GGGAAACCGT CCCGTTGAGG TTATAATCCA GCATCAGTCC      180
GGGAATGCCG TCGTCCCAGC GTGAGAGAGG CAGCCAGGTG GCATCAGAAT ACTCAAGCCC      240
AGCTGCGGCA TATTGATGG TAATACGCC GCTCCGGTAT CAGGACGAAT ATCCACTCCC      300
GGCAACCCAT GAAAATCCGC ACACTGACCA TCATGCCAGT AAACAACTTT ATCCAGAGAT      360

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TC TGCTGTTA ACCCCATCAG TCTGACCATA TCTGATGTCA GACAGGCCTG C 411

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 977 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TATTATCGCG CGCGCGCTGC ACAGGGGTTA TCTACATCTG CTGCTGCTGC CGGTTTAATT 60
 GCTTCTGTAG TGACATTAGC AATTAGTCCC CTCTCATTC TGTCCATTGC CGATAAGTTT 120
 AAACGTGCAA ATAAATAGA GGAGTATTCA CAACGATTCA AAAAATTGG ATACGATGGT 180
 GACAGTTTAC TTGCTGCTTT CCACAAAGAA ACAGGAGCTA TTGATGCATC ATTAACAACG 240
 ATAAGCACTG TACTGGCTTC AGTATCTTCA GGTATTAGTG CTGCKGCAAC GACATCTCTT 300
 GTTGGTGCAC CGGTAAGCGC ACTGGTAGGT GCTGTTACGG GGATAATTC AGGTATCCTT 360
 GAGGCTTCAA AGCAGGCAAT GTTGAACAT GTTGCCAGTA AAATGGCTGA TGTTATTGCT 420
 GAATGGGAGA AAAAACACGG TAAAAATTAC TTTGAAAATG GATATGATGC CCGCCATGCT 480
 GCATTTTTAG AAGATAACTT TAAAATATTA TCTCAGTATA ATAAAGAGTA TTCTGTTGAA 540
 AGATCAGTCC TCATTACTCA ACAACATTGG GATATGCTGA TAGGTGAGTT AGCTAGTGTC 600
 ACCAGAAATG GAGACAAGAC ACTCAGTGGT AAAAGTTATA TTGACTATTA TGAAGAGGGA 660
 AAGCGGCTGG AAAGAAGGCC AAAAGAGTTC CAGCAACAAA TCTTTGATCC ATTAAAAGGA 720
 AATATTGACC TTTCTGACAG CAAATCTTCT ACGTTATTGA AATTTGTTAC GCCATTGTTA 780
 ACTCCCGGTG AGGAAATTCG TGAAAGGAGG CAGTCCGGAA AATATGAATA TATTACCGAG 840
 TTATTAGTCA AGGGTGTGA TAAATGGACG GTGAAGGGGG TTCAGGACAA GGGGTCTGTA 900
 TATGATTACT CTAACCTGAT TCAGCATGCA TCAGTCGGTA ATAACCAGTA TCGGGNAATT 960
 CGTATTGAGT CACACCT 977

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCTTAAGT CCGGCATTGC CACGCGTAAC CCCCACTTCA ACCGCATGAT TGAGCAGATC 60
 GAAAAAGTGG CGATCAAATC CCGCGCGCCG ATTCTGCTTA ACGGTCCAAC CGGCGCGGGC 120

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AAGTCATTTT	TGGCGCGACG	CATCTTAGAG	TTAAAACAGG	CGCGGCATCA	GTTTAGCGGC	180
GCKTTTGTGG	AAGTGAAGT	CGCCACCCCTG	CGCGGCGATA	CCGCCATGTC	GACGCTGTTT	240
GGTCATGTAA	AAGGCGCGTT	TACCGGGGCG	CGGGAATCTC	GTGAAGGTTT	ATTACGCAGC	300
GCCAACGGGG	AAATGTTGTT	TCTTGATGAG	ATTGGCGAAC	TGGGCGCGAC	GAACAGGCAA	360
TGCTGCTGAA	ACCCATTGAA	GRGGA AAAAC	TTTTACCCGT			400

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GTATGCGTTT	TCATTAAGAT	ATTCTCTGCT	GTAAGAAAAC	TTATAGCAAT	ATAATCTGAT	60
AATATCTTTT	ATGTAAAATT	TAAATAGTTC	ACCTGTGACA	GATATATGTT	TTCTGCTCAG	120
TAACCTCTGT	GTATTAAGCC	ATTCCCGTGA	CCGAAGCACA	CCCTTGTAAG	AACTTTTTCT	180
TACTTGCTTT	GAGGCACGGC	ATTGATGTAA	TATTTTGTGG	TCCTCAATAA	TTCTCTTTCC	240
CGTTTTATTT	TTTGCAGCAT	CTCTTACTCC	ATAAAATATC	TCCCGGTCCA	GACTTTTGTC	300
ATATTTACTG	ATTATACGAC	AAATATTCCT	GACCCGACGA	TTCTCTTTAT	TTGCTTCCA	360
TAGCTTATAA	TGATCATCGC	ATAACCTTAA	GGCATTGTGC	TCATCAAATT	CTGAAACAGG	420
ATTACTGCAT	TTTTTATTCC	GACAAATACC	TTTGTTTTGA	GCCATACTCT	TCTTCCCGTC	480
AATGGAAAAA	TTTTCACACC	CATATTACCT	GAATGATAAA	CCGGATTAGT	GTGATCCGGT	540
TCAGTGAAAT	CAACAGGATA	CCGGTATGCC	ATTCAGCAAT	TCTTCCCTCT	CCGCGCAAGT	600
GAAATCATAT	CTGACGTTTC	TTCCTGAAGA	AATACGCCAG	AAAATCCTTG	AACATCTCCA	660
CGGTGTTATT	CATTACGAGC	CCGTGATTGG	CATTATGGGT	AAATCCGGCA	CCGGCAAGAG	720
CAGCCTGTGT	AATGCCATTT	TTCAGTCCCG	TATCTGCGCC	ACGCATCCCC	TGAACGGCTG	780
CACCCGCCAG	GCTCATCGTC	TTACCCTGCA	GCTCGGTGAA	CGCAGAATGA	CGCTGGTCCA	840
TCTGCCCCGC	ATTGGTGAAA	CACCGCAGCA	TGATCAGGAA	TACCGAGCGC	TTTATCGTCA	900
GTTACTGCCG	GAAGTGGATC	TGATTATCTG	GATCCTGCGG	AGTGATGAAC	GTGCGTATGC	960
TGCCGATATT	GCCATGCATC	AGTTTTTACT	GAATGAGGGC	GCAGATCCCT	CGCGCTTTCT	1020
GTTTGTCTCT	AGCCATGCCG	ATCGCATGTT	TCCTGCTGAA	GAATGGAATG	CCACAGAAAA	1080
ATGCCCGTCC	CGTCACCAGG	AACTCTCACT	GGCGACAGTA	ATAGCCCAGG	TGGCCACCCT	1140
GTTCCCTTCA	TCATTTCCGG	TACTCCCTGT	AGCCGCACCT	GCAGGCTGGA	ACCTTCCAGC	1200
GCTGGTGTCA	CTGATGATCC	ACGCGCTGCC	ACCACAGGCA	ACCAGCGCAG	TTTATTCACA	1260

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TATCAGGGGG	GAAAACCGCT	CTGAACAGGC	CCGGAAACAC	GCACAACAGA	CTTTTGGTGA	1320
TGCCATCGGG	AAAAGTTTTG	ACGACGCCGT	TGCCCCGGTT	AGTTTTCCGG	CCTGGATGTT	1380
ACAGCTTCTG	CGTAAAGCCC	GGGACCGCAT	TATCCACCTG	CTGATCACAC	TGTGGGAGCG	1440
TCTGTTCTGA	CACACTCACG	CCGACAGATG	TGTCGCTGGA	TTAACGAGCA	TTCTTCTTTT	1500
TATGAAATCA	TGCTTAAAAA	TCAGATAATT	ARAAGAATAT	TTTTTCTGCT	GCATTTTATT	1560
CCTGATTATC	CGGATGCGAC	ACATCCTTTC	AACATCATGA	TGCATAATAA	CATCATGAAA	1620
TAAAAGATGT	TTTCTTACGG	AGTGCACATC	TATGTCTGAT	AATCGTTCCC	GGCATGATCG	1680
CCTGGCGGTT	CGCTTATCAC	TCATTATCAG	CCGACTGATG	GCCGGAGAAT	CTCTGTCACT	1740
AAAAAACTG	TCAGATGAAT	TTGGCGTTAC	AGAACGTAAT	TTACAGCGCG	ATTTTCATCA	1800
GCGTCTGGTT	CACCTAGATT	TAGAGTACAG	AAATGGCAGG	TACAGCCTCA	GACGACAGAG	1860
CAGCCCAGGT	GCGATCCCTG	AAATGCTTTC	TTTTATACAG	AATACCGGGA	TCGCACGGAT	1920
ACTTCCGCTC	CGGAACGGAC	GACTGATAAC	CTGTCTTACC	GACAACCAGG	AGCCCTCTCC	1980
CTGCCTTATC	TGGCTACCGG	CGCCGGATAT	CACTGCAACG	TTCCCCGAGT	GTTTCTCGCA	2040
ACTCATCCTG	GCAATAAGAC	AGTGTATCCA	CATCTCTCTG	ATGACTGAGC	GATGGTATCC	2100
GTCACTGGAG	CCCTGCCGGC	TCATTTATTA	CAGCGGTAGC	TGGTATCTGA	TCGCGTTACA	2160
GAAGGGAAAA	CTGCAGGTCT	TTCCTCTGGC	AGATATCAAA	TCAGTCAGCC	TGACATCAGA	2220
ACGGTTTGAA	CGGAGAGGCC	ACATCCACAG	TCTGGTCGCT	GAAGAGCGTT	TTATCTCCGC	2280
CCTGCCACAT	TTCTCTTTCA	TCCATAAACT	TATCAACACC	TTTAACCTGT	GATCGCCGGC	2340
CTGCCAAAGC	CGTCCCGACA	GGTATGGAGA	CAATATGTTG	AACAGAAAAC	TAAATATACG	2400
GCTACGTCAT	TCCCTGAACA	GTCACTGCAT	ACCTTCCATC	ATTATCAATA	ACACCGTACG	2460
TTCATTTTCA	AGGTACAGTCA	TGAATACCAG	AGCTCTTTTT	CCCCTGCTGT	TCACTGTGGC	2520
ATCATTCTCC	GCCTCCGCCG	GCAACTGGGC	TGTCAAAAAC	GGCTGGTGTC	AGACCATGAC	2580
GGAAGATGGT	CAGGCGCTGG	TAATGCTGAA	AAATGGCACG	ATTGGTATTA	CCGGCCTGAT	2640
GCAGGGATGC	CCGAATGGTG	TACAGACGCT	CCTGGGCAGC	CGTATCAGTA	TTAACGGTAA	2700
CCTGATCCCC	ACATCACAAA	TGTGTAATCA	GCAGACGGGA	TTCAGGGCTG	TTGAGGTGGA	2760
AATCGGACAG	GCGCCGGAAA	TGGTCAAAAA	AGCCGTTTAC	TCCATAGCAG	AGCGTGATGT	2820
GTCCGTTTTA	CAGGCATTTG	GTGTACGAAT	GGAATTCACC	CGCGGTGATA	TGCTGAAGGT	2880
CTGTCCGAAA	TTTGTACAT	CACTTGCCGG	TTTTTCCCCG	AAACAGACGA	CCACTATTAA	2940
TAAAGATTCC	GTCTGCAGG	CTGCCCCGCA	GGCATAACGC	CGGGAATATG	ACGAGGAAAC	3000
AACAGAAACC	GCTGATTTTG	GCTCTTACGA	AGTAAAAGGC	AATAAGGTTG	AGTTTGAAGT	3060
ATTCAATCCT	GAAGACCGTG	CGTACGACAA	AGTGACCGTC	ACGGTTGGTG	CTGACGGTAA	3120
TGCCACCGGC	GCCAGCGTTG	AATTTATCGG	AAAATAGCCG	GTATGTCGGA	CTGCCACCCT	3180

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GTTTTATTGC	CCGAAGGCCC	TTTCTCACGC	GAACAGGCCA	TGGCTGTCAC	AACAGCTTAC	3240
CGCAATGTGC	TTATTGAAGA	TGACCAGGGA	ACGCATTTCC	GGCTGGTTAT	CGCAATGCC	3300
GAAGGGCAGC	TACGCTGGCG	GTGCTGGAAT	TTTGAACCTG	ATGCGGGAAA	ACAGCTAAAT	3360
TCGTATCTCG	CCAGTGAGGG	AATTCTCAGG	CAATAAACGT	CTTCATTTCA	TCCATCAGGC	3420
CGCGTCTTCT	CCGGGAGACG	CGGCCTTTTC	GTTTATACCG	CTAATTCATT	CATAAGGAGC	3480
AAAGTATGCA	ATTAGCCAGT	CGTTTTGGTC	ATGTAAATCA	GATCCGTCGG	GAGCGCCAC	3540
TGACACGCGA	AGAACTGATG	TACCACGTCC	CGAGTATTTT	TGGAGAAGAC	CGGCACACCT	3600
CCCGCAGTGA	ACGGTATGCG	TACATTCCCA	CCATCACCCT	CCTGGAAAAT	CTGCAGCGGG	3660
AAGGCTTTCA	GCCGKCTTC	CCCTGCCAGA	CCCGTGTGGG	CGACCAGAGC	CGCCGGGAAT	3720
ATACCAACA	TATGCTGCGT	CTGCGGCGGG	CCGGACAGAT	AACCGGTCAG	CATGTGCCTG	3780
AAATTATTCT	GCTCAACTCC	CATGACGGTT	CATCCAGCTA	CCAGATGTTA	CCCGGATATT	3840
TTCGTGCCAT	TTGTACCAAT	GGCCTGGTCT	GCGGTCAGTC	GCTGGGAGAA	GTCCGGGTGC	3900
CACACCGGGG	AAACGTGGTG	GACAGGGTCA	TAGAAGGTGC	TTACGAAGTG	GTGGGCGTGT	3960
TTGACCTGAT	TGAGGAAAAG	CGTGATGCCA	TGCAGTCGCT	GGTCCTGCCG	CCACCGGCAC	4020
GCCAGGCGCT	GGCACAGGCG	GCGCTGACTT	ACCGTTATGG	TGATGAACAT	CAGCCCGTCA	4080
CCACTACCGA	CATTCTGACG	CCACGACGCC	GGGAGGATTA	CGGTAAGGAC	CTGTGGAGTG	4140
CTTATCAGAC	CATCCAGGAG	AATATGCTGA	AAGGCGGGAT	TTCCGGTCGC	AGTGCCAGAG	4200
GAAAACGTAT	CCATACCCGG	GCCATTACAC	GCATCGATAC	CGACATTAAG	CTCAACCGGG	4260
CGTTGTGGGT	GATGGCAGAA	ACGCTGCTGG	AGAGCCTGCG	CTGATACCGT	TTCCCTGAAA	4320
GCGCAGTCCT	GTTACGGGCT	GTCCCTTCCC	CCAGACATTC	CACCATTCTAT	TTACTTTTTTA	4380
TAAGGAATAA	TCTCATGACA	ACCTCTTCGC	ATAATTCCAC	CACACCTTCT	GTTTCCGTGG	4440
CCGCTGCATC	AGGAATAAAC	CAGTCTCAGT	TGGTTGCCAC	TCCCGTCCCT	GATGAACAGC	4500
GCATCAGCTT	CTGGCCGCAG	CATTTTGGCC	TCATTCCACA	GTGGGTCACC	CTGGAGCCCC	4560
GTGTCTTCGG	CTGGATGGAC	CGTCTGTGCG	AAAACACTG	CGGGGGTATC	TGGAATCTGT	4620
ACACCCTGAA	CAACGGTGGC	GCATTTATAG	CACCTGAACC	GGATGAAGAT	GATGGAGAAA	4680
CCTGGATACT	GTTCAATGCC	ATGAACGGTA	ACCGCGCTGA	AATGAGCCCC	GAAGCTGCCG	4740
GCATTGCCGC	CTGTCTGATG	ACGTACAGCC	ATCATGCCTG	TCGTACGGAG	AATTATGCCA	4800
TGACGGTCCA	TTATTACCGG	TTGCGGGATT	ACGCCCTGCA	GCATCCGGAA	TGCAGCGCCA	4860
TTATSCGCAT	CATTGACTGA	AAGGGGCCGG	AATAATGCAA	CAGATTCCT	TTCTGCCCGG	4920
AGAAATGACG	CCCGGCGAGC	GCASTCACAT	TCTGCGGGCC	CTGAAAACCC	TGGACCGCCA	4980
TCTTCATGAA	CCCGGTGTGG	CCTTCACCTC	CACCCGTGCG	GCACGGGAAT	GGCTGATTCT	5040
GAACATGGCG	GGA CTGGAGC	GTGAAGAGTT	CCGGGTGCTG	TATCTGAATA	ACCAGAATCA	5100

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GCTGATTGCC	GGTGAAACCC	TCTTCACCGG	CACCATCAAC	CGCACGGAAG	TCCATCCCCG	5160
GGAAGTGATT	AAACGCGCCC	TGTACCACAA	TGCGGCTGCC	GTGGTGCTGG	CGCACAATCA	5220
CCCGTCCGGT	GAAATCACAC	CCASTAAGGC	AGACCGGCTT	ATCACCGAAC	GTCTGGTACA	5280
GGCACTGGGC	CTGGTGGATA	TCCGGGTGCC	GGACCATCTG	ATAGTCGGTG	GCAGCCAGGT	5340
TTTCTCCTTT	GCGGAACACG	GTCTGCTTTA	ACCCGTCACC	GTCACAATCA	CCTTCATATC	5400
ACTTCAGTTT	CTCTTTCTCA	GCTGTTTCTT	ACTTTCACAT	TCAGGAGGAC	TATTCTCATG	5460
AAAATCATCA	CCCGTGGTGA	AGCCATGCGT	ATTCACCGTC	AGCATCCTGC	ATCCCGTCTT	5520
TTTCCGTTCT	GTACCGGTAA	ATACCGCTGG	CACGGTAGCA	CGGATACATA	TACCGGCCGT	5580
GAAGTACAGG	ATATTCCCGG	TGTGCTGGCT	GTGTTTGCTG	AACGCCGTAA	GGACAGTTTT	5640
GGCCCGTATG	TCCGGCTGAT	GAGCGTCACC	CTGAACTGAA	TCAGGACGGG	CATTCAGAAG	5700
AGCAGAATTA	TCGCCACCAC	CGGACCATTG	TTAACCAATT	TTCTGTGAGG	ATTTTATCGT	5760
GTCAGACACT	CTCCCCGGGA	CAACGCATCC	CGACGATAAC	AACGACCGCC	CCTGGTGGGG	5820
GCTACCCTGC	ACCGTGACGC	CCTGTTTTGG	GGCACGTCTG	GTGCAGGAGG	GTAACCGGTT	5880
GCATTACCTT	GCAGACCGCG	CCGGTATCAG	AGGCCGGTTC	AGCGACGCGG	ATGCGTACCA	5940
TCTGGACCAG	GCCTTTCCGC	TGCTGATGAA	ACAACTGGAA	CTCATGCTCA	CCAGCGGTRA	6000
ACTGAATCCC	CGCCATCAGC	ATACCGTCAC	GCTGTATGCA	AAAAGGCTGA	CCTGCGAANC	6060
GACACCCTCG	GCAGTTGTGG	CTACGTTTAT	ATGGCTGTTT	ATCCGACGCC	CGAAACGAAA	6120
AAGTAACTCT	CCAGAATAAC	CTTCTGCCCC	GGCCTGGTGC	TTTACCACCG	CCACTTTTCC	6180
ATTTTTCATC	TCTGCATATC	AGGAAAATCT	TCAGTATGAA	CACATTACCC	GATACACACA	6240
TACGGGAGGC	ATCGCATTGC	CAGTCTCCCC	TCACCATCTG	GCAGACACTG	CTCACCCGAC	6300
TGCTGGACCA	GCATTACGGC	CTCACACTGA	ATGACACACC	GTTCGCTGAT	GAACGTGTGA	6360
TTGAGCAGCA	TATTGAGGCA	GGCATTTCAC	TGTGTGATGC	GGTGAACTTT	CTCGTTGAAA	6420
AATACGCACT	GGTGCGTACC	GACCAGCCGG	GATTACGCGC	CTGTACTCGT	TCTCAGTTAA	6480
TAAACAGTAT	TGATATCCTC	CGGGCCCCGC	GGGCAACCGG	CCTGATGGCC	CGCGACAATT	6540
ACAGAACGGT	AAATAACATT	ACCCTGGGTA	AGCATCCGGA	GAAACGATGA	AACTTTCCCT	6600
GATGCTGGAA	GCCGACAGAA	TTAATGTGCA	GGCACTGAAC	ATGGGGCGAA	TTGTCGTTGA	6660
CGTCGATGGT	GTTAATCTCA	CTGAACTGAT	TAACAAGGTC	GCTGAAAACG	GTTATTCACT	6720
CCGCGTGGTG	GAGGAATCCG	ACCAACAGTC	AACCTGCACA	CTACCACCGT	TTGCAACCCT	6780
TGCCGGCATA	CGCTGCAGTA	CCGCACATAT	CACGGAAAAG	GATAACGCCT	GGCTGTACTC	6840
GCTGTACAC	CAGACCAGTG	ACTTCGGTGA	ATCAGAATGG	ATTCATTTCA	CAGGTAGCGG	6900
ATATCTGTTA	CGTACCGATG	CGTGGTCATA	TCCGTTCTG	CGGCTTAAAC	GCCTGGGGCT	6960
GTCAAAAACG	TTCCGTCGTC	TGGTTATCAC	ACTTACCCGA	CGTTATGGCG	TCAGTCTCAT	7020

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TCATCTGGAT GCCAGCGCTG AATGCGTGCC GGGTTTACCC ACTTTCAACT GGTAACCAGG	7080
AACAACATGA AATCATTAAC CACGGAAACC GCACTGGATA TTCTGATTGC GTGGCTGCAG	7140
GACAATATCG ACTGCGAATC GGGAATTATC TTTGACAACA ATGAGGATAA AACGGATTCA	7200
GCAGCACTGT TGCCCTGTAT CGAAGAGGCC AGAGAGGATA TCCGTACCCT GCGCCAACTG	7260
CAGCTTCAGC ACCAGAACCG GTGAGTCTCA CTCATCATCT CACTCACCAG ACTTCATTCC	7320
ACTSACGCCA GCCTGAACAC GGCTGCGGTT TTCATTTATC TGCAAAAAGG AATATCGATT	7380
ATGTCTGAAA TCACAGTCTC CCGTCCGGAA GTGGTCAACG AGAATACGGA CGTTATCTGC	7440
TCCACCTCAG TCAGGTACAG GTCACTGGAA TATGATAATT TTCCGGAAAT CAGCGAAGCG	7500
AACATTCTGA GCACATTTGA ACAACTGCAC CAGAACAAAG ATGAAGTCTT TGAACGGGGA	7560
GTGATCAACG TCTTCAAAGG GCTGAGCTGG GATTACAAA CCAACTCACC CTGTAAATTT	7620
GGCAGTAAAA TTATCGTCAA CAATCTGGTG AGATGGGACC AGTGGGGATT TCATCTTATC	7680
AGTGAATGC AGGCAGATCG CCTGGCTGAC CTGGAAAGAA TGTTGCATCT GCTCAGCGGT	7740
AAACCGATCC CCGACAACCG AGGGAATATC ACCATTAATC TGGATGACCA CATAAGTCC	7800
GTTCAGGGTA AAGGACGCTA TGAAGATGAG ATGTTTCATCA TTAAATACTT TAAGAAGGGA	7860
TCTGCACACA TCACTTTCAA AAGGCTGGAG CTGATTGACA GAATTAACGA TATAATAGCC	7920
AGGCACTTTC CTTCTGTGCT CTCAGCCTGA CCCCAGATTT GATTCCCTTT CGATATCAAA	7980
AGGGACTGCG GGTACAAAAG AGGGTACATC TTTACCAAAA CCAAACAAAA TAAACTAATA	8040
TCAACATGAT AGAAGCATTG TTCGATTCCG AGTCCGGCAC CAAATTCATA TAAACGGACC	8100
TCCACGGAGG TCCGTTTTTC GTTTCAGGAC GCCACGATTT AAGCGTCCTG CCGCCAAATC	8160
AATTCTACCG AACTCAACCA GATTCTCCCC ACATCACCAG CAATTTGCGG GCATATCCCA	8220
ATTCGGGAAA ATTTGTTTCT GAGCTATAGC GCTGACTGAC GTGAAATGTC GTGCGGCCCC	8280
GTGATGCTGT TGAAMGTCAA ATGACGTCAT CAGGAGCGTA ACGCACCCTT AAAGCACAAC	8340
ATCGGGCAGA ACGCCAACTG ATGAGATTTT CTGAATGAGA ACAAAGAGAA ATGTATCAGT	8400
CCGTTTGCTC ATGCAAAGAC TAACAATCCA TTAAATAGT AAGCGCTCCG GACAATTTTC	8460
CATGGATTAT TTTCTGAACA TTTTCTTTG GCAAAGATGA TGAATTTTGA TGGTAAGGAA	8520
AATTACTTCT GGTTCCTCAGT AAAATCCTTT CGTAATACTA TGTAATCAAG AAGTTTATGG	8580
CTAGTAAAAA TAACGTCTTG CATTACCAAA TAATATGTAA ATAAACCCAT CTATAGATGG	8640
AAAAAATAGG TTATGGAATT ATCATTGCAT CATTCCCTTT TCGAATGAGT TTCTATTATG	8700
CAACAACCTG TAGTTCGCGT TGGCGAATGG CTTGTTACTC CGTCCATAAA CCAAATTAGC	8760
CGCAATGGGC GTCAACTTAC CCTTGAGCCG AGATTAATCG ATCTTCTGGT TTTCTTTGCT	8820
CAACACAGTG GCGAAGTACT TAGCAGGGAT GAACTTATCG ATAATGTCTG GAAGAGAAGT	8880
ATTGTCACCA ATCAGCTTGT GACGCAGAGT ATCTCAGAAC TACGTAAGTC ATTAAAAGAT	8940

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AATGATGAAG ATAGTCCTGT CTATATCGCT ACTGTACCAA AGCGCGGCTA TAAATTAATG	9000
GTGCCGGTTA TCTGGTACAG CGAAGAAGAG GGAGAGGAAA TAATGCTATC TTCGCCTCCC	9060
CCTATACCAG AGGCGGTTCC TGCCACAGAT TCTCCTCCC ACAGTCTTAA CATTCAAAAC	9120
ACCACAACGC CACCTGAACA ATCCCCAGTT AAAAGCAAAC GATTCACTAC CTTTTGGGTA	9180
TGGTTTTTTT TCCTGTTGTC GTTAGSTATC TGTGTAGCAC TGGTAGCGTT TTCAAGTCTT	9240
GAAACACGTC TTCCTATGAG TAAATCGCGC ATTTTGCTCA ATCCACGCGA TATTGACATT	9300
AATATGGTTA ATAAGAGTTG TAACAGCTGG AGTTCTCCGT ATCAGCTCTC TTACGCGATA	9360
GGCGTGGGTG ATTTGGTGGC GACATCACTT AACACCTTCT CCACCTTTAT GGTGCATGAC	9420
AAAATCAACT ACAACATTGA TGAACCGAGC AGTTCGGGTA AAACATTATC TATTGCGTTT	9480
GTTAATCAGC GCCAATACCG TGCTCAACAA TGCTTTATGT CGGTAAAATT GGTAGACAAT	9540
GCAGATGGTT CAACCATGCT GGATAAACGT TATGTCATCA CTAACGGTAA TCAGCTGGCG	9600
ATTCAAAATG ATTTGCTCCA GAGTTTATCA AAAGCGTTAA ACCAACCGTG GCCACAACGA	9660
ATGCAGGAGA TGCTCCAGCA AATTTTGCCG CATCGTGGTG CGTTATTAAC TAATTTTAT	9720
CAGGCACATG ATTATTTACT GCATGGTGAT GATAAATCAT TGGATCGTGC CAGTGAATTA	9780
TTAGGTGAGA TTGTTCAATC ATCCCCAGAA TTTACCTACG CGAGAGCAGA AAARGCATTR	9840
GTTGRTATCG TGCGCCATTC TCAACATCCT TTAGACGRAA AACAATTAGC CAGCACTGAA	9900
CACAGAAATA GATAACATTG TTACACTGCC GGAATTGAAC AACCTGTCCA TTATATATCA	9960
AATAAAAGCG GTCAGTGCCC TGGTAAAAGG TAAAACAGAT GAGTCTTATC AGGCGATAAA	10020
TACCGGCATT GATCTTGAAA TGTCCTGGCT AAATTATGTG TTGCTTGGCA AGGTTTATGA	10080
AATGAAGGGG ATGAACCGGG AAGCAGCTGA TGCATATCTC ACCGCCTTTA ATTTACGCCC	10140
AGGGGCAAAC ACCCTTTACT GGATTGAAAA TGGTATATTC CAGACTTCTG TTCCTTATGT	10200
TGTACCTTAT CTCGACAAAT TTCKCGCTTC AGAATAAGTA ACTCCGGGT TGATTCATGC	10260
TCGGGAATAT TTGTTGTTGA GTTTTTGTAT GTTCCCGTTG GTATAATATG GTTCGGCAAT	10320
TTATTTGCCG CATAATTTTT ATTACATAAA TTTAACCAGA GAATGTCACG CAATGCATTG	10380
TAAACATTGA ATGTTTATCT TTTCATGATA TCAACTGCG ATCCTGATGT GTTAATAAAA	10440
AACCTCAAGT TCTCACTTAC AGAAACTTTT GTGTTATTTT ACCTAATCTT TAGGATTAAT	10500
CCTTTTTTTCG TGAGTAATCT TAGCGCCAGT TGGTCTCGT CAGGAAATAG TTATACATCA	10560
TGACCCGGAC TCCAAATTCA AAAATGAAAT TAGGAGAAGA GCATGAGTTC TGCCAAGAAG	10620
ATCGGGCTAT TTGNCCTGTA CCGGTGTTGT TGCCGGTAAT ATGATGGGGA GCGGTATTGC	10680
ATTATTACCT GCGAACCTAG CAAGTATCGG TGGTATTGCT ATCTGGGGTT GGATTATCTC	10740
TATTATTGGT GCAATGTCGC TGGCATATGT ATATGCCCGA CTGGCAACAA AAAACCCGCA	10800
ACAAGGTGGC CCAATTGCGT ATGCCGGAGA AATTTCCCT GCATTTGGTT TTCAGACAGG	10860

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TGTTCTTTAT TACCATGCTA ACTGGATTGG TAACCTGGCA ATTGGTATTA CCGCTGTATC	10920
TTATCTTTCC ACCTTCTTCC CAGTATTAAA TGATCCTGTT CCGCGGGTA TCGCTGTTAT	10980
TGCTATCGTC TGGGTATTTA CCTTTGTGAA TATGCTCGGC GGTACCTGGG TAAGCCGTTT	11040
AACCACGATT GGTCTGGTGC TGGTTCTTRK TCCTGTGGTG ATGACTGCTA TTGTTGGCTG	11100
GCATTGGTTT GATGCAGCAA CTTATGCAGC TAACTGGAAT ACTGCGGATA CCACTGATGG	11160
TCATGCGATC ATTAAAAGTA TTCTGCTCTG CCTGTGGGCC TTCGTGGGTG TTGAATCCGC	11220
AGCAGTAAGT ACTGGTATGG TTAAAAACCC GAAACGTACC GTTCCGCTGG CAACCATGCT	11280
GGGTACTGGT TTAGCAGGTA TTGTTTACAT CGCTGCGACT CAGGTGCTTT CCGGTATGTA	11340
TCCGTCTTCT GTAATGGCGG CTTCCGGTGC TCCGTTTGCA ATCAGTGCTT CAACTATCCT	11400
CGGTAACCTGG GCTGCACCAC TGGTTTCTGC ATTCACCGCC TTTGCGTGTC TGAATTCTCT	11460
GGGCTCCTGG ATGATGTTGG TAGGCCAGGC AGGTGTACGT GCGCTAACG ACGGTAACCT	11520
CCCGAAAGTT TATGGTGAAG TCGACAGCAA CGGTATTCCG AAAAAAGGTC TGCTGCTGGC	11580
TGCAGTGAAA ATGACTGCCC TGATGATCCT CATCACTCTG ATGAACTCTG CCGGTGGTAA	11640
AGCCTCTGAC CTGTTCCGGT AACTGACCGG TATCGCAGTA CTGCTGACTA TGCTGCCGTA	11700
CTTCTACTCT TCGGTTGACC TGATTCGTTT TGAAGGCGTT AACATCCGCA ACTTTGTCAG	11760
CCTGATCTGT TCTGTACTGG GTTGCGTGTT CTGCTTCATC GCGCTGATGG GCGCAAGCTC	11820
CTTCGAGCTG GCAGGTACCT TCATCGTCAG CCTGATTATC CTGATGTTCT ATGCTCGCAA	11880
AATGCACGAG CGCCAGAGCC ACTCAATGGA TAACCACACA GCGTCTAACG CACATTAATT	11940
AAAAGTATTT TCCGAGGCTC CTCCTTTCAT TTTGTCCCAT GTGTTGGGAG GGGCCTTTTT	12000
TACCTGGAGA TATGACTATG AACGTTATTG CAATATTGAA TCACATGGGG GTTTATTTTA	12060
AAGAAGAACC CATCCGTGAA CTTTCATCGC CGCTTGAACG TCTGAACTTC CAGATTGTTT	12120
ACCCGAACGA CCGTGACGAC TTATTAAAC TGATCGAAAA CAATGCGCGT CTGTGCGGCG	12180
TTATTTTGA CTGGGATAAA TATAATCTCG AGCTGTGCGA AGAAATTAGC AAAATGAACG	12240
AGAACCTGCC GTTGACGCG TTCGCTAATA CGTATTCCAC TCTCGATGTA AGCCTGAATG	12300
ACTGCGTTTA CAGATTAGCT TCTTTGAATA TGCGCTGGGT GCTGCTGATG ATATTGCTAA	12360
CAAGATCC	12368

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 833 base pairs
 - (E) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GCAACGGCACT	CTGATGTANC	TTTTATCTST	TCCCAGTGGA	AGCATGCCCC	ACAACTGAGT	60
CATTAAGTGT	GGAAGAACAG	TTTTGTCCCC	GCCTGCAATC	TCTCCCTTTC	NAAAAACCAG	120
TATGTCGCCA	TGCCTCGCCT	TAATGGAGAG	CGCTGAACCA	TACCTTCTTT	TTCCCAGTAA	180
TAAACAGGTAA	TAGCGTGCCT	GGTAATCCGT	TACCGCCAGC	GCCTCCGCAA	TTTCTGCGGT	240
TTTCCCTCCA	TTATGCCTGT	TCAGAAATYC	CAGTATTTCA	TTCTTCATAT	ATTCACTCAT	300
CTCACTGTAA	CAAAGTTYCT	YCGAATAATA	AAAATCATGC	TTTCTGTTAT	CAACGGAAAAG	360
GTATTTTTAT	TCTCTGTGTT	TGCTTTATTT	GTGAAATTTA	GTGAATTTGC	TTTTTGTGGG	420
CTTTATTTGN	ATGTGTGTCA	CATTTTGTGT	GTTATTTTTT	TGTGAAAAGA	AAGTCCGTAA	480
AAATGCATTT	AGACGATCTT	TTATGCTGTA	AATTCAATTC	ACCATGATGT	TTTTATCTGA	540
GTGCATTCTT	TTTGTTGGTG	TTTTATTCTA	GTTTGATTTT	GTTTGTGGG	TTAAAAGATC	600
GTTTAAATCA	ATATTTACAA	CATAAAAAAC	TAAATTTAAC	TTATTGCGTG	AAGAGTATTT	660
CCGGGCCGGA	AGCATATATC	CAGGGGCCCG	ACAGAAGGGG	GAAACATGGC	GCATCATGAA	720
GTCATCAGTC	GGTCAGGAAA	TGCGTTTTTG	CTGAATATAC	GCGAGAGCGT	AYTGTGCCCC	780
GGCTMTATGT	CTGAAATGCA	TTTTTTTTTA	CTGATAGGTA	TTTCTTCTCA	TTC	833

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGCACCATCA	CTGATACCAC	CGGGACCCCG	GATTTTATCC	GGTCCCCGCG	GACTGACAGG	60
GTTTGTGACA	CCTGAGTCAT	ATCCGATGTA	AACTTCATTT	TCACGGGTTG	TACAGGAAAA	120
CTCCCTGTG	CCATTGAGTT	CTGATGTGTG	CCCTTCGCCA	CAACTCCAC	CGTCACGGCA	180
CCAGTTGCAT	CTGACGCCGA	CCAACTGCTG	AGAGCCATGC	CGTTTCCGGC	TTTGTCGACA	240
ACGCATGCTG	CAGTTCCCAG	CGATGCGAAC	TGGTCTGGCA	TGCATTACAG	AACCAACAGC	300
AGTGGTGCTA	CGTCCGATG	CAATTCGCAT	GAGCTCCAAC	CGCGGTTGTA	AGTTCAGCAG	360
CCCGGGCCTC	TGCCCCCGGC	ACAGTCGCAT	AAGTATTGCA	TACCGTGCGA	CACCATTACC	420
TTCAGGATAC	GCCACGGACC	CGTCACCCTA	CGAAAACGCC	GGAGCACCGG	CAATCAGCAA	480
AGGCAGCAGT	GATAAAAGAC	TGATATATTT	CCTGTCATTA	TTTTTCATAT	TAATTTAACT	540
CCTGATTAAC	CGGTTTTTAT	TGATATGAGA	AAGTAATAGT	TGCAATAGCC	TTCACTTTC	600
CAGGTGTAGT	TGCATCAGCA	ATTTTTATAT	AATTGGCTCT	TAAATTGATA	TGTGGATTTA	660
CCTCTCCCT	GTAATCGGAG	AAGTGCCATT	GACTGCCATT	TCCTTTCACA	GGGGAGTCTT	720

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CACCATAGCT GATGGCAGTT ACATCACTGT CTTTATATAG CCTGATGCCA AATCCTTTTG	780
CAGTGGATTG ACTGCTTAAG GTCAATATAT CTGTTCTGTT CACTGGCTGT GATGCATCTG	840
TCAATGTAGC ATAAACATCA ATTCCATCCG GGCATTGTAG GTGTATGTCA ATTTTACCTC	900
CCTGTATTTG TTTATACAAA GATGTGAAGT GTGATTGATA TACGGTATTT AATGGCACCA	960
CATAGTTTTT TTGCCCCATG GTACATGTCT GACTCTGTAC CTGAATGCGC CCACCATTTA	1020
ACATAACAGG TGCTGTCAGT CCTTTATTAT TTAAACTTGT ACGTTTTGCT TCCAACAAAA	1080
TAGTACCAAG CTGCCTGGTG GGTATTGTTA TATATCCATT GGTAATCTT CCGTTGCGA	1140
CAAAAGCAAC AAACAAACGA GCTCCGAAGC TTGCTGTGCG ACCGTTATAA GTATTGGGGT	1200
TTGTATTGGC ACCTACAGGG TCAATATATA TACCTGAGCT ATTTATGGGG ACCAGAGGCG	1260
TTGCGGGCCA ATAGCCCGCC ATGCCAATAA TAATACCCAG TCCGGATACA CCAATATCAT	1320
AGATATCAAA ATCAGATGAA TCACGGCTGT TTCCTTGATG GAAAGTATAC GTAATACTTC	1380
CAATTTTAGG CAGTGCGGGT GTAAACTTTC CACGCATCAG AGCGATGGCA CCGCCATTAA	1440
AAACATACTG GTTACTTGTT CCCGCCAGCT CTCCTATCAC CCGGGGATAG GTATGGGCAT	1500
CAGCAGGACC AATCACAACA CCTGGCAATG TGGATGTATT AACCGCTATC TGCGAAGGCA	1560
CATAATCATC CGGACCCGCT ACCGCCAGCT TAGGGAGTAA AATTAAAAAC AATGGTATGA	1620
AAAAGATTCT TTTCATGTTT TTTCCTGATT AGGGTGCTGT ATACACAGAA CAGGAACGAG	1680
CTGAGATTGC ATATCATCTT TATTGTGTGC AACATGATAT ACAAATGAAC ATCTGTCTTT	1740
ATTATCTGGT CCCCATACAA CGCTGAGATG ACCTTTTTCA GGGAGTCCCC TGGTAAATAC	1800
CTTCCCGGCC TGAGCGACAT ATCCGGCCAA CTGTCCATGT TCATCCAGAA CTTCAGAAGC	1860
CATTGGAGGG GGATTGCCAG TAGACATACG AATATCAAAT AACAGACTTC TTCCTGTTTT	1920
AGTGTCAAAT TTYACTAACG TGGCGCTATT AGCACGAGGA ATGATTTCCCT GCTCCGTCGC	1980
CGATAATTCA ACATTCAAAT CTAAATTGGA GGGATCGATG CTAATTTGAT TTTTCTCATA	2040
GGGTGTAACA TAAGGAACAA TACCATTTC CAAAAATCC AGACGACTAC CAGAGGCATT	2100
ATTGATGGCA GCCCCCTGAG CTCCTTCAGC ATGGATAATG GCAAAAGTAT CACTCAGGTC	2160
ATTACTCAAT GTCACTCCAT AGGGGTGTGC GACCACCGCT CCCGACGCA CAAATGACCT	2220
TTGATTATTA TTCTGAGTAT CATGCCCGAC TGTGTGGTT ATATTTACAT AAGGTGAACG	2280
ATAACCCCCA TTCATTGCAT AACCGGAAGG CCGTTTTTC TGGCTGTTTC CTGAAAGACC	2340
ATAAGAGAAC TGATTATCCT CCCC GCCAGT ACCACTAATT GATGTCTGAA TACTATTTTT	2400
CTCTTCTTTG CTATAATTTA AAACAGTGGG AAACACCGGG CTTTGAACAC TTNCCTCCCA	2460
GAGGGAGACT AAAATTAATA TAAATCTGT CATCACGGCG TTGTTGCTCA TTATCTCTTG	2520
ACTGAGACAA TCCAATTTGA TAGCCGAGTT GTTCCAGAA GTTGCTGTAC CCCATCTGGT	2580
ATTCATTACG ACTTCCTTTA TGTCCCCAGT AATTATAGGT TGTTCCTGTT AAATACATCC	2640

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CACCCCATTT TTCACCTAAT TCCTGGTTGA TTGAAATCTG GAATTGATTC CTGGGACGAT	2700
AAAACGCTGT ACTTTTTTACA GAAACATCAT CAATAAACGC GTTGTGATTA GCTGATAGCG	2760
CATCCTTCAG ATGATAAAAA TCTTTTGATG AATAACGATA AGCCGCCAGA GTTATATTTG	2820
TGTTTTGAGG GCTGGGAATA TTGGATGGCT AATAACTTGG AGTNGCAGGA CTAATAAACC	2880
TTTTACGGCG GTTACACCGG GAATACCNGG AAATGC	2916

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACCGCATCGC CAATCTCAGC GGCAGTGGTT TACATGTCTT CCGTGATGGA AGGTCATGGC	60
ATCAGCTACC TCCATCTGCT CTCCGTGGTC ATCCCGTCCA CCCTGCTGGC GGTCTGGTG	120
ATGTCCTTCC TGGTCACTAT GCTGTTCAAC TCCAAACTCT CTGACGATCC GATTTATCGC	180
AAGCGTCTGG AAGAGGGCCT GGTTGAACTG CGCGGTGAAA AGCAGATTGA AATCAAATCC	240
GGTGCAAAAA CGTCCGTCTG GCTGTTCTCT CTGGGCGTAG TTGGCGTGGT TATCTATGCA	300
ATCATCAACA GCCCAAGCAT GGGTCTGGTT GAAAAACCAC TGATGAACAC CACCAACGCA	360
ATCCTGRTCA TCATGCTCAG CGTTGCAACT CTGACCACCG TTATCTGTRA ARTCGATACC	420
GACAACATTC TCAAYTCCAG CACCTTCAAA GCAGGTATGA GCGCCTGTAT TTGTATCCTG	480
GGTGTTGCGT GGCTGGGCGA TACTTTCGTT TCCAACAACA TCGACTGGAT CAAAGATACC	540
GCTGGTGAAG TGATTCAAGG TCATCCGTGG CTGCTGGCCG TCATCTTCTT CTTTGCTTCT	600
GCTCTGCTGT ACTCTCAGGC TGCAACCGCA AAAGCAYTGA TGCCGATGGC TCTGGCACTG	660
AACGTTTCTC CGCTGACCGC TGTTGCTTCT TTTGCTGCGG TGTCTGGTCT GTTCATTCTG	720
CCGACCTACC CGACACTGGT TGCTGCGGTA CAGATGGATG ACACGGGTAC TACCCGTATC	780
GGTAAATTCC TCTTCAACCA TCCGTTCTTC ATCCCGGGTA CTCTGGGTGT TGCCCTGGCC	840
GTTTGCTTCG GCTTCGTGCT GGGTAGCTTC ATGCTGTAAT GACCCATYGC GGGGCGTTCA	900
CGCCCCGCTT TCTTTCCCGC CGACTAACAT CCTTTCCCCG TCCGTTGTAT AGTGACCTCT	960
CTCTTGCGGT TCCATCTGTT CTTGCGAGGT GTTTATGCTT GATGAAAAAA GTTCGAATAC	1020
CACGTCTGTC GTGGTGCTAT GTACGGCACC GGATGAAGCG ACAGCCCAGG ATTTAGCCGC	1080
CAAAGTGCTG GCGGAAAAAC TGGCGGCCTG CGCGACCTTG ATCCCCGGCG CTACCTCTCT	1140
CTATTACTGG GAAGGTAAGC TGGAGCAAGA ATACGAATGC AGATGATTTT AAAA ACTACC	1200
GTATCTCACC AGCAGGCACT GMTGAATGCC TGAAGTCTCA TCATCCATAT CAAACCCCGG	1260

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AACTTCTGGT TTTACCTGTT ACACACGGAG ACACAGATTA CCTCTCATGG CTCAACGCAT	1320
CTTTACGCTG ATCCTGCTAC TTTGCAGCAC TTCCGTTTTT GCGCGATTAT TCGACGCGCC	1380
GGGACGTTCA CAATTTGTCC CCGCGGATCA AGCCTTTGCT TTTGATTTTC AGCAAAACCA	1440
ACATGACCTG AATCTGACCT GGCAGATCAA AGACGGTTAC TACCTCTACC GTAAACAGAT	1500
CCGCATTACG CCGGAACACG CGAAAATTGC CGACGTGCAG CTGCGCAAG GCGTCTGGCA	1560
TGAAGATGAG TTTTACGGCA AAAGCGAGAT TTACCGCGAT CGGCTGACGC TTCCCGTAAC	1620
CATCAACCAG GCGAGTGGCG GAGCAACGTT AACTGTCACC TACCAGGGCT GTGCTGATGC	1680
CGGTTTCTGT TATCCGCCAG AAACCAAAC CGTTCCGTTA AGCGAAGTGG TCGCCAACAA	1740
CGAAGCGTCA CAGCCTGTGT CTGTTCCGCA GCAAGAGCAG CCCACCGCGC AATTGCCCTT	1800
TTCCGCGCTC TGGGCGTTGT TGATCGGTAT TGGTATCGCC TTTACGCCAT GCGTGCTGCC	1860
AATGTACCCA CTGATTTCTG GCATCGTGCT GGGCGGTAAA CAGCGGCTTT CCACTGCCAG	1920
AGCATTGTTG CTGACCTTTA TTTATGTGCA GGGGATGGCG CTGACTTACA CGGCGCTGGG	1980
TCTGGTGGTT GCCGCCGAG GKTTACAGTT CCAGGCGGCG CTACAGMACC CATACTGCT	2040
CATTGGCCTC GCCATCGTCT TTACYTTGCT GGCGATGTCA ATGTTTGGCT TKTTTACTCT	2100
GCAACTCCCC TCTTCGCTGC AAACACGTCT CACGCTGATG AGCAATCGCC AACAGGGCGG	2160
CTCACCTGGC GGTGTGTTTA TTATGGGGGC GATTGCCGGA CTGATCTGTT CACCYTGCAC	2220
CACCGCACCG CTTAGCGCGA TTCTGCTGTA TATCGCCCAA AGCGGGAACA TGTGGCTGGG	2280
CAGCGGCACG CTTTATCTTT ATGCGCTGGG CATGGGCTG CCGTGATGC TAATTACCGT	2340
CTTTGGTAAC CGCTTGCTGC CGAAAAGCGG CCCGTGGATG GAACAAGTCA AAACCGCGTT	2400
TGGTTTTGTG ATCCTCGCAC TGCCGGTCTT CCTGCTGGAG CGAGTGATTG GTGATATATG	2460
GGGATTACGC TTGTGGTCGG CGCTTGGTGT CGCATCTTT GGCTGGGCCT TTATCACCAG	2520
CNTACAGGCC AAACGCGGCT GGATGCCCGT GGTGCAAATA ATCCTGCTGG CAGCGGCATT	2580
GGTTAGCGTG CGCCCACTTC AGGATTGGGC ATTTGGTGCA ACACATACCG CGCAAACCTCA	2640
GACGCATCTC AACTTTACAC AAATCAAAAC AGTAGAT	2677

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATCCTGATGA CGCGTAAAT GTGCATTTGC CAGGATTGCC GCATAGAGGG CACGAAGAAA	60
AGGTCGGTTG TCAGGATGTA TCCAGATGAT TCTGCCACTG AAACCTTCAG GGATAAGACG	120

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ATTGCCAACT GCCAGTCCTT TAAGGSCAGC ATTCAGCGCC TTACGCGGGG CATTCTGCTC	180
CAGAAATACG TATGCCAAGT GAGCSTGTAC ATCAATAAAG TCATTCTCCT GTCGGGCAAG	240
GCGCCTGAGT TTGTTGATGT AACTTGTTTC GCTGATTTC A TCCGCATCGT ATGCATCAAT	300
CAGTTCTTCA AACTCATCCA GCAACGAGCC AAACCAGGTT TCCGGAATA TGAAACAGCC	360
CTGGTTATCG TTCACTTCAA AGCGTAATTT GCCAGTCATA TTCTGAACCT GTAAAAAAGG	420
ATAGACCATA ATCTGCAGGC TATAAAAATT GTGGATGCCT GGCATCGGGT GTCCTTTTAT	480
TGTCCGGGAT TAACGTTGCC CATGATAATA CAGTGAATCC NGTTCTGTGG TAAGACG	537

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CGCTCGAGCA CCAGATTCAC TGACATGCGC AAATCATGT GTAAATCCTG TCTGGGCATC	60
TATCTCAAGT AACAGTTCGG TTAAATCTAC CCGTGGGAGT AGCTGTTTGA TCCGATTATT	120
TAGACGAAGC AATGATGGTG GCTCTTCCTG TTTCTCCAGA CAACTGATAG TCAGGGATGG	180
ATATTTACCT TCATTACAGA TATGAACTTC CGCATTCTTT TCAAATCGTG ATGCCAGGCT	240
TTCCAGGTCT CATCCAGCTG AATAGCCAGT TGTGACAC CTTTACGTCC ATCGACAGGA	300
TGTCCAGTG CCCGACAGAC AGGAATACGC TGAGTCTGCC ACTCTTCACC TTGCAACAAC	360
TTCTCGCGAG GATCTCCCCA GCGATCACTG TTTTCAAGCC CAGATGTCCC CGGCGGCGCA	420
RTGCATCCTG AAGGCGTTCC AGCAAACATA GTGAATAACC TGCACGCTGT ATCCCGTCCC	480
TCCGCATCGT ATACGAGGCG TTTCCAGGGA CCGGTGATAA TATGTTCAGC GCATCATCAA	540
GGATGCGCTT TTTCGAACCA TTCAGTTCTG CCAGATAATG AATCGCAGCC AGTACATGTC	600
ACCTGCCGGT GCCGCACGGA AATGCAGGTC CCGCAACACC GCCGGAAGAA AACGTTTAAAC	660
CCGACCGTAC TGCTCAACCA TTTGTCATG GAAATTATTG TTCTGTGGAC GAGCAAGTTC	720
ATTAACCTTG CTTACAGATT CTGCCAGTCT GTTTTTGGGT ACGCACTTGA AGATAACCTG	780
CCTGAGATCT GGGACATCTG TATTATCATC CAGCAACAAT GCACATGCCC GCGCCAGTAA	840
CAATGCGGCC TGATCAAGAT CTTTCAGTGT CCTGAGTCTT TTTTTTTGCC CGGTTTTCTT	900
TGCTTCGCGG ATAATGTCCA GAATTAGCAT ATCAAGCACA TCAACGGCAT CGTCTAATGC	960
CGTTATTTCC TGTGCTTTAA CGAATGCAGT AAGTACAGCA AGCTTTCTCT GCTGTGGCAT	1020
TCGAGCGATA TATTTTACCG ACGCCATGCC AGCATGAACG AGCCAGATTA CGCNTTGGNA	1080
ATGGTCAGGC AGACCGGGAA AAGTTCCAGT CGGGNAAAAC TCCAAGAA	1128

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(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

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GGNTGATAAA AATCYTTTGA TGAATAACGA TAAGCCGCCC AGAGTTATAT TTGTGTTTGA      60
GGCTGGAATA TTGATGCTAT AACTTGAGTG CAGACTATAA CCTTTACGCG TTACACCGGA      120
ATACCTGAAT GCTSTTCTGG ACAATGTAAT GTCAGATGCT ATAGCACCCA GATGGGTATT      180
AAAGGCCAGG CCAGCTAACC CCGCTGTATA TCCTGAAGCT GTGGTAAGAC CACTGTTTAA      240
AGTAATATCA TTCGTCAGGC CGTATTGATA GGTGCCTTGT GCTATTAAAT CATTATATGT      300
TTTATTGCGA TAACGATACT TTCCCACTGA CATTTGCCAG CGACTAAATC CGGGACGAAT      360
GAGTTGAGCA ACGGCCGCAA AAGGAACCGT GAACATTCGT GTCTGGCCAT TAGACTCTGT      420
TATCTTAACG AGAAGGTCAC CAGCATATCC ACTGGGATAT AAATCATTGA TGACAAATGG      480
TCCGGCTGGC ACCGTCGTTT CATAGAGGAT ATGAGCATTG TGATAAATGG TTACTTTAGC      540
ATTACTGTTA GCTATTCCCC GGACAGCAGG RGCATAGCCA CGTAAAGAAC CGGGTAACAT      600
TCGTTTCATCC GATGCTAACC TGAATTCGTC TCTCAATGGG GCAAGGTCAT GCATTATACT      720
CGTATAAAAA TCCCCTAATG TGAATTGTGC TCTCAATGGG GCAAGGTCAT GCATTATACT      780
TGTTTCTATA TTCTGATATC CGGCAGGATA GCTATTATTC CAGCTCTCAC TGCCACGGTG      840
GCGCAAAGCC ATCCCCACAA ATTGAATCCA GCTTTTAATC CCAGATAAGT CTGTTTCGTTA      900
CTCGTCCCGG AAGAGCTATA CTGGTAATAG TTAGCATCAT AGTTTATAAA TGCTGCAGGA      960
ACACCACTTT GCCACTGAGA AGGGGAAATA TATCCTCTTG GACGTGTATT CAGCAGTGCT      1020
GCGGGATTTC GATATTCAAC CTTAAAGTCG ATAAGTCAAA ATTAATTCTG GCTGAAGAAA      1080
GCCCTGTTGA CGCCGGAAG CAGGAGGTGT TTCCCGACAT AGTATCTTTG ACTAAATCAA      1140
TCAATGAAAG CAGCTCAGGC GTCAGGCATA ACGTCGGAGC ACCGGTATTG GCAGTACGTA      1200
AATACTGCAA ATCAGCCTTC CCCTTCCATA CATTATTAAC ATAAATATCA GAATAATACC      1260
TGCCCTCAGG CACAGGGTTA CCATGACTAA AGCGGCGGAT ATCAATAGCA TTTATCCCTT      1320
TATCCAAATG CAAAACTCA GAATCAAAC T CAGCCTCTTC AGCAGCAAAT GAATGGTTTG      1380
TTACTGTAA CCCTAATGCA GCAAAAAGCA GAAGAGAACA ACGACAGTAA ATCAGGCATG      1440
ACAGATTATT AGCGTTCATT ATTACCTTAC TCCAGAACAG ATTCTCCTTG CTGATATCCT      1500
CCGTAATCAT TAACAATAAC CCAGGAAACT TTGCTGGTGG CGCAGTTCTG CCTTTAAGTG      1560
CAAATACTGT TGAAGAGAAA GGGGGAATCA TTCCACCATG TTCAACAGGC GTTAAGTGCT

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TATTCTGGTC	AACTGCAATT	TTGTTGTAGG	TTATGTAATA	AGGTGTTGGA	TTAACTGCTT	1620
TAATTCGGCC	TTCCTCCTGG	TGCCAGGTAA	CTTTCAGATA	AGCATCATTT	GGTGTAACT	1680
TCAGGTGASC	AGGACGAAAG	AAAAATTTTA	TGCGACTACG	AACAGCTAGT	TGCAAATAAT	1740
TATTATTCCG	CTGCTCTGAG	TTATCGGAGT	CTTTTTTTGC	CCTGGGCTTT	GCTGGAATAT	1800
CCAGAACATT	TAGATAGAAA	AGAGATTCTC	GGTCTTTCGG	TAGTGACTION	CCTGTATATA	1860
CAATTCTGAC	TGTTTGTCTT	GATTTAGAGT	CCATACGAAA	TATTGGCGGA	GTAATGATAA	1920
AAGGACGTGG	ACTGACTCAG	GGGGAGCTGC	TGCATCTCCA	TCGYCAACCA	GGACTGGACT	1980
AATGCCGAGA	TTTCATTGTC	ATTATTTNAA	CGTATGCTAA	TACTCTTTTG	AGTCGCCGGA	2040
TAAACAACAC	GGGTTCCCAT	GATAACTACA	CTACCCTGAA	CAACTGCAGA	TACAGATAGA	2100
GTAACAAAAA	ACAGCACAAA	CCTTAGCATG	GATCTCTCCAG	AAGAAAGCAG	GGCAGTATTT	2160
CCTGCCCCAA	AATACAAAAC	CGTTTGTTAT	TCGTAGGCGA	TGGTATAATT	GACTGTTGTT	2220
TTTACATTGC	CTGGAGTTGA	TGTCCCGGTC	GCATAATATT	GAGCCATATA	ACGTAATGTG	2280
GCATTACCAT	CCCCACCAAT	AGTTTCAGAA	T			2311

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TATTACCTGT	GATTTTTCCG	GGCGTAAATG	GAGTCCCTAA	AGTTATCGCA	GTCCCAATAT	60
TTCCTGCATT	ACTGTTATAA	AGATAAACGA	GTAACCCATC	AGAAGATGTG	TTTGATGTAT	120
TCTGAACTAA	AATAGCATTG	TNATAAGTGT	TTGTTGCCGT	TATCGTAACC	TTCATTGTTC	180
CCAGATTATA	GGGACACCGC	ATATTCACAG	TAAACTCTTT	TTCGTGANTT	CCATTTTGAC	240
TCAGGGTCTG	AATCTCTACA	NCCTGCCAGT	CAACAGTTGT	GTTGCTTACA	GTACAGGCAG	300
GAATAATCAG	TTTTCTCTG	AAGGTCAGAT	TATCAACTGC	ATGTACATGC	TGAGACATTA	360
ACACTGCCCC	CAGCATTACC	GGAAGACACA	AACCTCTTAT	CTTTTTCATC	TGAAATATCC	420
TGTACAAAAA	TTTGCTAAC	GATATGTCAA	TTCAAACGTG	GCTGTTGCTT	CATAATCACC	480
GGGTACCACA	CTCTTCGTCC	GCAGGGCTTC	CGGCGTTGCC	ACAACATACG	CGCCGAAAGG	540
AAGCTCAAGA	CTGTTTCCGG	TAACCTTTTC	CCCCTGGCCT	TTGTTATGGG	AGGTGCCGGG	600
TTTCAGCAGA	CTGCTGCCAT	CGGTGTCCAG	CAGTGCAATG	CCTAACCGGC	CAGCATTAC	660
TCCGGTTACC	TTCAGATGGC	CCGGGAGRCG	CYNTCTCCG	TCCCTTAAA	GGTCAGGGTC	720
ACAATTTTGC	CAACTGCTGT	TGCATGGCAG	TTTTCCAGCC	TGATGACAAA	CGACTCTGTC	780

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GGCGAACGTC CGGGCGGATA CCAGAAATCC CTGGACGCCC GGGTTTTGAA GACGACATGT	840
TTATTCAGAC TGTACCGGA CACATGSCAG GGTCTGTCAA GCAGATTACC CCTGAATGCC	900
ACATCTGAGG CTATTGCCTG TCCGGCAGAC AGTGCGGCAA ACAGTAAAAG AGCGCCTGTG	960
CTTTTTATCA TCACATCCC TTAATATAT TTTATGCTCA GACGCAGCAT GGCCGGATTG	1020
CTCCTGGCAT CAGAATACTC AACCTCTGT GCGGCGCTTT TCCTCCAGGC GGGCAAGCAT	1080
CTCCTCCTGG CGGCGGGTAA GCGGGGACA GTAAAAAA	1118

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTCGTGGGTG AAATCGTAGG CCGCGCTTTT TTGCTGATCG GCCAGTTGAT GAATAGGGTG	60
GCCAKGATCG GGATAAACG TACAGGCAGC GATAAACAGA CAGCCCGGAT AGCGGTTGTT	120
TTTAACGCAC TCCGATAACG CCTGATAACG TGCCAGCAAC TTTTGTTCGG CGGTTTGCCT	180
TTCGTCCAGC ATCAGCTGAC GACGCCAGAC ATCTATCTGT TGGCTAAGAT AACGCAGCGC	240
ATCGTAGAGG ATTGCTCTT TGTCTGGCCA GAAGCGGCGT ACTCGTCCAG TGGATAATCC	300
ACACGTTTAC CAACCATCTC CAGCGTGGTG TTGGCAATCC CTTGTAATTC TAATAATTTT	360
AGGGCTTCTC CCAGTACATC TTCAGTTTGC ACGCTATTTT CCTCCGKCTT TCCCACTGCA	420
ATGTTGCTC ACGGTTGGCG ATCGGSCAAA TGTGCGCTGS AAGGTTTCAG CATCCATAAA	480
GCCCGTGACG CGTGCTTGTC GATGCTCTG GCCTTGCTCC GGTCAAAAAA GAGAATTTGT	540
CCGGTAGGGC CAAGGATATT AA	562

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCATCGCTTT ACCCCAGAAA AGTTAAGCCA TATAATGTGA GGGATATAAG TCGTCGTATC	60
CGGTAAGTAC AGATAACCAC AACATAAGCT CATTCAGTAA ATTTTATCTC TGAACAAACG	120
ACTATGGCAT GCTCATTTAT ACTATTCATA AGAAAGTGTG ATTATCTGTA AGCATTAAAC	180
ATCAAAATCAT ATAACCATAC TAAACTGGCG GATCATCAGC ACCATTAGCA GGTAACCTAT	240

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TGAAATTTTA TTATGTGTTT TTTGTTGATA ATTAATATGC AATATGAATT TGCTATTTTA	300
GAATCATGAA CACCATTTAA AATTACCATC ATTAACATCA TATAAAAATA TATTTTACT	360
AAAACATGAA TTGTATATAT TTATTAGCTC AGGAAAATTA TCAGGGTTCA CCTTCAAATT	420
AACCTGAATG TTATGCTTAA TTTCACCCAG TAGTCTTCA TGTGTAGATT TTATTATCCC	480
ATTATTATAA TCGATAAATG CACACATGTT TTTTATGAAT TCAAAACCTT TTCCTGTATA	540
CAGTTTAATG AATGCCACCA GAGCAAACAT TTCAAGATGT AGCCATAATG CTACGTTAGT	600
TTTTTGCAA GTATAAAAA TTGAATTCGC CACTTTTTTA CTTATTGCTC TTTTATACTG	660
TGATCGAGCA AGATTCAGTA GCGGAAGTCC TCGTTCAATA AATGAATGTG AAAAGACTGG	720
ATAAATTGAT GTCGGAAACC TTTC	745

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGTTNATGC ATTTTCASAT TTTCCACTTC GTTCTGACGT TGCCTGCTT TGGCGTCATC	60
ATTACGTAAC GTATCGAGGA AATCGAGGTA GCCCTGATCA ACATCTTTGG TGACGTAGAC	120
GCCGTTGAAC ACCGAGCATT CAACTGCTG GATATCCGGA TTTTCAGCGC GAACGGCGTC	180
GATCAGATCG TTCAGATCCT GGAAATCAA CCCGTCAGCA CCGATGATCT GGCGAATTTT	240
ATCAACTTCG CGACCGTGAG CGATCAGTTC CGTGGCGCTC GGCATATCAA TACCATAAAA	300
CGTTCGGGAA AGCGAATTTT CGGTGCCGCA GAAGCGAGGT AACTTTCTT CGCTCCGGCT	360
TCGCGTGCCA TCTCGATAAT CTGTCAGAAG TGGTGCCACG	400

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGTCGACGAT GAGGCAGCCA GAGCATTAGA GCCGAAAAGA AGGGATGATG CCATGACTGC	60
TGTTGCTATA AAATGTTTCA TATATTCTCC ATCAGTTCTT CTGGGGATCT GTGGGCAGCA	120
TATAGCGCTC ATACTAGGGG TTTGAGGGCC AATGGAACGA AAACGTACGT TAAGGAGATA	180
ATTCGTTGTT TATATTTAAA TTTAGAGCTC TCAGTTCCCC TTTTAAAATA TCCTCTGGCA	240

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ACGTGAATGT ATAATGGCC AACATATTGA TATGCCCGTG CATCAGGGGA GATAGCCGAG	300
CGATATCTTC ATCTATAATT TCTTGGCCAT TACGGCGCAT CCAGCTCAAC GCTTCCTCCA	360
TATAGAGCGT GTTCCACAGA ACCACTGCAT TAGTAACCAG GCCCAGCGCC CCCAGTTGAT	420
CTTCCTGCC TTCACGATAA CGCTTTCTGA TCTCTCCGCG TTGTCCGTAA CAAATCGCAC	480
GAGCCACAGC GTGCGKTCCT TCTCCTCGAT TAAGCTGCGT CAGGATCCGC CGACGATAAT	540
CTTCATCATC AATATAATTG AGGAGATATA GCGTTTTGTT TACACGCCCT ACTTCCATAA	600
TTGCCTGTGC CAGTCCTGAT GGGCGCGAGC TTTTCAGTAA AGAGCGAATG AGTTCTGACG	660
CATGAATTGT ACCCAACTTC AGGAACCAGC GGTTCGCATC ATCTCATCCC ACTGACTCTC	720
CGCTTTTGAC AGATCTGCAT ATCCTCGGGC CAACTTATCC AGTACTCCGT AGTTTGCCGA	780
TTTATTCACC CGCCAGAACA CCGCCTCACC TGCATCGGCA AGCC	824

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACAAATCAGA CCAGTTAACC AGTCAGTCGG TTTTATGATT TCACTACTA TACTTTGTTT	60
CATAAGGATT TCAGGATCTG CCAGACTGCG CAGAAATGAT GCTTACGAAT ACACAGTAA	120
GGCAATGTCA TTTCCGATAC AGAGCCTGAC ATTGCCATAA TGAGCTATTT ATCTGAAAAA	180
CGACAGAATA TGATGTTTTA TCGTAACGTA ATTTTAAGTT CTCAACTTAT TGAGACATAT	240
TGTCTTTTTT ACCCATGTGG TCATTTTTCA TCCCATCCGT TTTGCTCATG TGTCTTTCT	300
CCATTTTCTC TTTATCCATT GCATTTTTGC ACATACCATC CTTGCACATT TTATCATGCG	360
CGCTGGACAT GCTGCCTTTT ACTTCATGTG TTTTATCCAT TGTGTCTGCT GCCTGAGCAT	420
TGAACATGAA CAGCGCGGAT AGTACAGTTG CAGAAATAAT ATTTTTCATG GTTCTTCCTC	480
ATTTTAAACA ATTGTATCAA CAACCACCAA ACCAGTTATA ACCCTGGTCT TCCCAGTACC	540
CCCCCGGAAA ATGATTAGTG ACCTCTATAA CCTGAACATG CTTGGGGTTT TTATATCCCA	600
GCTTAGTAGG GATACGTATC TTTATGGGAT AGCCATATTC TTTTGCAAT ACCCTGTTAT	660
TCCATGTCAA TGTCAGCAAT GTTTGTGAAT GTAGTGCTGT CGCCATATCA ATACTGGTGT	720
AGTAACCATC GACGCAACGA AAACGTACGT ATTTTGCCCG CATATCGGCA CCAATCAGCG	780
TCAGGAAATG CCGGAATGGT ATCCCTCCCC ATTTTCCTAT TGCACTCCAT CCTTCAACAC	840
NGATATGACG GGTATCTGA CTCACATGCT GCATGTTATA CAATTCAGAC CAAAAACCAG	900
TTACGGGTTA T	911

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(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

NGGGGCAGGA TAATTGTATC CTGCCCNGTA TATAATTCTC AGCACAGGTG TTGACTAAAG	60
AGCGTGAAAC TTTGCTATTA TGTCTTCGTA AGATTCACGG ACGGTTATAC TTGAGCCTGA	120
TTCTGTGAAG TAAACAACAG CAGAAGCATC GTTGCCTTTT TCAATGTATG AAACATTCCA	180
GTCATGGATA GCCACTGCGG GCTGACCATT ATCCCACGG TCGTCTTAA TGAATCGCGG	240
AAGTAATTCT GCAATATCGT TAAAAACACC ATTTACGGTA TGAGTGATAC CACCAACGCA	300
ATGTAGATGA GTTGACTCCG GGGTATCATT GTCTGCTTCT GCAAAGAGTA TAGCTGTCTT	360
GCTAATTGTA ACAGGCGCCT GTGARCGGGA TAATTCGAGA GAAATAAACC CGGATTCTGC	420
CATAAAACT CCAGTTTGTG ATGTTATATC ATTTCATATG TTT	463

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTCTAACCTC TGACCAAAAA CAGAATTACG GTTGTTATGC TGCAGAACCT AATGACGTGC	60
AACTGGCGCG CTATTTTCAT CTTGATGAAC GGGATCTGGC CTTCATTAAC CAACGACGGG	120
GCAAACATAA TAGGCTGGGC ATTGCGCTTC AGCTCACCAC AGCCCGTTTT CTGGGAACAT	180
TTCTGACGGA TTAACTCAG GTTCTGCCTG GTGTTCAACA TTTTGTCGCG GTACAGCTTA	240
ATATCCACCG TCCAGAAGTT CTCTCCCGCT ATGCTGAACG GGACACTACC CTTAGAGAAC	300
ATACTGCATT AATTAAGGAA TATTACGGCT ATCATGAATT TGGTGATTTT CCATGGTCTT	360
TCCGCCTGAA GCGTCTGCTA TATACCCGGG CGTGGCTCAG TAATGACGAC CGGGTCTGAT	420
GTTTGATTTT GCCACTGCAT GGTGCTTCA AAATAAGGTA TTAGTCCCCG GAGCAACCAC	480
ACTAGTACGT CTCATCAGTG AAATTCGTGA AAGGGCAAAT CAGCGGCTGT GGAAAAAGCT	540
GGCCGCACTG CCGAACAAAT GGCAG	565

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 512 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGATGGCGTC CGGGGTGAAC GCCGGATAAG TTTAATTTAT CCGGTCAGGC AAAAGGCATT	60
AATCTGCAGA TAGCTGATGT CAGGGGAAAT ATTGCCCGGG CAGGAAAAGT AATGCCTGCA	120
ATACCATTGA CGGGTAATGA AGAAGCGCTG GATTACACCC TCAGAATTGT GAGAAACGGA	180
AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTGCTGGGAT TCCGGGTCGA TTATGAGTGA	240
GTCCTCCGG TGAGATGTCC GGTTATTTAT CTTTTTGTG AATCTGGTGA TGCCTGGAAT	300
GAAAGACAGA ATACCTTTTG CAGTCAACAA TATTACCTGT GTGATATTGT TGTCTCTGTT	360
TTGTAACGCA GCCAGTGCCG TTGAGTTTAA TACAGATGTA CTTGACGCAG CGGACAAGAA	420
AAATATTGAC TTCACCCGTT TTTCAGAAAC CGGCTATGTT CTGCGGGGGG CAATATCTTC	480
TGGGATGTGG AATTGTTAAC GGGGCCAAAG TA	512

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGCCGGTGC GGTTANTAGT GGCAGTGGTG TCTTTTGGTG TAAATGCTGC TCCAACTATT	60
CCACAGGGGC AGGGTAAAGT AACTTTTAAAC GGAAGTGTG TTGATGCTCC ATGCAGCATT	120
TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC TTTCAAAAAG CTTCTTGAG	180
GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT TGGTTAATTG TGATATTACT	240
GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA AGCTGGCTTT TACTGGCCCG	300
ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG GTACGGGCAC AGCTATCGTA	360
NTTCAGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG AAGTGATGCT AATACCCTGA	420
AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTAA GAAGTCGTCA GCGTTGGTG	480
CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT CAACCTGACT TATCAGTAAT	540
ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATCCGCTG TTTATTTCTC AGGGTATTTA	600
TCATGAGACT GCGATTCTCT GTTCCACTTT TCTTTTTTGG CTGTGTGTTT GTTCATGGTG	660
TTTTTGCCGG TCCGTTTCCT CCGCCCGGCA TGTCCCTTCC TGAATACTGG GSAGAAGAGC	720

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ACGTATGGTG GGACGSCAGG GCTCCTTTTC ATGGTGAGGT TGTGAGACCT GCCTGTACTC 780
 TGGCGATGGA AGACGCTGG CAGATTATTG ATATGGGGGA ATACCCC 827

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CCAGGGGCCC AAAATCCGTG TATCCACCTT TAAAGAAGGC AAAGTTTTC TCAATATTGG 60
 GGATAAATTC CTGCTCGACG CCAACCTGGG TAAAGGTGAA GGCGACAAAG AAAAAGTCGG 120
 TATCGACTAC AAAGGCCTGC CTGCTGACGT CGTGCCTGGT GACATCCTGC TGCTGGACGA 180
 TGGTCGCGTC CAGTTAAAAG TACTGGAAGT TCAGGGCATG AAAGTGTTCA CCGAAGTNAC 240
 CGTCGGTGGT CCCCTCTCCA ACAATAAAGG TATCAACAAA CTTGGCGGCG GTTTGTCGGC 300
 TGAAGCGCTG ACCGAAAAAG ACAAAGCAGA CATTAAAGCT GCGGCGTTGA TTGGCGTAGA 360
 TTANCTGGCT GTCTCCTTCC CACNCTGTGG CGAAGATNTG 400

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CCGATTTTTT GCGAAACGTT CCGCCTGGCA TCAGGATAGT TTGTTGTTA TCCAGTTCGG 60
 ATAGCGCATT GACGATATGC AGGCTGTTGG TCATCACCGT GATGTNATTA AAGCGCGAGA 120
 GCAGGGGAAC CATCTGCAAA ACGGTACTGC CAGCATCAAG AATGATCGAA TCGCCATCAT 180
 GGATAAACT AACGGCAGCT TCTGCAATCA GCTCTTCTT GTGGGTGTTG ATGAGTGTTT 240
 TATGATCGAT AGGCGGATCG GATTCTCTT TATTCAACAC CACTCCGCCA TAAGTACGAA 300
 TGACGGTTCC GGCATGTTCC AGAATGACCA GATCTTTGCG AATGGKTGTG CCTGTGGTGT 360
 CAAATATTGC GCCATTCTTC AACCGAGCAT TTAECCTGCT TTGCAGATAC TCCAGAATGG 420
 CGGCCTGACG CTGACGAGTT TCATGGGCGT GATACCTGAT TTAGGTTCAA ATGATAACTC 480
 GCAAGCAGTA ACATCACACG NAATATCCAC GTTCAGTTAA GCGCCATGAT AGAGCATCCG 540
 TGATAGGGNC AGGGGNAGTC ACACGGCGTA ATCACCGC 578

(2) INFORMATION FOR SEQ ID NO: 39:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TGTTAGGTCA GGGCCCCACAG TCAAGCTTAG GTTTTACTGA ATATACCTCA AATGTTAACA	60
GTGCASATGC AGCAAGCAGA CGACACTTTC TGGTAGTTAT AAAAGTGCRC GTAAAATATA	120
TCACCAATAA TAATGTTTCA TATGTTAATC ATTGGGCAAT TCCTGATGAA GCCCCGGTTG	180
AAGTACTGGC TGTGGTTGAC AGGMSATTTA ATTTTCCTGA GCCATCAACG CCTCCTGATA	240
TATCAACCAT ACGTAAATTG TTATCTCTAC GATATTTTAA AGAAAGTATC GAAAGCACCT	300
CCAAATCTAA CTTTCAGAAA TTAAGTCGCG GTAAATATTG GATGTGCTTA AAGGACGGGG	360
AAGATTTTCAT CGACACGTCN GCGTGCAATC TATCCGTAT	399

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CAGCCTCCGT TACCGGACAG CAAGGAGGCT GAATGGAGTT TACAGGATTT GCTTTTTTTAT	60
AATGTCTGGC CATGCAGTMA AACCGGACAG GTTTTATTAT CATGTGAGGT ATTCTGACAT	120
AAAATGCTGG ATTTTTATTT TGTGACGAAT GCTGCAAAAT TGCATCTGCA CTCTGATGTA	180
GCTTTTATCT GTTTCAGTGA AGCATGCCCA CAACTGAGT TATTAAGTTG TGGGAAGAACA	240
GTTTTGTCCC GCCTGCATAT CTCCTTTCAA AAACCAGTAT GTCGCCATGC CTCGCCTTAA	300
TGGAGAGCGC TGAACCATAC CTTCTTT	327

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGAGATGGGC ATGGAACTCA CTTCATAATA ATGCCTACCG AAGAAATATT AATAGATGAC	60
ATTTCCACGA GNGATAGCAA TAAAACATCA GAGCAGTCTT CTCGCTTAGA AAAAGCTTTA	120

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TTAGGTTTTA CAAACACAAT GTACAGTGAT TCAAACCCCTC CTATTATAGC TCGTTTTAGA	180
GACTATCTGG AAGATGGTGA GTGCATTGAC AGAATTAGCG AATCAATTTT TTTTACACCG	240
CAAGAATTCA ATCTTGCGA TCACCACATT GAAGGATGGT TCAATGAATT TGGTCAATTC	300
AGTGGAAC TG TTTC	314

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TCCCAAGATC TTTTGGCCG CAAATCCACA AAACCCGTCG TTANTGTCGC GCAGCCANTT	60
GCAGGCCGAA TTTGCACCGT TTTAGAAAGC GCGTTTTTGT AGAGCAGCAC GCAGTGAGAA	120
GCCACCGCGC CACGACCTAC GNGCNCGCGC AGCTGGTGTA ATTGCGCCAG ACCCAGACGC	180
TCCGGGTTTT CGATAATCAT CAGACTGGCG TTAGGCACAT CAACGCCGAC TTCAATAACG	240
GTTGTGGCAA CCAGCAGGTG TAGCTCACCT TGTTTAAACG ACGCCATCAC CGCCTGTTTC	300
TCGGCAGGTT TCATCCGCCC GTGTACCAGG CCAACGTTCA ACTCTGGTAG CGCCAGTTTC	360
AACTCTTCCC AGGTAGTTCC GMCGCCTGCG CTTCCAGCAA TTCCGACTCT TCAATCAACG	420
TACAAACCCA GTATGCCTGA CGACCTTCAG TTATGCAGGC GTGGTGCACC GGGTGCAATG	480
GATGTCGGTA NNGCGGGTAT CAGGAATAGC GACCGTAGTC ACTGGGCGTG CGGCCTGGGC	540
GGCACTCCAT CTATACCGA GGGTATCGAG ATCGGGCATA CGCNTGCATT	590

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTGGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGGATA AATGCTTCAA	180
TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT	240
TTTGCGGCAT TTTGCCTTGC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA	300
TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGGATCTG CAACAGCGGT	360

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AAGATCCTTG AGAGTTTTTC GCCCCGAAGG AACGTTTTTC

400

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATTCGAAAAG ATGCTTCTAN TTTTTTTAAG CACGTATAAA CTGTTAATTC AGGTTCAATG	60
CTACGAAATG CACTAGTTAT AACCTGTATT GAAGGAAAGA TCTTCTGATA CTCTTTCCAG	120
AGATCTTCAA GTCTGGCCAT GGAAATTGAC TTGGCTGCAT ATTCTAGGTC AGTGTTTATG	180
ATAGTTTCTC TATTCTCTCT GAATGCGGAA AAAAAAGCTT CATTCAACAA TGATAGTAAA	240
TCCCTGGGCC GGTAAGGGT AAATTGCAAA CATCGCTTAA AACCATTCTT CCCTTTAAGA	300
TCATCCGCTG TGCATCTATC CCAAACCTCGT TGATCTTTCT CAATATCTAG CTTAAATGCT	360
ACTTTCATTC TTTTAGCTGA CAGCATTAGG AGTTGTGCCC	400

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TAATGTTGAA GACAGAGATA TAATNTACAG CATCATCCCA CAAGGCAGAT ATAACAATAC	60
TTGACTGGGA TATGCAAAGC GATAGTGGGC AATTGCTAT TGAAATAATA AAATCGATAA	120
TCGTTTCAGA TATAAATTCT GGAGGACGTT TACGTCTTCT TTCTATTTAT ACTGGTGNAC	180
ATGTTACTGC TGTTATAACT AAGTTGAACA ATGAGTTAAA GAAAACATAC CGTAGCGTAA	240
TAAAAAATGA TGATAGTATT TTTATTGAAG ATAACTATGC ACTCGAACAA TGGTGTATAG	300
TTGTTATTAG TAAAGACGTT TATGAAAAAG ATCTTCCAAA TGTGTTAATA AAAAAATTCA	360
CTAACCTTAC AGCTGGGTTG CTATCCAACG CCGCACTCTC TTGCATTTCT GAAATAAGAG	420
AWAAAACCCA TGGGATATTA ACAAATATA ATAATAAATT AGACACTGCA TATGTTTCCC	480
ACATCTTAAA TTTAATAAAA TCCAAGGRGT CAAGGCATA TGCTTATGAA AATGCTCATG	540
ATTATGCAGT AGATTTAATT TCTGAAGAAA TAAGATCAAT ATTGC	585

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

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ANTCATCCAA CTGGCCGATC AGCAAAAAAG CGCGGCCTAC GATTTCACCC ACGAACTGTT      60
AACCACGCTG GAAGTTGACG ATCCGGCGAT GGTAGCAAAG CAGATGGAAC TGGTGCTGGA      120
AGGCTGTTTA AGCCGAATGC TGGTGAATCG TAGCCAGGCG GATGTCGACA CCGCACATCG      180
GCTGGCGGAA GATANTCNTT GCGTTCGCCC GCTGCCGTCA GGGTGGTGCA CTGACCTGAC      240
AGAAACACAG AAAAGAAGCG ATTTGCCGCA ATCTTAAGCA GTTGAATCGC TTTTACTGAA      300
ATTAGSTTGA CGAGATGTGC AGATTACGGT TTAATGCGCC CCGTTGCCCC GATAGCTCAG      360
TCGTAGAGCA GGGGATTGAA AATCCGTTGT      390

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(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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GGATGCCAGT GTCAGCGACT GGTAAAGTG GTCGATATCG ATGAGCAAAT TTACGCGCGC      60
CTGCGCAATA ACAGTCGGGA AAAATTAGTC GGTGTAAGAA AGACGCCGCG TATTCCTGCC      120
GTTCCGCTCA CGGAACTTAA CCGCGAGCAG AAGTGGCAGA TGATGTTGTC AAAGAGSTATG      180
CGTCGTTAAT TTTATCTCGT TGATACCGGG CGTCCTGCTT GCCAGATGCG ATGTTGTAGC      240
ATCTTATCCA GCAACCAGGT CGCATCCGGC AAGATCACCG TTTAGGCGTC ACATCCGTGC      300
TCCCCTGGCA AACGGGGGCG ATTTTCCTCC ATTTGCCTCA GTGGCTGGCG TTTCATGTAA      360
CGATACATGA CAGCGCCCGA CAAGATCCTG ATACTCTTTG GGTATTCAAC CGTTTCCAGT      420
GTAATTGCTC GTTACNAAC ATTGGCGTTA CAGGCGGGGC TGGCNGTNAC CCA      473

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(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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GAAGTGACGG ATGGCTGTGG TTTCTCCATC GGTCACCAGC AGCAGTTNGC ATCATGGATT	60
GCCTATAAAG TCGCGCCGTT CCTCGSNAAA AAASAGGAGA GCCTTGAAGA CCTCAAATTG	120
CCGGGCTGGC TGAACATTTT CCACGACAAC ATCGTCTCCA CGCGATTGTG ATGACCATCT	180
TCTTTGGTGC CATTCTGCTC TCTTCGTAT CGACACCGTG CAGCGATGGC AGGCAAAGTG	240
CACTGGACGG TGTACATCCT GCAAACCTGGT TCTCCTTTTC GGTGGCGATC TTCATCATCA	300
CGCAGGGTGT GCGCATGTTT GTGGCGGAAC TCTCTGAAGC ATTTAACGGC ATTTCCCAGC	360
GCCTGATCCC AGGTGCGGTT CTGGCGATTG ACTGTGCAGC TATCTATAGT TCGCGCCGAA	420
CGCCGTGGTC TGGGGCTTTA TGTGGGGCAC CATCGGTCAG CTGATTGCGG TTGGCATCCT	480
AG	482

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GACGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA	60
AAACCCTGGC GTTACCCAAC TTAATCGSCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG	120
TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCANCT GAATGGCGAA	180
TGGCG	185

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAACGCTTCA ATACGCGCGA CCAGCTGGCG GCGCTCATAC GGCGTAATTT TGGCGTCGGC	60
GAGCAAAATC CCTTGTTTAA AGGTATTTTG CCAGCTGCCG TCGTCATATT GGCGAGCTTG	120
CTGACGCGAC TGCGCAGGCA TTAAACGATC AGCACAATCC ATCGCCCGCA GCCAGTAAAG	180
CGGATTGGTT TCGGTTGATT TACCTTGCGC CGCCAGATG TCGCTACATT CAGTAGAAAG	240
ATAGTCAGCC AGTTGATAAA CCGGAATTTT TTCTTCTGCT GGCATATCAA TGGCTGGCTT	300
ATTGTGATTC TGCACGCAAC CCAGCAATGC CAGACATGGA GACCCTGCCA GCCACAGCCG	360
TGGGGGCAAT AATCGTTGAA AAATGTGTGC CATATTCACC AGACTTAAAG CCTATCCCAG	420

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TGGGCGTAAT TGTTGCAGAC AGTCTGGACA TGGACAGCGC GGAGAAACCG GNAGCGTACA 480
 TATCGTACGT G 491

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTGAACGG CAATTATTAT TTATCCATGC AACTTCAAGT TGCAGTATCG GAACATTAAC 60
 TTTTCTGGGG TGAATATCAC TCTGATATCG TTTTGTAT GCGTNT 106

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTTATGTGCG GTATTGATGG CTGAAGCCTG TAATATCGGA CTGGAACCGC TGATAAAGCA 60
 CAATATACCA GCACTGACCC GCCATCGGCT CAGTTGGGTG AACAGAATT ACCTTCGTGC 120
 AGAAACGCTG GTCAGCGCCA ATGCCCCGCT GGTGATTTT CAGTCCACAC TGGAGCTTGC 180
 TGGTCGTTGG GGAGGTGGAG AAGTGGCATC AGCTGACGGC ATGCGCTTTG TCACACCAGT 240
 GAAGACCATC AACTCAGGAT CTAACAGAAA ATATTTTGGT TCTGGGACGA GGCATCACCT 300
 GGTATAACTT CGTATCTGGA TCAGTACTCT GGGTTCCATG GCATTGTGGT ACCCGGTACA 360
 TTACGGGRCT CGATTTTGTA CTGGAAGGAC TTCTTGAGCA GCAGACAGGG CTGAATCCAG 420
 TTGAAATCAT GACAGACANT GCGGGTAGCA GCGATATTAT TTTCGGTCTG TTCTGGCTAC 480
 T 481

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGGNCCGTAA TTCCCAACCA TTTGCCGAGG TCCAGNTTTT TCACCATGTT ACTCGGGATA 60

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GCCAAAACNG ATACCGATGT TGCCGCGGTC CCGGTGCGAG GATCGCGGTG TTGATACCGA	120
TCAGTTCGCC GTTCAGGTTA ACCAGCGCAC CACCGGAGTT ACCACGGTTG ATCGCTGCAT	180
CGGTCTGGAT GAAGTTTTCG TAGTTTTCGG CATTTCAGGC GTACGCCCCA GCGCAGAGAC	240
AATCCCCGAA GTTACCGTCT CGCCGAGACC AAACGGGTTA CCAATCGCTA CGGTGTAATC	300
ACCCACGGGC AGTGCATCAG AATCCGGCAT CTTAATTGCG GTCAGGTTTT TCGGGTTCTG	360
GATTTGGATC AGCGCGATAT CAGAGCGCGG ATCTTTGCCA ACCATCTTCG CGTCGAACTT	420
ACGGCCATCG CTCAGTTGAA CTTTAATGAC CGTCGNGTTA TNAACAACGT GGTGTGTGGT	480
GACGACATAG CCTTTATCGG CATCAATGAT GACGCCGGAA CCCAGCGCCA TGAATTCTGT	540
TSCTSSCGGC CACCATTA	558

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CACCTGCGTG ACGTGACCGA CCTTTTCTCC TCGCTGNTTG TTTCCCCTAT CGTCGGCCTG	60
GTCATTGCGG GAGGCCTGAT ATTCTGCTG CGACGCTACT GGC CGGGAC GAAAAAGCG	120
TGACCGTATT CGCCGCATTC CGGAAGATCG CAAAAAGAAA AAACGGCAAA CGTCAACCGN	180
CATTCTGGAC GCGTATTGCG CTGATTGTTT CCGCTGCGGG CGTGGCGTTT TCGCACGGCG	240
CGAACGACGG ACCAAAAGGG ATC	263

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTAACGCGTC TGGAAGATGG CCTGCCAGTG GCGTCGTCG ATGTGGTCGA GGGGCTGGAC	60
GGTGCCATT CCGCCAATAT CTCACCGGAC AACCGTACGC TGTGGGTTCC GGCATTAAAG	120
CAGGATCGCA TTTGCTGTT TACGCTCAGC GATGATGGTC ATCTCGTGGC GCAGGACCCT	180
GCGGAAGTGA CCACCGTTGA AGGGGCGGCG CCGCGTCATA TGGTATTCCA TCCAAACGAA	240
CAATATGCGT ATTGCGTCAA TGAGTTAAAC AGCTCAGTGG ATGTCTGGGA ACTGAAAGAT	300
CCGCACGGTA ATAATCGAAT GTGTCCAGAC GCTGGATATG ATGCCGAAA ATTCTCCGAC	360

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ACCCGTTGGG CGGCKGATAT TCATATCACC CCGSATGGTC GCCATTTATA CGCCTGCGAC	420
CGTACCGCCA GCCTGATTAC CGTTTTACGC GTTTCGGAAG ATGGCAGCGT GTTGAGTAAA	480
GAAGGCTTCC AGCCCAACGGA AACCCAGCGG CGCGGCTCA ATGTTGATCA CAGCGGCAAG	540
TATCTGATTG CCGCCGGGCA AAAATCTCAC CACATCTCGG TATACGAAAT TGTTGGCGAN	600
CAGGGGCTAC TGCATGAAAA AGGCCGCTAT GCGGTCGGGC AGGGACCAAT GTGGGTGGTG	660
GTTAACGCAC ACTAACCGCT GAT	683

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGATGCAGG GAAAAACATT GATATTACCG GGGCAACGTG CTCGTCCGGT GGAGACCTTG	60
GAATGTCTGC GGGTAATRAC ATCAACATTG CCGTAAACCT GATAAGCGGG AAAAAAGTCA	120
GTCCGGTTTC TGGCACACTG ATGACAACAG TTCATCATCC ACCACCTCAC AGGGCAGCAG	180
CATCAGCGCC GGCATAACC TGGGCGATGG CTGCAGGCAG AGATKCTGGG NTGTCACAGC	240
ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GT	282

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGAACGGCC CCCCCACAG CCGTTAACA AACGGNTGCC CCGGCGATAA TCGTACTGAT	60
AAGTTAACTC CAGCAGGCGG TTAATTGAAA GCGAACGGGA GGCTGATGCA TGGTAATAAT	120
CCCTTAAAC GCGACGGCAA CGCGCCAGTA AACCGTGAGA TGGTCAGGGG CAAGCCAGTC	180
CGGGTAAACC AGAGGCAGTC CGGCAGTGAA CGAACCGGAA ACATGACCAC TGGTGGTGCT	240
GAGCCCGGCA GCAGACCCC ACAGCGTGCC GGACGAGTAC GGGTCATCTC TGTCAGAGTG	300
CAGCCAGCCG CCGTCCAGTG CAGTCACTGC ACGGACTGTC CCCACATATG GCAGGGAGAA	360
CAGAGACCAG GACAGCTCAT TTCGCAGATA ACCGCCGTTA TTACCGGAGA TATACTGCTC	420
CTTAAAGCCA CGCACTGAAC TCTACCCCC GAGGCTCAST TGTTCCACAC CATGAAGACG	480
GTCCGGTGAC CACTGGGCAT AAGCGCTGGT CAGCCACCAC ACCCTGTCCG TGACGGGGCG	540

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CTGAAACTG GCACTCACCG ACCATTTCGG GAACGTATT ACAGGCAGGT CTCCCCCTTT 600
 CCGGTGGTGG CTTTCTGCGC CGAACCAGGG CATCCCCCGT GTGAATACCG GATTGAGTGT 660
 TCCGACACCA CCCAGAAACT TGTGTGTGTG ATTCANC 697

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4835 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TTGACTGAG CACCACAAAT ACTGGGTATC TCCCCAGATA GTTCATTGCG GTACAAGCAA 60
 TATAGGTGCA GAAAGTCAAC CTGCTGCACC CTATTGGATA ATTATATATG GCCTTCAATA 120
 AAGTTTGGCG TTGTCGACGT TGGCTATATC AGCCATTTCC AATGCATAGT TCTTTGGTTT 180
 AGCACCATCA AGTTATAGAT TTGGGAATAG TTTCAACTGG TATTGATTGA ATTGGGTTTC 240
 ATCGTCGATG ATTAATACTA TTTGTAAAGA CTTTATTGTT GATTTCTTAT TATACCACAA 300
 ACCCAAACCTG GTCTAGGTCA TCATTTGGTG TTGATAACGG GCTCTGATAA TTTCTGCTCT 360
 TCTGCTATAC TGGGGATTAT GAAGAATATT AAGGCTGAGT GTATTGAGGT AGTGTTCTTT 420
 GAACCGACCA TTCATGACAA TATATTCTTC AATTCGTGAG TGATCCAGCA ACTGGTTGAA 480
 TTTAAAACAC TGAGTGATGT TATCCTCTGT AATCGTATGG TTGCTGAACT AGTTGATGTA 540
 GCCGATAAGG TTTATACCAG ATATCTTTTG GGGGGATTAG ATAACGTAGC CGCGGATAGC 600
 AAACGAGATA GTTGAATTTT ATTACCGTAA TTTCTTCCAT TGAGAAAAC TTATTTTTCT 660
 TGGTGATATT CGCAGTTATG TATCTTCCAT AAAGACTTGG GAATATCTTG CTTGAAARGC 720
 TATCTGGAGA TAGCCTTAGT TATTTGATAA ATATTTCAA TAGGAGGAGC CGTATGGCTG 780
 TCATTTATAC CCTCACTAA TCGTCACTTG TCAAGTCTGG TGGTCAATTA CATTGGAATA 840
 TTGATTCGCC ATCAGAACAA CAGCCACAAA AGATCGTCAA TGGTCGGGTT GCGCTTCGGG 900
 GATGGTTACT GGCAGATGTG GAAAAAGATC TCCGTGTTGC GGTAAAAATT GAACATTTGA 960
 CATAAGTTT TCCCTTCAAT ATAAAGCGCC CTGATGTTAT TTCAGCTATA CTGAAACAGC 1020
 CACCTGAAAA ACATCAAAGA CTTTATTGTG GATTTGATAT CAATGTCCCA TTTCTACTA 1080
 AAATAATTAT TGGCCTTGAG TCTGATGGGT TGATTACCTG GTTGAAGAG TTATTATTTT 1140
 TCCTGCCTGA TAATTGAATT AAGTATCTAT ACCGATAGTA TCGCGATAGA TATATTTTTT 1200
 TACAGGATGA TAATTTGAGA ATCTATATAG CCGCTATTAT CAAGGATGAG TATTCAAGTT 1260
 TACTTGAATG GATTGCCTAC CATCGAGTAT TAGGTGTTGA TGGGTTTAKT ATTGCAGATA 1320
 ATGGCAGTCG TGAWGGTAGC CGAGAATTAC TATTTTCCCT CGCTCGCCTA GSTATTGTGA 1380

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CGATGTTGGA	ACAACCGACT	TTGGTGAATC	AAAAGCCACA	ATTACCTGCA	TATGAACATA	1440
TTTTACGTAG	CTGTCCGAGA	GACATAGACC	TGCTTGCATT	TATAGATGCT	GATGAATTTT	1500
TATTGCCACT	TGAATCGGAT	ACCAATTTGT	CAGATTTTTT	TTCTGAAAAG	TTTCAGGATG	1560
AGAGTGTGAG	CGCTATTGCA	TTGAATTGGG	CAAATTTTGG	TTCTAGTGGT	GAATGGTTTG	1620
CTGAAGAGGG	GTTGGTTATT	GAACGTTTTA	CCTATCGTGC	CCCGCAATCC	TTTAACGTTC	1680
ATCATAACTT	CAAAAGCGTG	GTCAAACCCG	AACGAGTTAA	CCGCTTTCAT	AATCCGCATT	1740
ATGCTGATTT	GCGTTATGGT	CGATATATCG	ATGCATTGGG	TCGTGATTTG	ATTCTGCACC	1800
CGAGGCATGG	TAATGGGGTT	AGTGCTGAAG	TGACTTGGAG	CGGTGTCAGG	GTAAATCACT	1860
ATGCAGTTAA	ATCACTTGAG	GAATTCTTGT	TGGGCAAGCA	TCTGCGTGGT	AGTGCTGCCA	1920
CTGCTAATCG	AGTAAAGCAT	AAAGATTATT	TCAAGGCACA	TGATCGTAAT	GATGAAGAGT	1980
GCCTTCTCGC	TGCCGCATTC	TCAGAACAAG	TAAAAGCTGA	AATGGAACGA	TTAAGTGTGA	2040
AGTTGACTGA	GTTACCAGCA	GTTGAACCTA	TTCTACTGG	TTCTTGGTTC	AAAAAAAAAA	2100
TGAAGAAATG	GATGGTTTGA	ATATATTGAG	CAAGCACTTT	GGTATTTATT	TCTGCTCTTA	2160
TCTACAGGTC	TGCTAATAAG	GATCTGTATC	CCCCAGGTGT	TACCTTGGAC	TGTAAGTTAT	2220
ATTATGTGTA	GCTATTGCGA	TTGGCAGCCT	CTGACATTGC	CAGACTCGTT	TTCTCTTCAT	2280
TCTGGTTGGC	TTCTGATTCG	GGGGCGCGTG	TTGACGACTC	AAACTCGAGG	TGAAACTCGT	2340
CTGCGCTGGC	AATGCGGACA	AGGAATATGG	CATGAACAGA	AGTTGCCGGT	CACTCGTCGA	2400
GGCACGTTGC	TGGAGCTGGT	TTATCTACCY	TCGGGAGCTA	GTCATTKGTC	TTTGCTGGCA	2460
AGTAATAAGG	GCGCTGAGTG	TAATGTTGAA	ATTACTCAGC	TTTGTTGTGT	ATCCCGTGCC	2520
GAGAGTCTCT	GGCGTCGATT	GCGCCGGGTT	GTACCTTTTT	ACCGACGCTT	AACGAAGTCC	2580
AGACGCAAAA	GGTTAGGCCT	TTCATGGCAT	TTGTGGCTCA	CGGACTTGCA	GCAAGCTTAC	2640
CAACTTGTCA	GCAGAGTTCG	CGATGATAAA	CCACTCAATA	GCTATGATGA	GTGGCTAGCA	2700
GACTTCGACA	CCCTTGAACC	CGCCGAATAC	AAGCTGATTA	AGCGCCAGCT	GGCTCGCTGG	2760
GGCACATTAC	CACGTTTCTG	TTTGCATCTT	GTTGGCGTTG	GGGATGAACA	GAGCCGCCAC	2820
AAGACCCTGG	AGAGTATTCA	GGCACTCTGT	TATCCGGCAA	GCAATATAAA	CCTGCAGGAG	2880
CATGGTGCAT	ATCCAGAAAT	CTCCAGTCAG	TCAAGCGGCG	AATGGCAGTG	GGTGTTGCCT	2940
GTAGGGGCAG	TGGTTTCGCC	AAGCGCCTTA	TTTTGGGTTG	CCCACCAATT	ACGCCAGAAT	3000
CCTGATTGTT	TATGGATATA	CGGTGATCAC	GATCTGCTTG	ACGAGAGAGG	TGAACGTCAC	3060
TCTCCCAACT	TCAAACCTGA	TTGGAATGAA	ACGCTGCTAC	AGAGCCAAAA	CTATATTAGT	3120
TGGTGTGGTT	TGTGGCGTGA	ACAAGGTGCT	GGCCGTGTTT	CCTTTGATGC	GGCGACATGC	3180
CATCAGTGGT	GGCTACAGTT	GGCAAAGATG	TGTGAACCGA	AACAGATAGT	CCATATTCCA	3240
TCATTGATGA	TGCATTTGCC	TGCAAGAGCG	TTGATTTCCG	ATGATTTTGA	GTCGCTGAAA	3300

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GATAAAGAAG ATTTACTGCC ATCAGGAGTG AGCATTGAGG CAGCACCTCA TGGTGTATGT	3360
CGTTGGCGCT GCGCGTTGCC AGCGCAATTG CCATTGGTTT CAGTGATTAT CCTACTAGA	3420
AATGGTATTG CTCATTTACG CCCTTGTTATC GAAAGCCTGA TACAAAAGAC GCAATATGCC	3480
AATATGGAAG TCATAGTGAT GGATAATCAG AGCGATGAGG AGGAGACGCT TGCTTATCTT	3540
GCTCATATCG AACAGGTTTA TGGCGTTAGG GTGATTTCTT ATGATCAACC GTTTAACTAT	3600
TCAGCCATCA ACAATCTGGC AGTGAGAAAC GCACATGGAG ATATGATATG TTTGCTGAAT	3660
AATGATACTC AGGTAATCAG TATTGACTGG CTGGATGAAA TGGTTTCTCA TTTATTACGC	3720
CCCGGCGTGG GTGTGGTAGG AGCAAAGCTG TATTACGGAA ATGGCTTGAT TCAGCATGCA	3780
GGCGATGCTG TCGGCCCTGG CGGTTGTGCA GATCATTTTC ATAATGGTTT GTCAGCTAAC	3840
GATCCTGGAT ATCAGCGTAG GGCTGTTAGT GCCCAAGAGC TGTCAGCTGT GACTGCAGCT	3900
TGTTTATTGA CTCATAAAGA GTTATATCTG GCGCTCGGAG GACTTGATGA AACGAATTTG	3960
CCGATAGCTT TTAATGACGT RGATTATTGT CTCAGAGTTC GAGATGCTGG CTGGAGAGTA	4020
ATCTGGACTC CCTTCGCTGA ATTGTATCAT CATGAGTCTA TTTCCCGTGG TAAAGATGTA	4080
TCAAAACAAC AGCAGATACG AGCGAAATCT GAGTTGCGCT ATATGAAAAA ACGATGGGCA	4140
TGTGCACTTA AACACGATCC AGCCTACAAC CAAAATTTGA GTTATGAACG TCCTGATTTT	4200
TCTTTAAGTA GAGCTCCTAA TATAGTATTG CCATGGATGA ATTAATTCGC AGGAAACTAT	4260
TTAAGCCTTA TCGTAAATTA AATAAACAGA GTTATAGAAG TCCGCAAAGC TCTGAGATTA	4320
ACTTTGAACG ATTGTTTATA TTACATGAGG GAAAATCACC TACATTAGCC TATTTTGAAT	4380
CGGCTATTAT AAGTCGGTTT CCTGATGCAG AATGTCATTT TATCGACACA TTAGCATCCA	4440
CTGATATATT TATTCCTAGA GGATCTGCCC TTGTCGTCAT TAGATTCATC TCCCCAAAAT	4500
GGCAACAGCA CATAGAAAGA TATAACGACA GGTTTTCTCG AATTGTTTAT TTTATGGATG	4560
ACGACCTGTT TGACCCGACT GCACTATCTA CGTTACCAA AGAGTATCGT ACCAAGATAA	4620
TAAGGAGGTC GCGGCTCAG CATCGATGGA TTACGCAATA TTGTGATAAC ATTTGGGTTT	4680
CAACTGCCTA TTTGGCTAAT AAATATGCAC ATCTTAACCC GGAGATTGTT TCTGCTAAAC	4740
CGTCACTGGC ACTCATTGAA ACACATCGAT CAGTAAAAAT CGCTTATCAT GGCTCAAGTT	4800
CTCATCGGGA AGAAAAATAT TGGTTGAGAC AAATC	4835

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

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GAAAAATGNC ATAACCGCAT TCCATCAAGC CCGTNAATAT CCGGSACTTT CATTATTTTC	60
TGAGGCGTAC AGGGAAGCAA TAACTGCTGG TCAGATATTG CTGTCTCCGG TACATTTACC	120
TGACACTGTA TTTTTCATC CCASTTTACC GACAGGGTTT CCGCCGGCGT CACGCCACTC	180
AGCCAGGCAA GGCCTTCGTC GGCCACCATG CCASTTCCC GGCCTTTTTT ACTGTTTACA	240
CTGGCACCAA ACGGGGGCTG AGAGCCATCA GCAAGACGCA GTATTGCAA CAGACGTTTC	300
CCTTTAAGCA CGCTGAATTT CCGGTAACCA ATGGCACCTT CTGTACAGCG CGATTCCACA	360
ACAGAACGGG TTGCTTCCAC ATCATCCGGT AAGCGTTCA GGTCAACAGA GGTTSTATTC	420
CGGTAATAAC TGCTGATGTC AGTCACCAGG CCGTTCCCC AGCGATTTGT CACCACCTGC	480
CCGCCATCAA CCGGTACACC TCCCACACCA TCCGTGTCAA CAAGAAGACG TGTTCCACCG	540
GACATTCGCC CTGCATGTAA CGCCGCACCT TTTCGGTAA TTGTTGCCCC ACCGGAAGCA	600
CTGACGCGGA AAGACGTATA TCCTTTCTGC AGGGATGCAA TATTCGCGGA CAAATTTGCC	660
AGCGGACTAC GATGACTGTA ATAGGCATTA ATCTGACGTT GCGATGTCAG TCCACCGCCA	720
CTGTTAAGGC CGGCGTTTCA GCTGTAGCTG TCCAGACCGT CATTGAACGT GWCAGTGTAG	780
CCGGCCATAT TCACATAACG GTCATTACTC ATACTGCCAC TGTAGCTCGC TGTCCCCGTC	840
CCCCAGCGGC ACGGATATAC GCAGGTAAGC AGAATCNTTA TCACGCCCCA GATATTTAGA	900
CCTTGAGGCT GACAATCCAA CCGCCACACC CTGCASTCCG AAAACATTAA AGTAGCGGTT	960
GACGCTCACC GTATAATAGT CCGTTTTCCG TATGTCCCAG TATGTCTGAC GGCTGTACTG	1020
CAGGTAAAAA GAGGTGTTCC AGTCCGCCAC GTTTTTATTC AGCGTAACGG TATACATCTC	1080
TTTTTCCCGA CTGCTGTAAT CATTACGGTA GCGGGCGTTC AGGTACTGCT CCATGGTCAT	1140
ATAGTTTCGC TCTGAGAAAC GATACCCGGC GAACGTAATG TCGGCATCCG CATTATCAAA	1200
CCGTTTGGAG TAGCTCAGAC GCCAGGATTT TCCCTGAAAC GTTCTCTCTC CCTCAATACG	1260
GGCTACTGAC TGCGTGATAT CAGCGGAAAG GGTCCCCGGC ACACCCAGGT CCCAGCCGGC	1320
ACCGGCTGCC AGTGATTAT AATCACCGGC AAGCACAGCC CCGCCATACA GCGACCACTG	1380
GTTACTGAGC CCCCAGGATG CCTCTCCGGT CGCAAATACA GGCCCTTCGG TCTCATGCCC	1440
GTATCCACGG GAACGACCGG AGACAAGTTT GTACCGGACC TGTCCCGGAC GCGTCAGATA	1500
AGGAACCGAG GCCGTATCGA CCTGAAAGTT TTCTCCGTC CGTTCTGTTC AATAACCTCA	1560
ACATCAAGAC GTCCGCGAAC TGAAGTGTCC AGGTCTTGAA TACTGAATGG CCCTGCGGGG	1620
ACCATCGAGT CGTACAGCAC CCGTCCCTGC TCGACACCA CAACACGGGC ATTAGTCTCC	1680
GCAATCCCGG TAATCTGCGG TGCATAAGCC TTGSCATTCT TGGGGCGGCA CATTCCGGGT	1740
CAGCGN	1746

(2) INFORMATION FOR SEQ ID NO: 60:

(1) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TGTA	CTG	CGG	CGA	ATA	TCC	AGT	GT	TTC	AA	ATT	CC	ACT	TT	G	CAG	C	GAC	TG	CAT	G	AT	GT	60	
CT	GC	GG	CG	CG	G	TA	ACA	AT	CA	GG	G	ATT	ACT	GT	G	TTT	G	CT	G	CG	G	AT	GG	120
AC	GC	CC	G	CTA	CC	G	ACC	GT	C	CT	CC	G	CT	C	T	CT	T	T	A	G	CC	G	CC	180
CT	G	CT	T	C	A	G	C	A	C	A	G	A	C	A	G	A	T	T	G	A	T	A	G	240
GT	T	G	CC	G	CT	G	CG	T	TT	T	CC	AT	T	T	CT	G	A	G	T	CC	A	G	300	
CG	T	G	CC	CG	GG	TC	AC	C	A	T	C	A	C	A	C	T	G	T	CG	T	CG	G	CA	360
TT	T	C	A	G	CG	T	C	A	G	G	CT	GG	T	T	CT	C	G	C	T	T	T	A	G	420
G	AT	T	CC	G	A	A	G	A	G	G	CG	T	T	A	C	C	T	C	T	T	C	A	G	480
AT	CC	A	C	A	C	G	C	T	G	A	T	C	A	C	T	T	CC	G	T	C	A	G	540	
A	A	T	C	A	C	G	T	T	G	A	G	G	A	T	C	G	A	A	C	G	T	G	A	600
G	C	G	C	A	A	T	C	G	A	G	T	T	G	C	C	A	G	T	T	G	T	G	A	660
C	A	T	T	C	A	T	C	G	C	G	T	A	T	T	G	T	C	C	T	T	C	A	C	720
CG	G																						723	

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TAG	AGG	AT	CC	CC	G	G	C	G	T	T	G	C	G	A	T	C	A	G	A	C	C	A	T	60
TT	AC	CC	T	G	A	C	CC	G	Y	T	CC	A	T	A	C	C	T	T	A	C	GG	C	T	120
AT	C	A	G	C	A	C	A	T	AG	T	G	C	T	T	C	A	G	C	G	G	G	C	A	180
A	CC	C	A	G	C	G	C	C	CC	AT	C	G	T	A	T	G	C	A	G	C	A	G	240	
T	G	A	C	G	G	T	A	C	A	G	C	A	T	G	A	C	T	T	A	G	C	C	A	300
GG	A	C	T	G	G	C	G	T	C	A	T	G	G	G	T	T	T	G	G	T	G	C	G	360
C	A	C	C	G	G	C	T	G	C	A	G	G	C	A	G	T	T	T	G	G	G	C	A	420
A	T	A	T	C	C	A	G	T	T	G	C	C	G	T	T	C	C	C	A	G	C	G	480	

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CATTCGGTTT	CTGCCGGGGA	GATAACCTTC	CTGTACGGG	GAASTGTTGC	CGGAAGTGCT	540
TTGCCGACGG	GAGASTCTGA	TGTTTTGGGC	GCTGTCTCTC	CGGCCATTGA	GGTGAGTTGC	600
AACTGCGCCT	CACCAAGCCT	GTTCTGAGGC	TCGGTTATAC	GCGTTTCTGC	CCGTGCGATC	660
TTCTTTTCTA	TCTTCTCGCG	GCTTTTCTCG	CTGCTGCGAC	CGAACAACAT	TCTCTGTAGT	720
TTAGCGACCA	GCGCTCTGAG	TGAGCTGATC	TCGCGGCATA	GCCGGTTATT	TCACCAGACA	780
GACGGACGAT	AACAGCCTGC	TGTGCGATCA	GCAGGGCCTT	CAGTTGCTCG	ATGTCGTCGG	840
GGAGTGTGTT	GTTCAATCCC	CTGTTTTATC	ACGGGTTATA	TCCGGATGCC	AGGCCGTTCT	900
GTCCGTTTGG	GATGTTGCCA	CGCGATCCCC	TCCAGTAGCA	TGGATAACTG	AGCTGGCGTC	960
AGGTGCACTT	TCCCTTCCCG	GGTTACCGGC	CAGACGAAGC	GGCCCCGTTT	CAGGCGTTTG	1020
GCGAACAGGC	ATAACCCGTC	ACGATCGGCG	CACAGTATTT	TCACCATTTT	GCCACTGCGG	1080
CCCCGGAAGA	CGAAGATATG	CCCGGAGAAC	GGGTCATCTT	TCAACGCTGT	CTGCACCTTC	1140
GAAGCCAGGC	CGTTGAAGCC	ACAACGCATA	TCTGTGATGC	CAGCGATGAT	CCAGATTCTG	1200
GTACCGGTTG	GCAGCGTTAT	CATCGGGTAC	CTCCTTTTAT	TTCGCGGATT	AGCGCCCGTA	1260
ACATTTCCGG	AGTGAGAGGG	TCAAACAGTT	TTACCACACC	TGATTTAAGA	TGCAGCTCGC	1320
ACCGTGGGAC	GTTTCCGGGA	TCACACTCAG	GGCACTCATC	AGGCTTGTTA	CGCCAGAAGG	1380
GATTTGTAAC	TGGTCTGGTC	GGCTCTGGCG	TATCAGTCAG	AGCCACCGGG	ACAGGCATGC	1440
ATTCCTGTAT	GTCATCATCG	CTCAGTAAGC	CGTCCTCGTA	CTGGCTTTTC	CATTTAAACA	1500
GCAGGTTATC	ATTGATACCG	TGCTCTCTGG	CGATCCGGGC	AACAACAGCA	CCGGGCTGTA	1560
ATGCCTGCTT	AGCCAGACGG	ACCTTAAATT	CACGGCTGTA	GCTGGCTCGC	CGTTCTTTTC	1620
GCCATGTGCC	TTGCTGATT	TGAGGCTCTG	TTAATTCCTT	CTTTCTGTTG	GCATAAAGGA	1680
TGGCGTCAAG	CTGAGCTAAT	GAAACTGAAT	CGGGCAATGG	CCATGCGATA	CCGGATGCAA	1740
TAAATCGCTG	AAAAAGCGTA	TGTATTGTGG	AATGACTGAG	ACCTAGACGC	TGAGCGATGG	1800
CCCGGATGGT	CAGTTTATCT	TCAAATCTTA	AACGCAGAGC	ATCAGGCAAA	TAAGAACGGA	1860
AGCAGGGAAT	ATCTTTTTTT	GTCTGGGAAT	TCATCGTTTC	TGTCCATCTA	TATAGATGGG	1920
CGCGATTGTT	GCCAGACAGG	ACAATTTTCA	CAAGACGTCG	CAGATGGGGC	GCTTACCAGA	1980
AATGCGCGGG	TACGACAGTG	ACTCGTCAAA	TCTCAGTTGT	AGCACACGCG	GGATCAATTC	2040
CGGATTGTCT	GCCAGTACCG	CCTTTCGTGC	ATTCATCTTA	AATGTCCCTT	TACTGCAAAA	2100
ATGGACATTA	GTATCGGAAA	CAGGAAAGGG	AGGCGAAAGA	CGGTTTAAAT	GAGACGGTTA	2160
CCATTGTGTC	GGGCTGTGTA	CGTTCTCCCC	GGACAGACAG	CCTCAGTTTC	TAGAATCTAT	2220
AAATTACTGC	TACTGATGCT	GCCGGGGAAA	GGCGTAACGA	AAAAACAGCC	TCCGTTACCG	2280
GACAGCAAGG	AGGCTGAATG	GAGTTTACAG	GATTTGCTTT	TTTATAATGT	CTGGCCATGC	2340
AGTAAAACCG	GACAGGTTTT	ATTATCATGT	GAGGTATTCT	GACATAAAAT	CCTGGATTTT	2400

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TATTTTGTGA CGAATGCTGC AAAATTGCAT CTGCACTCTG ATGTAGCTTT TATCTGTTTC 2460
 AGTGAAGCAT GCCCACAAAC TGAGTTATTA AGTTGTGGAA GAACAGTTTT GTCCCGCCTG 2520
 CATCTCTCCT TTCAAAAACC AGTATGTCGC CATGCC 2556

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CAGTTAGTGT TAAAAAATNT CCTCTGCTNC AGAAATTACA CCCACCAATA TACAATNATT 60
 AATAAATTTT CGGTTGGGTT AGGTAATGGC TGGGATTCTA TAATATCTCT TGATGGGGTT 120
 GAACAGAGTG AGGAAATATT ACGCTGGTAC ACAGCCGGGT CAAAAACAGT AAAGATTGAG 180
 AGCAGGTTGT ATGGTGAAGA GGGAAAGAGA AAACCCGGGG AGCTATCTGG TTCTATGACT 240
 ATGGTTCTGA GTTTCCTCTG AATAAGATGA TGGATTATCT GACTGGCTGT TCATCAGTCG 300
 GATAATGATG AAAACTGATG AGCAACAGGT TGTGCGGGCA ATGTGCAGGA TCCGTCACCA 360
 AAGGGTGGAA GTTGCGGGCG ACTCAGATAA ACGGGTTACA TGAGCTATTT CTGGAGTTTG 420
 ACGAAGCCGT CTGGAAGGGA GAAGAGGCGA TTCCATTGAT GTCTCTGGAA AACATCTGTC 480
 AGTCGTGCTG CTGGAATAT TGATAGAGCA ATGGGAATGG TTATCCAACA TTGATGAACA 540
 TATTGTATAT TTACAGAAAT TTTTAAAAAC AGGACTCAGC AGGTAAATC GTGTAAAAAT 600
 TACTCATGAA TACCATTATG GGCTTACAAA GCGATGTGGT TAAGCAGATC TTATTCAGGC 660
 CTGTGCAGCG TAGGATTACA ATAGGATCGA ATAACGCCAT ACAGGGGAAT GGGAGATAGG 720
 CTGATTCATC CTGTGGCTAT AACCAGGAGC ATATCGGGAA TCMANTATGT TACCCAGAT 780
 GGAACACCAT 790

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10906 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCGGCCGCAG TACTGGATCT CTTTGCGGCA TGACGATGAG GGGGAGAGAA ATAACTTAA 60
 CCCAGTCATG GCAGATGAAG AACAGGCTTA CGTAAAAGGG TTATATGAAG GGATTATGCT 120
 GATTGGTAAT ATAATCAATA AGCCTGAAGA AGCTAAAGCG TTAATCAAGG CAACTGAAAA 180

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TGGCTGCAGA ATGGTGAGTA ACCGCTGCA ACTTCTACCC GAAGAGCAGC GTGTTTCGTGC	240
CTATATGGCG AATCCTGAAT TGACCACTTA TGGTTCCGGA AAATATACAG GATTAATGAT	300
GAAACATGcT GGC GCAGTAA ACGTCCCGC TTCCACCATT AAAGGTTTCA AACAGGTCTC	360
GATAGAGCAA GTCATTGAAT GGAATCCTCA GGTAAITTTT GTGCAGAATC GTTATCCTGC	420
TGTAGTGAAT GAAATACAGT CAAGCCACCA GTGGCAGGTA ATAGATGCTG TCAAAAATCA	480
TCGTGTTTAT TTGATGCCAG AGTATGCCAA AGCATGGGGC TATCCGATGC CCGAGGCTAT	540
GGGGaTTGGG GAATTGTGGA TGGCGAAAAA GCTGTATCCA GAAAAATTCA ATGATGTTGA	600
TATGCATAAA ATAGTCAATG ACTGGTATAG AACSTTTTAC CGTACTGATT ATCAGGGTGA	660
AGACTAATGC GAGTGCTTGC TGCGGGCAGT TTACGCCGGG TATGGAAATC ACTTGTGTCA	720
GAGTATCAGG CCGATAATAT ACASTGTGAT TTTGGACCAG CGGGTATATT AAGGGAGCGT	780
ATTGAGGTGG GTGAGGCATG CGATTTTTTT GCATCAGCCA ATATGACTCA CCCACAGATA	840
TTAATGtCCG CAGGanGAGC ATTSTGTATT AAACCTTTTG CCAGAAATCG TTTGTGTTTG	900
TATGTTCCGG CGAATAAATT CAATGAGAAT GACGACTGGT ATTCTTTATT AAATCGGGAA	960
ACATTGCGAA TCGGAACATC AACGGCGGGA TGTGATCCAT CTGGTGATTA CACTCAGGAA	1020
CTGTTTGAAA ATATGGGGAG GTTCGGTGAA AAAATAAGGC AACGGGCTGT AGCATTAGTT	1080
GGGcgGGAGG CATTTCGTTTC CTCTTCCAGG AAATGCGATA gcAGCGCAGT GGTTAATTGA	1140
AAATGATTAT ACTGATCTGT TCATCGGTTA TGCCAATTAC GCTCCTGGCT TGCAATCAAT	1200
TGATTCAAGTA AAAGTTATAG AAATACCGGA ACCTTATAAT CCGATTGCTA TCTATGGATT	1260
TGCCTGTCTG ACCGATAATG CCCTGCCACT TGCCGACTTT ITAGTTTCAC CTGTTGCCAG	1320
AGGTATACTT GAACAGCATG GGTTTATGCC TCCAGGTACG TTATAGCCCC CTGTCTTACA	1380
GCTGtCTCTT gATCAGATCT CCTGATCAAG AGACTTCATC ACCAGGTAAC CCTCAACCAT	1440
ATCCTGCATA TCCTGAAGTC TGAACCAGCC ATCCACATA ACTACCCAAC CGGGGCGGCC	1500
TGTGCGTTTG CTGTCATGCC ATCGCCCCAG TTTCGCCAGT TTCAGACAGG CCCATTTAG	1560
TGTCGGCGTC TGTGACGGAA GCGGTTTTCC TTCCAGCTTA ACCCACAGCA GTTTCCACTC	1620
TGTCGGCGTC AGTATTTTCT TACAGCTGTC ATTTTGTGTT TCTTCACTGA TACCTCCCTG	1680
CCGCAGGCCa GCACCCGTAC CGCGATAAAC GCCTTGATAA CCACCATGCG CTCAAGGTTA	1740
TCCCGGGTCT GCATTGCGAG CGATTCCACA CATGTACCAC CACTTTTCCA CGCCTTGTGG	1800
TATTCCTCTA TCAGCCaGCG TCGCTCGTAA TGGCTGACGA TACGTCGCGC ATCGGCGGCA	1860
CTCGCCACTT TTTCTGACGT CAGCAGATGC CAGCAGGCAC CGTCTCTGC CTGCTCCCGG	1920
CAACAGACAT ACGTGAGCGG GAGCGCCTGG CCGCTGTTGT CGGGATTTTT TATGCTGAcT	1980
TCGTTGTAAC TGATGAACAT CCGGGCctgg CGGGCTGCCC GCGCGCCTTT TTGCATCACA	2040
TTCAGCGTGT GGCTTCCCGC GGTTGCCAGG ACTTCCGGCA GTTCGAAGAG CTTGCCGGGT	2100

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GCTTCTTCCA	GCCGGCGATT	CTGTGCAGCA	CSCACCACGA	AGCGCTGTCC	GTGGCTGACT	2160
TTATAATGCA	GSTAATGCTA	GATATCCGCT	TCCCGGTCAC	AGACAGTGAT	TACCCGTTTC	2220
TGTATCTCCC	CCAGCCGTTT	GGCCATACGC	TECGAAGCCT	GCTGCCAGCG	GTAACTTTCT	2280
TTTTCTTCAT	AGGGACGTTT	TTTTCGCTGG	TGCTTAACAC	CATAGGTgtC	CGTGACCCGA	2340
CTCCAGCGCT	GCTGTTTCAT	AAGACCGACT	GGCAGGGGCG	TGTCGGGGGC	GTACATCAGG	2400
ACAGAGTGAG	CCAGCAGCCC	GCGCGTCTTC	GGGTAGTGG	TGGTATTCCC	CAGGTCATCA	2460
GATGCCGTAC	TGTGGCTGAA	GTTAATGGTG	GTGGTGTCTT	CCAGTGCAG	GAGCAGCGGA	2520
TGAGCCTCAC	ATGCCCTTAC	AGTGGCGGTA	AATCCGGCTT	CGGCAATGGC	TTGCGGGGAC	2580
ACAGACGGGT	TACGTATCAG	GCGGTACGCA	CCTTCAACCT	GAGCAGTGA	CTGGGATGAT	2640
TTCACAATAG	AAAGACCTGC	ATGCTGAGCG	AGAGAAGAGG	TCACTGACAC	AAGGCGTCGT	2700
GTACGACGCG	GATCACCGAG	ACGGGCATGT	CCAAACTGCT	CGTTAGCCCC	TGAATAACAA	2760
TCAGAAAGTA	CCATAACAGA	GTCGAATAAA	ATGAAATATA	AGAGAAGATC	AACGGGTGAA	2820
GAAAAAGTTC	AAAAAATGGC	TACCGGGGAG	GAAGGAAAGT	ACCGGATGGA	AAGAGCCCCC	2880
CTAAAGCAGA	CTGACAGACA	TCACAAATCC	CCGGGGGGGA	CTTGTGTATA	AGAGACAGGT	2940
CTTACAGGGG	GAGCGTCCGT	CTTTTTATCA	ACATCAGGCA	ATGACATAAC	ATTATGAACA	3000
AGCTCACAAG	TCTGATGGTT	AAATTTTATA	ATGCTCCTTA	CTAAGACCGT	ATTTTTTCAT	3060
TCTGAGATAG	AGTTTTTTCC	GCGGGATTTC	TAAATATTCA	GCAACCTCAT	TGATACGCCC	3120
CTGATGGATA	TTAAGTGCCT	CTGTGATTAT	CTGTGCTCA	GCGTCTCCA	CTCGTCTGTC	3180
AAGCGGTGTC	GGGGTTCCGA	CGTGCATCAA	CGGATTGCT	GTTTCTGCCA	GCGGTAATAC	3240
TCCTACAGTA	AATAGTTCTG	CTGCATTGGC	CAGCTCTGCG	ACATTATTTG	GCCACATGCG	3300
GCGCATCATC	TCTTTGAGCA	TCTCTTTTCC	CACTTCCGGA	ACAGGATGGT	TAAGCCGTTG	3360
ACATGCTTTA	CAAAGGTAAT	GGCGAAACAG	TGGTTCAATA	TCATCGGGGC	GTTGAGTTAA	3420
TGGCAGGCAA	GCGATTTGTG	TCATTGCAAA	GCAGTAATAG	AGCTCCGCGA	TGATATGGTT	3480
GCTGGCGGCC	AGCTCGACCA	GCGAAGTGTC	TCCAATACCA	ATCAGGCGAA	AAGGTCGGTG	3540
TTCCTGGCTT	TGTAAGTGAA	CCAGATGGTA	CTGCTGTTCA	CGCGTCAGGT	GTTCAGGATG	3600
GCTGAGCACT	AATGTTCCCC	CCTGAGCCAG	CGCAATGAAA	TCATTAAGCT	GTGGTGCATT	3660
GTCTGGTGTC	AGCTCGCGGT	AGATAAATTC	GCCTTGTCGA	TTACGTCCAA	ATTGGTGCAG	3720
ATAACGTGCA	CCGGTCATCC	GTCCTGTGCC	TGGGGCACCG	TAGAGCCAGA	CGGCAATATC	3780
TGTTTCAGAC	AACTGCTGTA	AACGTCGCGG	ATACTGATTT	ATCCATTAC	TTCTCCCTAT	3840
CAACTCCACC	TGCAACGTCT	GTTGGCAATA	CTGACGACGC	GCAATGATTG	ATTGACGCTG	3900
GCGTAgcGCC	TCTTCAACCA	GAGAAAGCAA	TTTGCCGGGA	TCAACCGGTT	TTTGCAAAAA	3960
ATCCCACGCG	CCTTTTTTTT	CCGCATCAAC	TGCCATTGSC	ACGTCGCCGT	GCCCCGTaAT	4020

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AAGCAGAATG GGGATCTGTT GATCATCCTG GTGAAATAAC ATCATCAAAT CGATACCAGA	4080
GCAGCCAGGC ATACACACAT CACTTAGCAC AATACCTGGC CAGTCTGGTT GTATCCACGT	4140
CTGCGCCTCA AAAGGATTGT TACAGGCAAA AACCCGATAG CCTGACTGTT CAAGTAACTG	4200
TGTGTAGGCG TCCAGCACGT CAGCATCATC ATCAATCAGC AGAATCGAAT ATTCACTACT	4260
TAGCATCTTC CACATCCGTT AGTCTGAATT GCAGTACCAC ACAGGCATTC CTGGTCATCG	4320
TTGATGCCAG CCGTAATTCA CCTTTCATTT GCTCCATCAA CGACACACAA ATTGAAAGAC	4380
CAATACCCAG TCCTACTTCT TTA CTGGTGG TAAACGGCTT CAATAACGAA GGCAACAATG	4440
CCTCAGGCCA GCGCGGGCCA TTATCGCCAA TGAATACGTT CAGCGTTTTA CCCTGCATTT	4500
GCCAGTTAAC GGTAATGACA GCGCCTTGCC CACAAACATC AAGCGCATTC GCCAGTACGT	4560
TAACCAGTAC CTGCTGGGTT CTGACCTCAT CGCCTGAAAC TGTGGCTGTA CCTTGCGGCA	4620
GAACAAGCGT AGCTTGCAAA GGGCGATGAC GCATGGCCAG AAGTTCCCAG GCCGCACTGA	4680
ACATCTGTGC TAAATCAACG GAATGGAGTG ATATTTCCAG TTCGGCGCGC CGGGTAAACT	4740
GCCGTAGTGA ACGGATAATG GCGTCAATGC GACCAATCAC CCCTTCGGCT TTACCAAGCA	4800
TCATGCTGGC CTGTTCTGTC TGGGTCTGTT cAaTGcCTGC GGGCTGTAAA CAGATACATC	4860
GACAGCGCAT TTAGCGGCTG ATTGATCTCG TGGGCCAGCG TGGTCATCGT TTGCCCCGACT	4920
AnCCGCaGct TCGCTGTCTG AATCAGTTCG TCCTGGGTGG CTCGCAGATC GGCTTCTATC	4980
ACCTTTCGAT CGGTAATTTT TTGTTCAAGT TGCTGTTTTT GCACATTGAG CTGCCCCGAGA	5040
GTATGGCGTA ATAATCCTGC AATTCTCCCC AGTTCATCAT TCCCATAAAC AGGAATAGCC	5100
GTTTCCGTGC CTCCCAGACC AATTTCACAA ACGGCCTGAT TCAGTAGGGT AAAGCGTTTC	5160
ACCAACCGTG AGCGGATAAA ATAATGGTTG AATACCCATG CCAGCAGTAA CGCCAGTGcT	5220
GTCGCCACCA GGATCAGCCC ACCgctAACG CGAACAATTT GTTCCATTCG TTGATTAAAC	5280
ATCTGCATTT GTTGATGAGT ACTGCcAAGT GCGCTTCCAG TAACGTTCTG AAGCGACCCA	5340
GTGTGCTTc CCTGGTGCGA CTGGCATCCT CTAAGGCTTT TTGGGCGGTG ACATATTCAC	5400
GCATCGTAGC CGGCATTTTG TTTTTTACGA TTCCCATATC CAGCAATTCA TCGATAGTCT	5460
GCCTCAGGGT AATGGTGCCA GGCCAGTCAT CCAGCATACG TATATTTTCA TCTGCCGTTT	5520
TTTTCAGATT TTCAAATAA CGGAGATGAG TTTCCACCTG TGTGTCGTCA TCACGTCCTG	5580
ATTTGAGTTC ATTGAGTCTG TCACGCAGAT CGTCAACAAT CTGATTTTCA ATGCGTGCCA	5640
GGGTATAAAC CTGCTGCTGT TCATTTTGCA CTTACGAGA TCGCTTCAGG TATTGCGCCG	5700
TATCGCCyTG TCGGGAGGCG ATTTGATCCA GCAGCGTTCC CTGCTGCCAG GTGAAATCCT	5760
GCACTAAAGA ATTAAGCTCG GTAGTAAAT CATCGTGTA CCAGTCAATC CTCGCTGATA	5820
GCTCACTCAC CTTTTCCCGT AGTAAAAACA TGTTGTAAAG CGCACGATCC AACTCGGATA	5880
ACAGTGATCG ACTGTCCTGC AAAAtGACCG TCAGTTGTTG GCGTTCCCGG GATGACAGCC	5940

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CCCGACTAAG	CCGTTCTATG	GTGTGAGAT	GCTGAATAAT	CTGGGTACGA	AGTTGCAATC	6000
GCACCGTGGT	GTTGGGAGCC	TGCAAAAATT	CATTTAGCTG	GTCTACCACC	AGATTCAGGT	6060
TCCCTTCAAT	AAGGAAAGCA	GAGTGAATAC	GGGGAAAATA	CTCATCCAGC	GAGTAACGAA	6120
TTTGTGAGCT	TTGTTTCATG	CATGAATACA	GACTGACACT	ACTGACAATC	AGGGTCAGAA	6180
GTGCCCCCAT	CAGAAATGCG	CAACGTAAGC	TGGTACTGAT	ACTGACCTGT	CTTAAACGCT	6240
GCCACAGCGT	TATGTTTTTC	ATTTTCAGCTC	TTCCAGTTTT	TTTATCGCCA	GGCGCTGGTT	6300
ATTCAGAAAC	CAGAGTTGCC	ATTCCATCAT	TTGCTGCTCG	GCAAAGCTTT	TGTTATCGAA	6360
CTGTGCCAGC	CAGACGGGAT	CTTCACTGCT	GGCCGCTGCA	ACGGGCACTT	GTGTTAACAG	6420
TGCACGTATT	TCTGGTAATG	GTTTCTTCAG	ACGTGCTCTG	GTACTGTGCA	GCGCTCGCCA	6480
GGCATCTTTT	AGCTGTGCTA	ACCGAAAGCT	AATTGCCGTA	TCAAACAAGC	GCTGCACCAG	6540
ACGCTGACGT	TTCAGGATAA	GGTGATAATT	CAGCGGGGGT	TGATTCATCA	GGAGCTGTTG	6600
TTGCGTTGCC	CGCGGATTGT	CTGCGGCAAG	TGGTGTCAAC	GGATATTTTC	CTGTATTGGC	6660
ATCGGCCAGA	ATACGCTGTC	CTTTCGGACT	TAACAGGTAG	TGAATAAAGC	GACGGGCTGC	6720
ATCGACGTGT	GGGCTTTTCC	TGAGAATTGC	AACGTAGGTG	GGGGATACCG	CAGACCGGGG	6780
GAAATAGGTA	AAAGAGAGAT	GGGGGTCATT	TAACAGTAAA	TTAGCATAGT	TATCGATAAC	6840
GGGGCCGGCA	ACGCCGAGTC	CGCTTTTTAT	TTTAnTCGcT	ACGCCAAAAC	TGCGGGAGGA	6900
GATTGTCACC	AGSTTTCTCT	CACTTGTCAG	CAACGTTTCC	CATCCTTTCA	CCCAGCCTTT	6960
TTGCTGTAAT	AATGACTCAA	CCATTAAATG	GTTAGTATCT	GAACGCGACG	GACTACTCAT	7020
CAATAAAGCG	TCCTGATAGA	TCGGCAAAGC	AAGATCGTCC	CAGTCAGCAG	GGGCAGGAAG	7080
GTGTTTTACA	GAAAGCGCCG	GACGATTAAT	GAGCAGACCA	AAACCTGATA	TTGCTACTGC	7140
AACGGAGGTT	GCACGGATCG	ACTCGGGCAC	CAGGTTTTGG	CTTTCTGCGG	GTSCATCATC	7200
AAACGGGGCC	AGTTTCTGGT	GCTCCTGAAG	GTGCTGGAGC	AGCATTGGTG	ATGAAGTCAG	7260
GATAAGATCG	AGSTTTTCTA	CGTTGGCCGT	ATCAAGCAAC	TGTTCCAGTG	AGGCACTGGT	7320
GCGGTTAAGC	GTACGGATCA	TTACCGACTC	AGGCTCTGTT	TGCCAGCGCT	GTATTATCCA	7380
CGCGGTAGCT	CCGGGTGAGA	ATGTGGTGGC	CATCACCAGT	TCATTTCTGT	GAGCCcTGAC	7440
GGCCCCGGCG	TCATCAGCA	ACAGTAAAAG	AATCATGGTT	TTGATGCCGA	TTTCGCACCA	7500
GCTAAAAAAT	CGGTTTGTGA	TCCAGGTCAT	AAATATTAAT	ACACCGCAAA	AATCGCATTG	7560
AGACAAAAAT	TACCCGTTTC	AGACATTCTG	CTGATAACAC	GTCTGCTCAA	AGAGACCGTT	7620
AATATATTAA	TCAGAGATTA	CCCGATAATC	AGCATGAGAT	TTGTTAATAT	CCGCACATGC	7680
TAACAACAAA	CCAGATAAAG	CATAAATCTA	CCTTGTCTAT	GCATCAATAA	AATGGGTCAA	7740
AAACAGGCTT	TGATTTTATT	ATTTTGTGTC	AATTGTGACA	CATTTTTTCA	GTTTGATGTT	7800
TCATYTCAAT	TATATGACTC	TCATTGTGAG	AATACTCCTG	ATGTTTCATAT	CAATATAAAA	7860

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TACAGGTGAA	GACATGTTAT	CAATATTTAA	AACGGGGCAA	TCGGGGGATA	GTGTTCCGGT	7920
GGAGAAAATT	CAGGTGACAT	ATCGTGGCTA	TCGTATGCAG	GGGTTACTTA	GGGTATTTCT	7980
GGGGTATCTT	GCATACTATA	TCGTGGGTAA	TAATTTCACT	TTATCGACGC	CTTATCTTAA	8040
AGAGCAATTA	GATCTCAGCG	CCACACAAAT	TGGCGTACTG	AGTAGCTGTA	TGCNTATCGC	8100
CTATGGTATC	AGCAAAGGAG	TGATGAGTAG	CCTTGCCGAT	AAAGCCAGTC	CGAAAGTCTT	8160
TATGGCGTGT	GGGCTGGTGT	TATGTGCCAT	CGTTAACGTT	GGCCTGGGAT	TCAGCACTGC	8220
ATTCTGGATT	TTTGGGGCAT	TGGTTGTTCT	GAATGGTCTT	TTCCAGGGAA	TGGGCGTTGG	8280
TCCTTCTTTC	ATCACTATTG	CTAACTGGTT	CCCTCGCCGG	GAGCGTGGTC	GGGTTGGTGC	8340
TTTCTGGAAT	ATCTCTCATA	ACGTCGGTGG	TGGTATTGTT	GGCCCTATTG	TTGGTGCCGC	8400
TTTTGCCCTA	CTCGGCAGCG	AGCACTGGCA	AGGTGCGAGC	TATATCGTTC	CGGCCCTGCGT	8460
GGCTATCGTT	TTTGCGGTAA	TTGTGCTGAT	TCTCGGTAAA	GCTTCCCCAC	GTCAGGAAGG	8520
TCTACCCCTCT	CTGGAAGAGA	TGATGCCGGA	AGAAAAAGTC	GTCCTGAATA	CCCGACAGAC	8580
GGTAAAAGCA	CCAGAAAACA	TGAGCGCCTT	TCAGATTTTC	TGCACTTATG	TATTACGCAA	8640
CAAAAATGCC	TGGTATGTCT	CACTGGTTGA	CGTATTTGTA	TACATGGTGC	GCTTCGGGAT	8700
GATTAGCTGG	TTGCCTATTT	ACCTGCTGAC	GGTGAAACAT	TTTTCTAAAG	AACAAATGAG	8760
CGTCGCGTTT	TTATTTTTTG	AATGGGCCGC	AATCCCTTCC	ACGCTACTTG	CCGTTGGTT	8820
GTCAGACAAA	CTGTTTAAAG	GGCGTCGTAT	GCCATTGGCG	ATGATTTGTA	TGGCGCTGAT	8880
TTTCATTGTC	CTGATTGGCT	ACTGGAAAAG	TGAATCGCTG	TTTATGGTGA	CAATTTTTGC	8940
TGCCATTGTT	GGTTGCCTGA	TTTACGTTCC	ACAATTTCTG	GCTTCCGTTC	AGACTATGGA	9000
GATCGTTCCC	AGCTTTGCTG	TTGGTTCTGC	AGTAGGCTTA	CGCGGTTTTA	TGAGCTATAT	9060
CTTCGGTGCG	TCTCTGGGCA	CCAGCCTGTT	TGGTATTATG	GTCGATCATA	TTGGCTGGCA	9120
TGGCGGATTT	TATCTTCTTG	GCTGCGGTAT	TATTTGTTGC	ATCATTTTCT	GCTGGTTATC	9180
ACATCGTGGT	GCAATTGAAC	TTGAACGTCA	CAGAGCCGCA	TATATAAAAG	AACACTGATT	9240
ACCTTCCCCA	GGGCCGTCTC	CCTGGGGAGT	GGAGTATATT	ATGATTTATA	AGATATCTGG	9300
AAATCAGAGA	TTAATATGGA	AATTTTATAA	GA CTGATTAC	AATAAATGGA	GATGGTATTG	9360
TCATGAGAAA	AATGGATATC	TTTTGTCTCA	ATCAGATAAC	GCATATAATT	CGCAATTGTT	9420
ATGCATTGAA	AATGCTAAAA	AACAGGGATA	CTCAGACGAA	TCGGTCTTGC	CACTTTTTCT	9480
ACATATTTCC	TATATTCAGG	AAAAAGGCTG	GAAATGGTAT	CAATGTTATG	ATTGTGGATA	9540
TATTGTAAAA	GAAACCTCTG	TTTTTTTTTC	GACATACCAG	GAATGTGTCA	ATGATGTAA	9600
AAGGAATATA	CTAGCATCTA	TGTGTAGTGG	TTGTAGTGGC	ACAGTAAATT	TGGCCACCTG	9660
ATTAAAGGTG	ATATTCTCAC	CACAACATAA	AACAACAAGA	AAACAAAGCG	TACCTTCTCT	9720
CCTGAGTTTA	AACTGGAATG	CGCCCAACTT	ATCGTTGATA	ACGGTTACTC	ATACCGGGAA	9780

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GCTACTGAAG CTATGAATGT TGGTTTCTCT ACTCTGGAGG CATGGGTACC TCAGCTCAGA 9840
 CGGGAACGTC AGGAGATCAC GCCTTCTGCT GCAGCACCAC TCACATCAGA GCAGCAACGT 9900
 ATTCGTGAGC TGGAAAAGCA GGTGCGTCGT CTGAGGAAC AAAATACGAT ATTAATAAAG 9960
 GCTACCGCGC TCTTGATATC AGACTTCCTG AATAGTTACC GATAATCGGG AAACCTCAGAG 10020
 CGCATTATCC GGTGGTCACA CTCTGCCATG TGTTCAGGGT TCATCGCAGT AGCTACAGAT 10080
 ACTGGAAAAA CCGTCCTGAA AAACCAGATG GGCTGTATTA CACAGTCAGG TACTTGAGCT 10140
 ACATGGCATC AGCCACGGTT CGGCCGAGC AAGAAGCATC GCCACAATGG CAACCCGGAG 10200
 AGGCTACCAG ATGGGACGCT GGCTTGCTGG CAGGCTCATG AAAGAGCTGG GGTGGTCAG 10260
 CTGTCAGCAG CCGACTCACC GGTATAAACG TGGTGGTCAT GAACATGTTG CTATCCCTAA 10320
 AAGCAACAGC AAACAGCGAC CACTGGGGAG CCCTGCATTG CGGATTTGTA TTGTTACGCG 10380
 GGCCATGCTG ATGGCGATGG GGCCGAGGAG AGTGATTTTC ATACGCTCTC ATATGGTTTT 10440
 CGACTTGTGC GAAATGTCCA CTACGCGATC CGCACGGTGA AACTGCAACT CACCGACTTC 10500
 AGGGGAAACT CGGGGCCGCT GGGTAATCTC ACATAAAAAGT TCTTCGGTGT CATAAACAAC 10560
 GAGAGTATTT GATTCTTTTA TGGTGGCCTG GTGCAGAGCT GCCCTTTCCC AGGACCTCCA 10620
 TATAATTTTT GTAGCGGCAG TCAGTGGCAC ACTCAGTTAA CTACTTTCAC TTCAGTGACT 10680
 TTGAATGAGT CAGGGCTGCC GTTAAAGGTG TTAATGAAGG CTTGTATTTT CCACTTCTGG 10740
 CCTGGTTCAA GATTGGATGC TGTGTCGATT GTTTGACCGA TAACGACTCC ATCTTTTAAN 10800
 AGATTAAATT TTACATAAGC ATTTTGTACA ACAGAGTTTG ATTTATTNC AGCATAACCC 10860
 ACAATTGCCT TCGTCCCACT TGGGGTGTTT TCCACATGAA GGTTAG 10906

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ATGGTTATTT TTATTTCTG CACCTTGCTT CATTGAAAT AAAACATAT GCATACGACG 60
 CTGCCATTGA GCAGAAAAT ACAGGAATTA ATGTTATGAG TTAACCATAA TACCTGTGTT 120
 ATGAATATCT GACATAAACA AGAACAAATC ATATCTTCTG TATTCAGCAG AATAATAAAA 180
 GTTCGTCTGC CATTCTCAA CTTATTCTTC GGAATACGTT GTTTCATGAA AGAAGGGGCC 240
 GGAATAAAAG CTGGTCACCG TAATGCTAAT ATTAATGCAG ACTACCGCCT TCTGGAATTA 300
 ACAGTCATCA ACCAGCACAA ACCATTAGCA ATCAAACAA TTTTAATTAA CAAAATTTTA 360
 GCTAATACAA TTAGTCATT AACCCTCTG CAGTTTGCTT TCTCAATAAG TTACAGATGC 420

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CAAACAATAC TCTTTTATAT GTTATAACAT AACACAAACA ATAAATAAAG AACAGACGGC	480
ACTCCATTTC TCCACGTAAG TGAGCCATCA GAATCGCTTA TGAATGTGTA CGGCAGACGT	540
ATACTCGTGT TTTACTGCAG CAACCGGAGC AAAAGTTGCA CTTCACAGC CTGGGTAAAG	600
TTTTTCATGC TTGTGGGCTC GTCCTCCCTC CATTTCACC GCGGGCAAAC AAGGTCATCT	660
TTTGTCTGGE CACACAGCAG ATGSAGAGTC GAATTATGCT GTCTGACGAC ACCGGAACA	720
AATATGCCAT GCCTTCGCAC AATGAACCCG GGCATCATCG TTTTATCTTT ATAATCGAGA	780
CAGGTATGAG GGAAAGTCGG ATGATAAGCA GATASTGAGT GAGGCGCTGG AACATGGCGC	840
TCTGGCAAGA GAAGTGTAC AGGTTACCTG ATGATATGGG GCAACCTGAT ATCTACTTAC	900
TTTTTTGCCT ACTCTCTTAC TTCATGCCAG CAGCGAGGT ATCGACATTG TGTTTGAACG	960
CTGCCGTGTA GGTAGCAGCG AGGCCGCTAC TGTCGGTAAAG TGCTTCCGGA TAAAGCTCTC	1020
CTCCCGCTTG TGCACCACTG GCATTGGCGA TTTGTTTCAC CAAACGGGGA TCTGTCTGGT	1080
TTTCGATAAA GTACAATTTT ACGTGCTCTC TCTTAATTTG ATTAATCAGT TTCGCCACAT	1140
TTTTACTGCT AGCTTCCGAC TCASTGGAGT ACCCCACTGG CGACAGAAAG CGAACCCCGT	1200
AGGCGGCAGC GAAATACCCA AACGCATCAT GACTSGTCAG TACTTTACGT TTTTCTCTTG	1260
GAATAGCAGC AAACGTCTGC GTGGCGTAAT TATCCAGTTG CTTCAACTGC TGGATATAGC	1320
TGTCACCCTG TTTTCGATAA TCGCTGGCGT GCTCCGGGTC TGCTTTGCTC AGGCCATTGA	1380
CAATGTTGTG AGCATAGACA ATACCGTTTT TCATGCTGTT CCAGGCGTGC GGATCAGTGA	1440
TGGTGATCCC ATCCTCTTTC ATTTTCAGTG TATCTATTCC GTTAGACGCG GTAATTACCT	1500
CACCTCTGTA GCCAGAGGCT TTCACCAGAC GGTCCAGCCA TCCCTCCAGT CCCAATCCAT	1560
TGACAAAGAC AACATCCGCC TGTGCCAGCG TTTTGCTGTC TTTCGKCGAC GGTTCAAATT	1620
CATGTGGATC ACCATCCGGT TGCACCAGAT CAGTGACATG AACGTATGGG CCGCCAATCT	1680
GGCTGACCAT ATCGCCAGT ACCGAGAAAC TTGCCACCAC ATTCAACTCT TTTGCAATCA	1740
CCAGTGGGCT CACTAGTAGG CTGGACAGTG CCACAACCAA AATGGACCGT TTCATCTTTC	1800
CTCCTTCATC TCGTTGCTAT GTGTAAAAAC ACTTCTTGTC AGCGACATCT GCATAACATG	1860
CCGCCATTAG AGCCAAACAG AACTGAAAAG CAGAAAAACA GAGTGCTCGT GAGGATGACT	1920
GCAGGACCTG CAGGCAAATC AGCGTAATAA GACCAGATCA GTCCAACCAG ACTGSCGCG	1980
GTACCAATAC CCACTGCAGC TAACAACATG ATGGACAGAC GTTGACTCCA GAAACGCGCG	2040
CTGGCAGCCG GTAACATCAT AATACCGACT GTCATCAGGG TGCCAAGTAG CTGGAAACCT	2100
GCCACCAGAT TGAGTACCAC CATTGACAAA AACAGGCAGT GGATCAGGCG CCGCGACCGA	2160
CGTGACAGAA CTTTCAGGAA AGTGACATCA AACGACTCAA TCACCAGCAC CCGGTAGATC	2220
AACGCCAGTA CCAGAACCGA ACCGGAACCTA ATTATGCCGA TAGTGATCAG AGCATTGGCG	2280
TCAATAGCCA GAATGGAACC GAACAGCACA TGCAGCAGGT CGACACTGGA GCCACGCAAA	2340

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GAGACCAGGG TGACGCCAAG TGCCAGCGAG CCGAGGTAAA ACCCGGCGAA ACTGGCGTCT	2400
TCTCTCAATC CAGTGCGGCG GCTGACCACA CCAGACAACA TCGCCACAGA CAGCCCGGCA	2460
ATGAAGCCAT CGACTCCCAT CGCAACCAGC GACATGCCCC ATACCAGGTA GCCAATTGCT	2520
ACTCCCGGGA ACACCGCATG GGACAGTGCA TCACCGATCA GGCTCATACG GCGCAGTAGC	2580
AAAAAACAGC CAAGTGGCGC GGCGCTCAGG GTCAACGCCA GACATCCGAC CAGCGCCCGA	2640
CGCATAAAAA CGAAATCGCC AAATGGCTCG CACAACAGGT GCAGTAACAT CATGGCAGCA	2700
GGCCCTGCTG CGGTGGCGTG GCTGCAGCCG TGAGGGAATG GAGTATATCG GCACTTCTCC	2760
CCCATCGGTG GCCTTCCGCA CTGAGCATCA GTACATGAGG AAAGTATTTT TCTACCTGTT	2820
CCATGTCATG CAACACCGCA AGAATTGTAC GTCCTTCCAG ATGTAGCTGC CGAATAACAA	2880
CCAGCAGAGT ACGGATAGTC TGAATATCAA TGCCAGTAAA TGGTTCATCC AGCAGAATAA	2940
CCGACGGCTG CATCACCAGC AGTCGTGCGA ACAGTACGCG CTGTAAGTGA CCACCGGAAA	3000
GTGTGCCGAT GTGCATCGGC GAAAATTCTG TCATACCGAC GGTATCCAGC GCTTCGATAG	3060
CTTTTTTTTG CCATAGACCG GAAATACGAC CGAACATCCC GCTGTGTGGA ATACATCCCA	3120
TCAGCACCAAT ATCGTTAACA CTCAGTGGAA ACTGGCGATC AAATTCAGTC AATTGGGGCA	3180
AATAACCTAA CTGGCGTTGC CCCTGCGGTG CCATGCAGAA GCAACCACCC AGAGGTGGCA	3240
GCAGACCGGC CAACGTTTTA AGCAAGGTGG ATTTACCTGT GCCATTGCTT CCGATAATGG	3300
CAGTCAGTGA ACCGGTGTCA AAACATCCAT TCAGCGTACC CAGCGGGTGC TGTCCCGAAT	3360
AGCCAAATGC CAGTGAATGT AATGCGATCA TGTCAGTACC ACCGCCCAGG AAATAAGAGT	3420
CCATAACAGT ACCAGCAGCA CACCGACGAT ACCCAGTCGG GCTATTGCGG AAAAAGCATA	3480
AAGACTGACC ACAGTATCCC CCATCAAAAT TGTTATAGTA TAACATTATT GCTTTATGGG	3540
TGCCGATGAT AGGTAAGAAA ATGTGTCATG GCTTCTGCAG CGTAAGCATA CAGCGAGAGC	3600
AGTATTGACA GGGATGCGTT AGTCATTTAG CAGTGTAATG CGCTAAATAG NTGCGCGGAA	3660
TAGTAGATCA CTTTGAGGGT ACTCAGCCCG GATTGTGCGC TCTGATCAAT CGCCAAATCA	3720
AAACAAATCA CCAACCGAAC TGAGCAATGC CGATCATAGC ACCAATTTCC CGTGACGAAC	3780
GACACCGGAT GCAGAAAGCC ATCCATAAAA CACACGATAA AAATTATGCC CGCAGACTGA	3840
CTGCCATGCT GATGCTGCAC CGGGGCAACC GTATCAACGA CGTTGCCAGA ACGCTCTGCT	3900
GCACCCGTTT ATCTGTTGGA TGCTGGATTA ACTGGTTACT AAAATCATTC CCTGCCGGGC	3960
GTGCCCATCG CTGGCCATTT GAGCATATCT GCACACTGTT ACGTGAGCTG GTAAAACATT	4020
CTCCCGACGA CTTTGGCTAC AAGCGTTCAC GCTGGAATAC AGAACTGCTG GCAATAAAAA	4080
ATCAATGAGA TAACCGGTTG CCTGTAAAT GCCGGAACCG TTCGCCGTTG GTTGCCGTCT	4140
GCGGGGATAG TGTGGCTAAG GGTTGTGCCA GCTCTGCGTA TCCGTGACCC GCATAAAGAT	4200
GAAAAGATGG CAGCAATCCA TAAGGCACTG GACGAATGCA GCACAGAGCA TCCGGTCTTT	4260

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TATGAAGATG AASTGGATAT CCATCTTAAT CCCCCAATCG GCGCTGACTG GCAGTTACGC	4320
GGACAGCAAA ACGGCTGATC ACGCCGGGAC AGAATGAAAA ATATTATCTG GCCGGAGCGC	4380
TGCACTGCAG GACAGGTTAA AGTCAGCCAT GTGGGCGGCA ACCGCCAAAA TTCGGTGCTG	4440
TTCATCAGTC TGCTGAAGCG GCTTAAAGCG ACATACTGTC GAGCGAAAAAC CAGCACGCTG	4500
ATCGTGGGCA ACAACATTAT CCACAAAAGC CGGGAAACAC AGCGCTGGCT GAAGGAGAAC	4560
CCGAAGTTCA GGGGCATTTA TCAGCCGGTT TACTCGCCAT GSGTGAACCA GTTTGAACGG	4620
CTATGGCAGA CACTTCTCGA CACAATAATG TGTAATCATC AGTACCGCTC AATGTGGCAA	4680
CTGGTGAAAA AAGTTCGCCA TTTTATGGAA ACCGTCAGCC CATTCCCGTA GGGGAACATG	4740
GGCTGGCAAA AGTGTAGCGG TATTAGGAGC AGCTATTTAG GAGAACAGCT CGCTGACCCG	4800
GTTGACTATG ACTCAAGCCC ATGACGAAGA TAGCTTTCTG GATCAACATC GTTCAGTCTG	4860
CACGTCCCAA TCCAGCCACC AGCCACCAGC CACCAGCCAC CAGCCACCAG CCACCAGCCA	4920
CCAGCCAGGC TACAGTGCCA TCCCGACCTC CCCACGTAAA CCCAGGGACA GGCTAAAGGC	4980
AGAAAATGGG GAAGGCAGTA TGA CTCTCCG TGACACAGAT GCGGGTACCT GATGGGAGTG	5040
AGATCATCTT CCCCTCCCGG TCAGTTCCCG GATCAACACC GTGAGCAGCT CTGGCGAAGG	5100
TTTTTCCAGC GTCATTTTAC CGTAACGAAA TTCAACCTTA CAGGAACTGG CACAGACTGT	5160
GCACTAAGTG GCAGTGGATA AAAGCGGAGT AAGAGCCGCC ACAGGCTCTT TCTGCTCATC	5220
AGGCATTATC TCAACAGGTA ATAATTCAAC GCCAGCGCCA GAAGAGGTTG TTACCGGAAG	5280
ACGCCGCGCC CCCCTTCGTT CAGCCAGAGC CTGAGCCATT TGACCAGGAG GTTATCATTG	5340
ATATCGTGTT CCTGGTCAAT ACGGGCAACA GAGGTGCCTA CGACGTTTTT TCAGTTCGGT	5400
TATCTATTGA CTTAACTCTT TGGCCAGTAA TGCTGCAGCC CCCGTGCCAT GAATAAACGA	5460
GTGGTCGCAG ACCACGCAAC ATGCAACATC ATTCAGATCC CCCGCTAATA TTACAGGTAA	5520
TTCAGAAATCA GCAATACTTT TCCCGACCAT TAAAAGTTCT GATCACGAT CAGTTGACTC	5580
ATCACTTTCA GTCGGGCTCG GTGGAACAGG ATGAAGACAA TGTAATCTTA TTCTCAAACC	5640
TTCTGGCATA TGA ACTATCA TATTCATGGA GGAATTTCC TTGTCCACTA AATACTGTAT	5700
TTCTGCATCA CTTAAAATCA TCCAGGAATA TACATGCATG CCATATAAAT TTTCTTTCGG	5760
GCATTTTCAGG GAGTATGGAA ACACTTCATC CAGAGGTGAT AGTTTCTGTT CCCACCATAA	5820
GTTTGTTTCA AGAAGAACAA GTATATCAGG TTTTCTTTA TTTATAAGTT CAAGAATGGG	5880
TATATATTTT TTATTGGTCA TAAGAACATT GAATACCAGT ATACTTAAAC CCAGAAATCC	5940
ATCAGAGTCC TTTATTTCTT TTACCTGCTT CTTGCCAATT ACTGTATAAG GAATTATCCA	6000
TACCAACTGG TAAGCGACAC AAATTAAACT TATTATCCCA ACAAACAACCT CTGTAAATAA	6060
GTCAAGAAAA ACAACAGACA GAAAAACATT CAAAGTACAC AGCAAAAGTA TCTGTAGTCG	6120
GGGAAAATCC CATCCCCGA CAACCCATGA TGTATTACCG GAAACAGGGA TAAAAGTTAT	6180

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GACTGCCAGA AGGATAGCAG TAAAAATAAA AACACAAGTT ATCACAATC GTCCTTGTT	6240
CTGAACCGGA ACACAAAAC TGCATATACG TTTCAAAAGT AAAAATACAC TGCTGCCACA	6300
AGATTTACAG CGTAACCGGA CAGCATATCC TGATTACGGA CAATCCATGA AACCGCCTCA	6360
CCAGAAGCGT CCATCACATC CGTTTTTTCC CTGTTTTATA TTCCCGAAA CATTTTATTT	6420
TCAGGAATCT CCGGGCCTTT ATCCCGCATC ATTGCAAAAT GGCATCTGAA TCGATCATGA	6480
TTTGGCATCC ATCTCCGATC ACAGTTTGGC ATCACAATCG ATCAGATTT GGCATGCTTC	6540
CGATCATTGA TTAGCATCCT GCCAGTCACT CCGGGAATTA ACTCTTTTCG CCACAGTCTT	6600
CATTGCCGTG TTAAACCAA TGGAGACGGC AATGTCCAAA AAGAGAATAT CCAGGAGCAC	6660
TATGGATACC TGTTTTAAGA TCCTTCAGCT CAAGTTCGAC CAGAAGCTGG CTAACCGTTG	6720
TATCGGACTT GCAAACACC AATGGGGATT GATCTCTATT TTGCGACACA GACGCATTAT	6780
CAATACATCG ATGGTGGGAT CAAATACCTC AGTGGTCTCA CCGTGGATCA AATCCAGCAA	6840
TTGCTCACAG ATTAAGACTC GTCGGGAGTT TTGAGCCAAC ACCAGCAGTA ACCCATATTC	6900
ACCTTGAGTG AAATCTACAG GCTGTTGATG AGCATCAACC AGCACGTAAC GGTCCGGGAT	6960
CAAGTGTCCA GCCGTTAAAA AAACCACTCT ACTACCCTGC TCGACCTAAG CCTCGGCGTT	7020
CAGCCGCCTG AACGGGTATG GCAAGGGTGA AAAGAAACAG CATCCCCACA GTACCGACCA	7080
GACGACAGGA TGATGCTGGA ACAGAAAGCA TTCGCACCTC TCTTAGAATT AGACAGTGCG	7140
TACAGGATAC GTAAGACAGG GTGACGGGGC GGCGATAAAC TCTATTTACA AAGCTGAAAA	7200
TTTTCTGACG ATGAAAAACT ATTCAACAAG GTTATCTGAG GCGTTAAAAAT AACCAGCTCG	7260
ATTAACGACT AACTTGAGGT GAATATGAAT TTAAAAATA TAATTTTAAG TACTGTTTTA	7320
TCAATCGCTA GTTGTCATGC CCTGGCTGTA GGTAATTCTC CAAATAGCGC TATCTAACCT	7380
TCATGTGGGR AAACACCCCC AGTGGGGACS AAGGSCAATT GGTGGGGTTA	7430

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGATTATTCT GGCTCAGATT CATTTTTCAT CAGTCGCTTT CCCCTATAAA CCGTAAGGTT	60
CCATAGTGTC GACGCTCTCG CTTAATTCCC ATATCGTCGA TAGTCTTATT AGCCGCTTCT	120
GTCAGGTCAG AAAAAGTATC ACGCTTCTTT GGGAGTTCAA GTCAGATTTC TCGCCGTCGG	180
GCGATGCGCT CAAAATGTTT GTCTGTATGG GGTGCTTCA TCACGTCAAG CCATCGCGCT	240
GCCGCTCTCC GCCAGAGTAC AAGCTCTTCC AGTTGTTCTG CTTTTTATCT TATCTGTGGC	300

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GATGCAGTAT CCTCCTCCGT TTGTSTAAAT CGTTGAGTGG TGAATCACGC AAAGGGGCTT	360
CTTTTTTCTG ATCTATCCCC ATATTCTTTA GCGTTCTGGT CGCAGCATCT CTGATGTCGC	420
AGACACTGAA CCTTTGTATT TTCCATGATC TTGTGGAGTT TTCSATACAT CTGCTCCGAT	480
GCTGGGTTAT AAAGATCCGC TCTTTATCAT CCTTGGCTTG TGTAAAGCAAT TCTCCCAAC	540
GTTCTGCTGC ACGCCGCCAT AACTCTCTTC TTTCAGTTC CTCAGCTTTT TCATCATGTA	600
CCATTCGTGT ATCCCCGTTT ATCCAGTCTG AACCGCACCG GGTTCCTGG AGAATGTTTT	660
CTCTGTGAAC TCAGGCTGCC AGATCATCGT TTCCGATGGA AGCATAATAA GCTTTTTCTG	720
CTTCTGCCGG ARGAAATATGG CCCAGCTTTT CCAGCAATCG TCGATTGTCA TACCAGTCCA	780
CCCACGTTAG TGTGGCCAGC TCCACTTCTG TCCGTTTTTT CCAGCTCTTA CGTTATTAC	840
CTCCGTTTTG TAAAGACCAT TGATGCTCTC CGCCATTGCG TCGTCATACG AGTCGCCTGT	900
ACTCCCTGTT GATGCCAGTA ATCCGGCTTC CTTAAGCCGT TCGGGACACA TAATGAGAGC	960
CTTTATCGCT GTAATTGTCA ACGACGGATG AAAAGTGATC CACTTATATC TCCACCAACG	1020
GCCCAATATT GATCCACCGT TTTACTCAGG ATTAGCTTCT GCTATAACCC CGGCCTTTCTG	1080
TTTCTGTCTG AGTCGATAGC TTTCTCCTTT GATTTGAACG ACATGTGAGT GGTGTAAGAT	1140
ACGGTCCAGC ATCGCTGAGG TCAGTGCTGC ATCACCGGCG AACGTTTGAT CCCACTGCCC	1200
GAACGGCAGA TTGGATGTCA GGATCATTGC GCTCTTTTCTG TAACGTTTAG CGATGACCTG	1260
GAAGAACAGC TTTGCTTCTT CCTGACTGAA CGGCAGATAG CCTATTTTCA CAATGATGAG	1320
CAGGCGGGGG GCCATTACTC CACGCTGAAG CGTCGTTTTA TAACGGCCCT GACGTTGTGC	1380
CGTAGATAAC TGAAGTAACA GATCTGCTGC TGTGTGAAG CGAACTTTGA TACCTGCACG	1440
GACTGCTTCA TAGCCCATCG CTATTGCCAG ATGGGTTTTT CCACACCTG ATGGCCCCAG	1500
TAATACGATA TTTTCATTAC GTTCTATGAA GCTGAGTGAG CGTAACGACT GGAGTTGCTT	1560
CTGCGGTGCT CCGGTGGCGA ATGTGAAGTC AACTCTTCTG AACGTTTTCA CCGCCGGGAA	1620
GGTGCCATT CGGGTATACA TCGCCTGTTT ACGTTGATGA CGTGCCAGTT TTTCTTCATG	1680
AAGCAGATGC TCCAGGAAGT CCATATAACT CCATTCTTGG TCTACTGCCT GTTGTGACAG	1740
CGCAGGCGCT GCGCTTATAA GGCTTTCCAG TTGCAACTGC CCGGCGAGCG CCATCAGTCG	1800
TTGATGTTGC AGTTCCATCA TCACGCCACT CCTCTGCAGA ATGAGTCGTA GATGGAGAGT	1860
GGATGATGCA GGGGGTGTTT GTCGAAGTTC ACCAGATTTT CATCAAGATG CACGTCATAC	1920
TCTTTTTTCT CCGGAGCAGT GCCAGCATGG ACTGCTGTCT TCGAGCCAGC GATCGCAGGG	1980
ACGGGCCTGG ATTGTTTCAT GCTTTCGTTG GTTAGCGACA TCGTGCAGCC AGCGCAGACC	2040
GTGGCGGTTG GCTGTTTCAA CATCGACAGT GATCCCCATC GGGCGCAGGC GAGTCATTAG	2100
TGGGATGTAA AAAGTGTAC GGGTGTACTG CACCATCCGT TCCACCTTAC CTTTAGTCTG	2160
TGCCCTGAAG GGGCGACACA GTCGGGGAGA GAAGCCCATC TCCTTGCCGA ACTGCCACAG	2220

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CGAAGGATGG AACCGGTGCT GACCGGTCTG ATATGCGTCA CGTTGCAGAA CCACAGTTTT	2280
CATATTGTCA TACAACACTT CGCGCGGCAC ACCACCAAAG AAGCGGAACG CATTACGATG	2340
GCAGGTCTCC AGCGTGTCTT AACGCATATT GTCAGTGAAT TCGATGTACA GCATTGCGCT	2400
GATCCGAGA ACAGCAACGA ACACGTGAAG CCGTGAGCGA CCATTACGCA TAGTGCCCCA	2460
GTCAACCTGC ATCTGTCGTC CGGCTTCAGT TTCGAACCGA ACGGCAGGCT CCTGCTCCTG	2520
AGGAACCGAG AGAGAACGAA TGAATGCCCT GAGAATGGTC ATTCCGCCAC GATATCCCTG	2580
GTCTCTGATC TCGCGAGCGA TTACCGTTGC CGGGATTTTG TAAGGATGAG CATCGGCGAT	2640
GCGTTGACGA ATATAATCCC GGTATTTCATC CAGGAGTGAA GCAACAGCAG GTCGCGGCGT	2700
ATATTTTGGC GGCTCAGATT TTGCCTGCAA ATAACGTTTA ACCGTATTGC GGGAGATCCC	2760
CAGTTCTCTG GCAATCGCCC GGCTACTCAT TCCCTGCTTG TGCAGGATTT TAATTTCCAT	2820
AACTGTCTCA AAAGTGACCA TAAACTCTCC TGAATCAGGA GAGCAGATTA CCCCCTGGAT	2880
CTGATTTTCTG GCGTTGGGTG TGGATCACTA TTGCACCGTT CGTGACAGTA ATGGATTGTG	2940
TCAGACGGAC GACGGGCCCC TAACGCCTGC TCCAGTGCAT CCAGCACGAA TGTTGTTTCC	3000
ATGGACGATG AGACTCGCCA TCCCACGATG TATCCGGCGA ACACATCAAT GATGAACGCC	3060
ACATAAACAA AGCCCCGCCA TGTGCTTATC CCGGTAAAAT CAGCTACCCA CAACTGGTCC	3120
GGGCGTTCTG CGATGAACTG ACGGTTTACA CCGTTGCATG CGGCAACAGC TTTCCGGCTG	3180
ATTGTCATGC GAACCTTTTG CAAACCCCAT ATATTTTCTG CGATACCGTT CAACGGTAGT	3240
GAACCCACCA TCACCGCTCC CGGTATCCCG CTCATGCTGG TATACCCAGA CATGCAGGGG	3300
TTCCAGCGTA CAGCCAATCT TTGGGGCAAT GGAACAAATT GACGCCCACT ACGAGTCATA	3360
CGACTTTTCCA GAACAATACG GAGCGCCCGC TGACGGACCA CCAAAGAGCC GCCATTATTC	3420
TTATTACCTT TAACTAATAA TGCCAATTCA GACCCAAACA CGGCATCATT CGCTTCAGCC	3480
TCTGCGCCAT TAATTAATGC CAGGACTTGG TCAAGAAAGC GTTGCCTTC GTTTACATCT	3540
GTTGCTTGTC GCAGGTAATA AGGTATTTCG TCAACAAACT CGGAACGTGA TAAAGGCTGA	3600
TGCTCCAGCA AAACCTCAAG CATTGCGGGC CGCAACAAAC GACGCTCAGC ATCAACATTG	3660
GGAAACTTAA CCTCAATGGC ATATGTGGCA AAATACTTAA GTTGCTCCTT AAGCCCCAAA	3720
TTAGGCATAA GAGAATCAAT TGAGCCAGAC GCCACTGCAG CGCTTGATTC AATTGTTTCT	3780
ACATACTCGT AGGAAGGTAC AACAACATCT GGAGCCAATG TTTTAAGCTC ATGGAGTTGA	3840
CGGATAATCG GGGATAGAAC CTCATCAGGA TTAAGTGAAC AATCAGTGGA CCAAATACGG	3900
CTAATTCTCC ACCCCAAACG CTCCAAAACC TCTTGACGCA AACGATCAGC GGCAGATTTA	3960
GCTGAATGAT AAGCCGCACC ATCGCACTCT ATACCCATTA AGTAACAACC CGGATCTTCT	4020
ACCGACAGAT CAATAAAGAA TCCTGCAACC CCACCTGAGG TTCACACTCA AACCAGCGT	4080
GATTGAGTGC TTCCATTATA GCAACCTCAA AGTCACTATC CGGAGCCCTG CCCGTATACG	4140

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TCGTGAGGGA ATCTAATTTG CCACTTTTGG CAAACTGTAA AAAACCTTTC AACGAAATAA	4200
CACCAAATTT ACTGGTTTCA CTCGTCAATA CATCTTCAGA ACGCATTGAA CTAAACACAT	4260
GCATCCGTTT CTTTGATCGA GTTAAAAGCA CATTCAAGCG GCGCCAGCMA ACATCGGAAT	4320
TGACAGGCCC AAAGCGTTAA TAAACCTTTC CACCATGCTC AGAAGGTCCA CAGGTAAAGG	4380
AAATAAAGAT TACATCACGC TCATCACCTT GAACGTTCTC AAGTTTTTTC AAAAAAGTG	4440
GCTCTTCCAT GGCATATAAG CCATCAATTG CATCGTTAAA TTCAGTGCGA TTTCGGCGCA	4500
ATTCATCAAT AGCGCGCTCA ATCTGATCGC GTTGCTTGGA ACTCATGGCC ACTACCCCAA	4560
GAGATTTCATC CAGCCGGTGT TGCGCATGAT GAAGTACAGC CTCAGCAACT GCTTGGGCTT	4620
CTTCAATATT GTGTGATTA GAGCAACGAC CTTTGTATAC ATAAGTAAAT TTGATTCCAT	4680
ACTCTGGAGA CTCAGCATTT GSAGAAGGGA ATATCACCAA ATCACTGTTA TAAAAATGGC	4740
GGTTAGAGTA TGCAATTAAC TTTTCGTGTC GTGAACGATA GTGCCAATGC AAACGTCTCA	4800
TAGGAAACAG TGSCAAAGCA GCATCCAAAA TGCCGTCAGT ATCACTTAAA GCCGCGACAT	4860
CATCGTCATC TTCTCCGGCG GAACTTCGAT CTGAAGTGGC ACACTGAATT TGGCCACCTG	4920
AACAGAGGTG ATATGCTCAC CTCAGAACAA CACAGGTGCT CCAATGAAAA AAAGGAATTT	4980
CAGCGCAGAG TTAAACGCG AATCCGCTCA ACTGGTTGTT GACCAGAACT ACACGGTGGC	5040
AGATGCCGCC AAAGCTATGG ATATCGGCCT TTCCACAATG ACAAGATGGG TCAAACAAC	5100
GCGTGATGAG CGTCAGGGCA AAACACCAA AGCCTCTCCG ATAACACCAG AACAAATCGA	5160
AATACGTGAG CTGAGGAAAA AGCTACAACG CATTGAAATG GAGAATGAAA TATTAAAAAA	5220
GGCTACCGCG CTCTTGATGT CAGACTCCCT GAACAGTTCT CGATAATCGG GAAACTCAGA	5280
GCGCATTATC CTGTGGTCAC ACTCTGCCAT GTGTTCGGGG TTCTATCGCAG CAGCTACAGA	5340
TACTGGAAAA ACCGTCCTGA AAAACCAGAC GGCAGACGGG CTGTATTACG CAGTCAGGTA	5400
CTTGAGTTGC ATAACATCAG CCATGGTTCT GCCGGGGCAA GAAGCATCGC CACAATGGCA	5460
ACCCGGAGAG GCTACCAGAT GGGGCGCTGG CTTGCCGGCA GGCTCATGAA AGAACTGGGA	5520
CTGGTCAGTT GCCAGCAGCC TGCGCACCGT TATAAACGAG GTGGTCGTGA ACATGTCACT	5580
ATCCCGAATC ACCTTGGGCG GCASTTCGCA GTGACAGAGC CAAATCAGGT ATGGTGCGGC	5640
GACGTGACGT ACATCTGGAC GGGGAAACGT TGGGCATACC TTGCCGTTGT TCTCGACCTG	5700
TTTGCAAGGA AACC GG TAGG TTGGGCAATG TCGTTCTCTC CGGACAGCAG ACTGACCATC	5760
AAAGCGCTGA AAATGGCCTA GGAAATCCGC AGTAAACCAG CCGGGGTAAT GTTCCACAGC	5820
GATAGTAATA ATGCCGGTAT CAGTTTTTAT CATCACTCTG TTTGCTGTTT AACCAGACTG	5880
GTGTGATTAC TGATGCAGTG AAGACCTTCC CGCATCTGA CTCACACAGC GATCGACCCT	5940
TTGTGTCCTG CCTTGGACCT GTCGGTTGCC GGAAGCGCCT TCATGCGAGG CGTCTCCTCA	6000
CCGATGCGCG TGAICTAAGA AGGSCCTGAC GTTTGTCTC GTTACTGTCC TGTCCGGGTT	6060

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ATCTGTCTGG AGATTCAACT CTGTTTCCTC ACAGGAGCTC TGTTATGGCA GGTAAAGTTA	6120
CGGAAACCGC TGTGTGGGT GGGCTGGATA CACATAAAGA TCTGCACGTT CCCGCTGTCTG	6180
TAGATCAGAA CAATAAAGTT CTGGGGACCC AGTTTTTCTC CACAATACGG CAAGGTTACC	6240
GGCAGATGCT GGCATGGATG ACTTCGTTTG GGGCATTAAA GCGAATTGGT GTTGAGTGTA	6300
CTGGCACCTA TGGATCAGGT CTGCTTCGCT ATTTACAGAA TGCCGGGTTA GACGTTCTTG	6360
AGGTGACTGC GCCAGATCGG ATGGAGCGAC GCAAACGGGG TAAAAGTGAC ACGATTGATG	6420
CTGAATGTGC CGCTCACGCC GCATTCTCCC GAATAAGAAC CGTCACACCC AAAACGCGCA	6480
ATGGCATGAT TGAGTCTCTG CGGGTATTAA AACTTGCCG AAAACAGCA ATATCAGCCC	6540
GCAGAGTCGC TCTCCAGATT ATCATTCCA ATATTATCTC TGCCCCGGAT GAATTACGTG	6600
AACAGCTCAG AAATATGACG CGCATGCAGC TCATCAGGAC TCTGGGATCC TGGCGGCCTG	6660
ATGCCAGTGA ATACCGCAAT G	6681

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TATTCGCGCA TACGCGTTGC ACATGTTCTT TTGGCGAACG ATCATCGGCA ATACAGAGTT	60
CCCAATGGGG ATAGCTTTGA GCCAGGACAG AATCCAGACA GGCACGCAMG TAGATCTCCG	120
CTGGATTATA AACAGGAATC ACAATAGATA TAACTGGAGG GTGAGTCATA CTGGCAAGCA	180
TCAGACTCAC CWCTTCKTTG CCAGGCAACG AAGGTAATTC CACCGTTTCT ATCCATTCT	240
CATAACCGAC AGAAGACGGG GTAACGCTGA ACGTYTCGTT ATAGAATGCT TGCAGGCGCT	300
CTATTGACAT ATCGCCATTG TSCATCAATA TGGATTTTWT GATTTTTTCT AGCGGCATGT	360
CACGATAGCT TTGGTGTCT TTTTGAATGC GAGCCAATAG TGCAGACTCG ACTACTTTCA	420
CATCAACAGC CGCTATTTCA AACTGATTAA TTGCAAATTT TGCTGCCTGT TCTAATGGAT	480
CAAATCGTAA TGCACAAGAG GCGATTCCAG ATAGAACAAC GACTGACGCT GACCGCTCGT	540
TTATATGGCA ACGTTACTGT TTCAAACCTA TTGAACCCCT TACCTGTATC CAAATRTAAC	600
TTAGCTAATC CTTGCTTTGG TTGGGCAATT AATAGAGATA TTAAATTGAT ACCATCCCTT	660
GCTAATATTT GAGAGCTGCT CCAAATCAAT AATGAAAAAT GGATCATTTT CCTCTGCAAC	720
CCAACCTTGT GAATTATCTA TATCTATCGA GAGCTGATTT GTTGCCAGAT AGGGCAGCAC	780
AACTGTATTT TGCATTTTAC TCACTGCAGG AGAAACGTCC CATGCTTCGC ATGGTTTCCT	840
ACCAAGTAAC ATCCATAAC GCTTAAAATG TTCTCTTGCT GACAACCCGG TCTGTTTCAC	900

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ATCCAAATAG TTATGCAGAT ACCAATGTTT ATCAAAGTGA GCTAGCAACT CGTCTTGGTG	960
ATTTTAAACC ATCACTTTTA TTCTCCCTTA TTGACAGGCA GGCAACTGCG CTGCTCAAAC	1020
TTCCCATACA TAATGTAATG AAGCAGCGGA TTAATGCCTC CTTGGGCCAC ATCCGGATAG	1080
GTTTGCAAAT ACCAGCGAGT ATCAAACTGC TCACTAGGGC TATAACCTTT ATCCGCCCCC	1140
ACGCTAATAA AATGCTCAAG AGCTGAGAGC CCAGTGTCTG CAACCTCTGG GTAGCGATGT	1200
TGATACCAGA GTTCATCAA CAATCTTGAA GCGGCAANTA CTCCGCGGCA CTCTCTGTAG	1260
CTGTTGTTCT GGATGGAGTC TCCTCTTAA ATGTTCTGCC AAGAGCACGA ACTGGGGCTG	1320
TAATCTTCCA AGAGACGGTT CT	1342

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CGAAGGAAGC AGTNTGCNGC CTGEGCTGGC GGAGTTGCGC CTGTTCCAC CGATGATGCT	60
GTACATGAAT CCTCCGGCGA ACAGAGCGGT GAACTGGAAA CCATGCTTGA ACAGGCCGCG	120
GTCAATCAGG AACGGGAATT TGATACCCAG GTGGGGCTGG CGTTAGGGCT GTTTGAGCCG	180
GCGCTGGTGG TGATGATGGC GGGGGTGGTG CTGTTTATCG TCATCGCCAT CCTCGAGCCG	240
ATGCTGCAAC TGAACAATAT GGTGGAATG TAATTTACGG AGTTATCACA TGAATTCGTT	300
ATCCCGCACA CAAAAACCAC GGGCAGGTTT TACCCTGCTG GAAGTGATGG TGGTGATTGT	360
TATTCTTGGC GTCTGGCAA GTCTGCTGGT GCCTAACCTG TTGGGCAACA AAGAGAAARC	420
CGATCGGCAA AAAGCCATCA GCGATATCGT GCGCTGGAG AATGCGCTGG ATATGTACCG	480
ACTGGATAAC GGGCGTTATC CGACCACTGA GCAGGGGCTT GAGGCGCTGA TCCAGCAACC	540
GGCCAATATG GCGGATTCCC GTAACCTACG TACCGGTGGA TACATTAAAC GACTGCCAAA	600
GGATCCGTGG GGCAATGATT ATCAGTATCT CAGCCCGGGT GAAAAAGGSC TGTGATGT	660
TTATACCCTG GGGGCAGATG GTCAGGAAAA TGGGGAGGGC GCTGGCGCAG ATATCGGTAA	720
CTGGAATTTG CAGGAGTTTC AGTAATCAGT GCCTGAACGC GGATTCACAC TTCTGGAAT	780
CATGCTGGTG ATTTTCCTTA TCGCCCTTGC CAGTGCGGGC GTGATACAGA CGTTTTCGAC	840
CGCTTCAGAG CCGCTGCGA AAAAAGCGGC GCAGGATTTT CTGACTCGCT TTGCGCAGTT	900
TAAGGACAGG GCAGTGATCG AAGGGCAAAC ACTCGGTGTG CTAATCGACC CGCCTGGCTA	960
TCAGTTTATG CAGCGTCGTC ACGGACAATG GCTACCCGTT TCTGCGACCC GCTTATCGAC	1020
ACAGGTTACG GTGCCAAAAC AGGTGCAGAT GCTGTTACAA CCCGGCAGTG ATATCTGGCA	1080

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GAAGGAGTAT GCGCTGGAGC TGCAACGTCG TCGCCTGACG CTGCACGATA TTGAACTGGA	1140
GTTGCAAAAA GAGGCGAAAA AGAAGACGCC ACAGATCCGT TTTTCGCCTT TTGAACCCGC	1200
CACGCCGTTT ACGCTGCGCT TCTACTCAGC GGCGCAAAAC GCATGTTGGG CGGTAAACT	1260
GGCACACGAT GGCGCGTTAT CCTCAGTCA ATGTGATGAG AGGATGCCAT GAAGCGTGGA	1320
TTTACCTTGC TGGAAGTGAT GCTCGCGCTG GCGATTTTTC CGCTGGCTGC CACGGCGGTG	1380
TTACAGATTG CCAGCGGCGC GCTGAGTAAT CAGCACGTTT TTGAGGAAAA AACGGTAGCG	1440
GGCTGGGTAG CTGAAAACCA GACCGCACTG CTCTACCTGA TGACCCGCGA ACAACGGGCG	1500
GTCAGGCACC AGGGCGAGAG CGATATGGCA GGAAGCCGCT GGKTCTGGCG AACCCACCA	1560
CTGAATACCG GTAATGCGCT	1580

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTTAACCATT ACCCAGCATT TGGTAGTTAA ATAGTCGTTA AAAGCATAAA ACATGGACAT	60
TGTGCCATCC CAGCTAAAGC ATCCATTACC GCCTGACAGG GATAAAAATA AAAAAGCAGG	120
GAACCATTTT TTCATCAGAA ATCACTTCCG TAATTACAGT TATTCATTTA GGTATGACTC	180
AGTTATAAAT CATGCTCATA CTGGCCGTGG TCTGGRAATC CCCGCCATTC AGTATCCCGC	240
TGCCATTACG AAAGGGCACT GAAGTAAAGG TGAACGTTGA ACGTGCTGTG TCCAGACCTG	300
CTGTCACTCC GTAACCATTT CCTGAACCAT TACCTAATAT AAGAGGTGTT GACATTCCTT	360
TTCCCTGATA CAGCGCTATA CCAAATGAG TTATATTTGT TGCCAGTACA TTATTCTGAC	420
CTCCTCCCAT AGTATTTCCC GTAACCTTTT TCCAGAGAGA GCCACTCTTA TACGGACAGG	480
ATATGCTTAT GGTTTTTGTG ACTTCACCAC GTGAGTTGTC CACGTGCTCA GGATTAATAT	540
TCCCAAAATC AACAACAATA TTCTGCCCGT TATTAATGGT GCATGGGGGG ATATAAACAT	600
TCCCCCTGAT GTTAATCTGC ACATCAGCCA GTACAGCGAC CGATGTCAGA AGCAACGATA	660
TAAATAATGA TAAACGAATC ATCCCCCTCC GGAGAGCGGT ACAGAAAACA TTTTATTTTA	720
CGAGATATAA AATTAACGTA TTTTAGTTGA TACTATTACG AATATGATGC AACCAGCGTT	780
GCTGTTGCAG AGAAAAGACC GGCTATCAAA TTCTGCATAT TCCCTTTATA TCCAAGTTTG	840
GCATGAAGTG ATATAGTTTT ATCTGCATTA TTACCTGTGA TTTTCCGGG CGTAAATGGA	900
GTCCCTAAAG TTATCGCAGT CCCAATATTT CCTGCATTAC TGTTATAAAG ATAAACGAGT	960
AACCCATCAG AAGATGTGTT TGATGTATTC TGAACATAAA TAGCATTGTT ATAAGTGTTC	1020

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GTTGCCGTTA	TCGTAACCTT	CATTGTTCCC	AGATTATAGG	GACACCGCAT	ATTCACAGTA	1080
AACTCTTTTT	CGTGATTTCC	ATTTTGACTC	AGGGTCTGAA	TCTCTACATC	CTGCCAGTCA	1140
ACAGTTGTGT	TGCTTACAGT	ACAGGCAGGA	ATAATCAGTT	TTCCTCTGAA	GGTCAGATTA	1200
TCAACTGCAT	GTACATGCTG	AGACATTAAC	ACTGCCCCCA	GCATTACCGG	AAGACACAAA	1260
CCTCTTATCT	TTTTCATCTG	AAATATCCTG	TACAAAAATT	TTGCTAACGA	TATGTCAATT	1320
CAAACGTGGC	TGTTGCTTCA	TAATCACCGG	GTACCACACT	CTTCGTCCGC	AGGCTTCCGG	1380
CGTTGCCACA	ACATACGCGC	CGAAAGGAAG	CTCAAGACTG	TTTCCGGTAA	CCTTTTCCCC	1440
CTGGCCTTTG	TTATGGGAGG	TGCCGGGTTT	CAGCAGACTG	CTGCCATCGG	TGTCCAGCAG	1500
TGCAATGCCT	AACCGGCCAG	CATTCACTCC	GGTTACCTTC	AGATGGCCCG	GGAGGGCGCC	1560
TCTTCCGTCC	CCTTAAAGGT	CAGGGTCACA	ATTTTGCCAA	CTGCTGTTGC	ATGGCAGTTT	1620
TCCAGCCTGA	TGACAAACGA	CTCTGTCGGC	GAACGTCCGG	GCGGATACCA	GAAATCCCTG	1680
GACGCCCGGG	TTTTGAAGAC	GACATGTTTA	TTCAGACTGT	CACCGGACAC	ATGGCAGGGT	1740
CTGTCAAGCA	GATTACCCCT	GAATGCCACA	TCTGAGGCTA	TTGCCTGTCC	GGCAGACAGT	1800
GCGGCAAACA	GTAAAAGAGC	GCCTGTGCTT	TTTATCATCA	CATTCCCTTA	CTCATATTTT	1860
ATGCTCAGAC	GCAGCATGGC	CGGATTGCTC	CTGGCATCAG	AATACTCACC	CTCCTGTGTC	1920
GCCCTTTTCC	TCCAGGCGGC	CAGCATCTCC	TCCTGCCGCC	GGTCAGGCCG	GCACAGTAAA	1980
AAGGTATCAC	CATCGTGTAT	AACAAGATGG	TCACAGCCGG	ATAGCTTACG	GTCAGGAAGT	2040
AAAGCACTTC	CGTTTCCGGG	ACCGGTTACC	AGTGAGCCGG	AGACTGTCAT	CGCAACGCCC	2100
CGTTTTCCGG	GCTGAAGTGC	ACCACCGTCC	CCACATCCTG	CCAGCCTCAG	CATCAGAGGT	2160
GCTCCGGCTG	CCGCAGAGTG	ATTTTCCGGC	CGGAGGYTTA	ACGGCACCTC	ATTACTCACC	2220
AGCGTGCAGG	GTGAGGACAG	CAGTGCACCA	CTGACGGTCA	GGCTTCCGGT	GCGTCCCCCC	2280
CGTTCATTTA	TCCGGTAATG	ACGCAACTCA	TCTGCAGTAA	AGACGTCATC	GTATATACCC	2340
CGCTCTTCAG	CCCGCAGGAA	AGTATGGATG	AAACCACTCA	GCGACAGTGC	AATAAGATAC	2400
AGTACTGCTG	TTGTTTTATT	CACAACCATA	ATATCCCACC	CGCATTTAAC	CGTTATTGCG	2460
GTACATTATT	TCTCTTTTTT	CACAGAGCAA	CGGCTACCAT	TACAGATAAA	CGACAGTACC	2520
GGGCGACCAC	CATAGTCATT	AATATAAGAC	AGATAAGGGG	TATTATAATT	TGCCGATTTT	2580
ACTGTCTGCT	CTGAACGGGG	AGACAGCATC	ACGGTTTCAA	ACTCACCTTC	CTCTGCCTGC	2640
TTTTCACTTC	CTCCCAGACC	AATAACAGTG	ACATAATAGG	GCGTTGGGTT	TTCAATACGA	2700
TACCCACCGC	TGACTTTGTT	CAGAATTAAC	TGGTCTGCC	ATACTTCATT	TGGTCTGGTT	2760
TTAATTGCTG	CCGGGCGATA	AAAAAGCTTT	ATTTTGGTCT	GTAAGGCTAT	CTGCAGTACA	2820
TTGGCCTTTT	CACTCCTCGG	CGGTATTTCC	CTGAGATTAA	AATAAAACAG	TGATTCCCTG	2880
TCCTGAGGAA	GTTTACTGAT	ATCCGGTGTG	GTACTCAGCC	TGACCATGCT	TTTCGCACCC	2940

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GGCTCAAGGC GCTGAACCGG AGGGGTGGCA ATAACCGGCC CTGTAATAAT TTTTTCCTGA	3000
TTTTCATTTT CTATCCATGC CTGAGCAAGA TAGGGCAGTT GTTTGTTATC ATTGGAGATA	3060
TCAAGCGTCA TTGACTTCTC ACTCCCGTCA AACACCGCGC GGGTTCTGTC CAGCGAAACA	3120
GCAGCGTCTG CCCC GGATAT AACAAACAGG GGGATGGCAG CCATCAGAAT CTTTTTTCGA	3180
ATCATACTTA ATTTCCACAT TCTGTAATTT CACTGGTCC GGAAAATGGC ATAACCGCAT	3240
T	3241

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AACGTGGATC TCCAGCTGAT CGGTGCCGTA TTCCAGGTCG TAAGTTTCAC TGATGGTTTC	60
ACGCGGCAGT TTGCCCCGTT TACGGACCGG TACAAAGCCA ACGCCCAGAC CCAGAGCTAC	120
CGGAGCGCCA AACAGAAGC CACGCGCTTC GGTGCCGACA ACTTTGGTAA TGCCCGCATT	180
TTTGTAACGC TCAACCAGCA AGTCGATGCT GAGAGCGTAA TTTTCGGGTC TTCCAGTAAG	240
CTGGTGACAT CGCGGAAAAG AATGCCGGGT TTTGGGTAGT CCTGAATGCT TTTGATGCTA	300
TTTTTGAGAT ACTCAAGCTG CTGTGCATCG CGGGKCATAA GTGTATGCCT GCTTGTTACG	360
GTGGTACTCA CGGCGCGTTT TTAAACGTAT CAAAAGTT	398

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CAGTTNCNGT TCTCATAGAC AGATTGATAA AATCGTAAAC AGCCCCTAGC ATTCCCGTTT	60
CCTTTGCACA CATATTCAGG CACGGGGATA AAGTATAAAG AATGTCGTAC TGCTGCTACC	120
AGAGCAATAT TCCCCCTGA TGGCCGTATC AGAGATAGTA TGCCGGTATT TTGCGGGTGG	180
TTCCCGTCAG GTTATCGTGT ACCTCCACGG TCGTAGTCAC CACCGGCATT CCGGCYTTTC	240
TCAGCCTCAA AACATCAGCT GCAATACGCT GACTGCCGAA CCAGAACAGG CCGTCCAGTG	300
CAGTCACCAG CAACCCCGCC TCCAGCGCAT GCTTCAGCCG TTCACGGGGC GCTTTCACTT	360
CCCCGGCAAT CTGCTGGTAT GSCGATGATG TGTTTTTCATT CCCAATCACC CGGCGAATAC	420

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GATGAGACAG	ATGATACCGG	TATGTATCCG	GCACACCGGA	AAGGCTGGCC	TTCAGGCTGT	480
ACACGCAGGC	AAATCGTTTA	TCATTGAACA	CCACATTTTT	CTGGCTGATG	CCCCATTCTT	540
CACGCAGCGC	GGCAATCAGT	TGTGGTGTAC	GGGTAAGCAA	CAAGCGAAAA	GGCAGTTCAA	600
AACTGGTGAC	ATAATCCACA	TTCAACAGGG	CAATGCGAAG	TCGTTCTTCT	GGTCCGGCTT	660
CTGTCTGCGG	GCACTCCTCC	AGGACATCCT	GCCACTGCAG	GCGAAGACGG	GAAGACTCAT	720
TCAGTTCTGT	AAAGCAGTAT	TTATCCGCCA	GATAGTCAAT	TCGTGTATGC	ATACTGAAGA	780
GTATTCCGTA	TAAAGATTCA	GCTGGCAAAA	CTTTATCAGT	CTGTAAAAAC	TAACGGAAGA	840
GTCGATATTT	CTCCCGACAA	TCACCGGATG	ATTGTTGCAA	TACCTCGTGG	CATCAGAGAC	900
TGAACAGCAG	TTTTTAACGC	AACGTATTGC	TCTGATGTAT	CAGGCCGGAC	AACCCGAAAA	960
CAGCCTTCCA	CCCGGCATTG	TCCGCCAGCG	CTTATCACCG	GCCAGGTCTG	TTGCAGTAAA	1020
TCCGCCACTT	GCGAACATGC	TTCATCAACT	GTGACACTGG	CCCGCGGATG	GCAAATGCTC	1080
GTCTGGGTGA	GCAGCAACAG	GCATCGCATT	GTTGCTCCTC	TATGTTGTTC	CCGCAACCAG	1140
CGTAATACCA	CCGGCGAGGA	TGGACAGGCA	GTGTGATTAC	GCTCCGTAAT	ACGTTTCGTGC	1200
ACCCGTCGCT	GAAAGGAACT	ACAGAATGTC	TGAATCTGTT	GCCCGTTGAT	GTATCCTTCT	1260
GTGGAATGAA	GTGTGAAGTG	GATTGCCAGC	AGATGCGGCC	AGTGATCCAC	CGCCTGCTGA	1320
ACAAAACGCC	GGATTTCCCC	CGGCTCTGAA	AGTAAGGCTT	CGGTTATTTG	CACTATTTTA	1380
TCTCTGTTGA	ATTTGGTTAA	GTCGGTGCAG	ACGCATCAAC	ACAAGTACGG	TTGATGCAA	1440
ACAGCTGTGA	CTGGCAATAT	GAAAGGAATG	ATGAATCAGT	CAGGATGACA	AAGTGCCGGC	1500
TGACCGGAGG	GGACGCAGGA	AGATTACCGG	GGGGACCAGC	ACCAGGGAAC	AGCGCCACAA	1560
TACCAGCGCT	GACACGTTGA	ACATTGCCAG	CGTACCGGTA	TCACAACACG	TTTCATACTT	1620
CTGCCCCCGT	GATTCTTCGA	TTGTTACTG	TATCTACTGT	GACACTTCGC	TTTTATACCT	1680
GCGGCTGGAT	CGGCCCGGCT	TGATGAATCT	TCACTGATCA	GCTTATAAAA	CCCTCTGTCT	1740
GTCATACCGG	TGAAACTGGT	GATATAGTTC	ATGTCAATCA	GGGAATTATC	GGCACGCAGA	1800
AATACGCTGT	CGTGGCTTGT	TGTAGTCAAC	ATGGTCAGAA	TGTCCTCTGT	GAGATTTATG	1860
AAGATTGTGC	GAATGCGGGG	AATCTACTGA	GCTGTGCTTT	CAGAACTGGC	CTGTTACGGG	1920
AKRSCAGGGA	TTACCGGCGG	GGTAACGGGC	TTCCGGATCA	TACACACCAC	GATTATCGCG	1980
GACAAAATCA	CTGAACGCCC	ATATCACCTC	TTTAAGTATG	TCTTCGCAGC	CCGGTACATG	2040
ACGATCCAGC	GCCACATCCC	GAGTGGTACT	ACTTTGATGC	GCCCCGTGAC	ACAAAGCCCCG	2100
GATTGTTCCA	GACATCCTGA	ATCAAACGCC	CCAGATTAGG	GGCGTCGAAA	TATGCCTCTC	2160
TGACCATTAT	ATTCCGGTGT	ACAGGTAGCA	GSTCAGAAGT	GACAATGCGT	CACCTGACGT	2220
TAAAAGTCAC	TACACCCAAG	ATGACGTTCA	ACAGCACCAT	GCGATTCAAT	GTAAGCCCCG	2280
GCTGTCTGTT	CCAGTACACC	AGGCTCAGCG	TTGTATGTGT	TAGCTGCATC	AAATACCAAC	2340

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GACAGCACTT	CAGGATACAC	AACCAGATGT	GTAATGGAGT	TATCTTCACC	CAATACTTTT	2400
CCCCACGECT	GCTCAATCAG	ATTTCTGAGA	ACCACACCT	CACGACTCTT	ACACCAGACA	2460
TCGTTATTAA	GTAGCAGCAC	CATAAGATAA	GGAGTGGTAT	CGTTAGTCAC	AGCCTCCCTA	2520
CTCCAGAGAT	AATATAAAGG	GGTGGGCTCA	ACAGATTTAT	CTTTACGTCG	CTTACACTGC	2580
AAATATTGAG	AAATGAGTCT	ATGCAGTTCA	CCAGTAAAAT	CCGCCATCAG	AGAGGGGAATG	2640
GCCTTATTAA	TACCAGGGCA	AGGTATTAAT	TTAAATTGTA	ATAATTTAAT	TTCAGGATGT	2700
GTGGCTGCAG	CCCGATACAG	AGTTGCAAGG	ACACACTTTT	GCCAGAGGGC	GTTACTGGAA	2760
AGCTTAACGT	TTGATTCTGT	ATACATAATA	AATCACCTTA	CAGTTACAAC	AGGTCAAAAA	2820
CCGCTGTAGC	CAGAGTTACG	CTGGCCTGAT	GCTTTAGTAC	CGGGCTTCGT	CAGATAATCC	2880
AGACGCTCCA	ATAAGCGCTG	ATACTGCTCA	GGGAAATCAG	GATCATGAAT	ATCCTGGATG	2940
TCACGTCCAT	TAGCAGGGAA	ATGAATAACG	CAGCCCCCTG	GATTAACAAT	GCAGAAATCG	3000
TCCTGAGGTA	CTGATCAATA	CGGAGAGGAC	TCTCGCGTGT	GGTTTATTGA	CACCACAGTG	3060
CAGATTCGGC	GAATCCGCGA	TCACGGTGCG	ATTTCGTTCC	ACAGCACACA	ATCATGACCC	3120
CGGGTTTTAT	TCAGGTAAGC	AGGATTGCGG	ATATCCGGTG	TCGCGCCTTT	CTGTCACGAA	3180
CGGGGTAGGT	GCGAAACACC	GGATAAAATG	CAGGCTGGCA	ATACCTCTGA	ACGCCCTGCG	3240
CAGAGCGGAT	ATTTTGGATT	AAGTACTCGC	ACCTCCGCAG	TCCTGAAACA	AGTCTGGCTG	3300
GTAGCTGTAA	ACAGACTTCG	TACATGTTGC	TCTGGAATAG	ATCCCCGTGC	CACAGGCTTC	3360
GCAGAACTTT	TTCCCGGGAA	AATGCTGCCC	GCACATCACA	CAATGCCACT	CCAGCACGAC	3420
CGGTAATGGC	GATAGAAACA	TCGCCATATC	CTCAATGTAA	GGGTGGGACT	TTTCCGGATT	3480
CAGCACCACG	CAGGCCGCCT	TCTGTTGCGC	GCTCAGGGCA	TGTAAATCGT	GCTCAAACCA	3540
CGCCCCCTGA	GCATCTGTCT	GCAAAATCAA	CCGACCACGA	CAGGAAAGGC	AGAAACAATG	3600
CCTGATATTT	CTGCTAAGGC	TGAGGCCGCA	CTGATAATGT	GTTACCCCGG	CGTGATCCCC	3660
AGCCCCGTTT	TTATACCGTT	CATTGAGCCA	CTCCCTCCTC	ACTGAAGTGC	CCTGTATGGC	3720
AGTGAGTGCA	GTACCGCTCC	CCATAATAAT	CGTGGTGACA	TTGTCTGCAG	TGCCAGCTGG	3780
CTTTACGCAC	CACGGGTAAG	GCATCCGGTA	CGAATTTCTG	CAGACGCTTA	ATCAGTTGTA	3840
TTTCTCTGCG	CTCCGGTCTG	ACATAAGGAC	ACTGTTGACC	GTGCTCCGTC	AGCCCGTCGT	3900
CAGTGTGTTG	AAACCAGGGA	AGTTGAGTGT	CGTATTGCGG	ATGGTATCTG	AGCGCACTGC	3960
CGCAAAGGTG	GCAGGTGTAG	CGGTGCTAAG	GTGCAGTCTG	TGCGGTACGG	GCAGCGGTCA	4020
GACGTCCGTT	GCCATCAAAT	GCGAGAAAAG	ATTTTGCCTA	CATAGTATAT	GTTCTTTACC	4080
GCCAGACGAC	ACGCAGGCGT	CAGCGTCCCT	TTACGGGCAG	CGTGGGCAGG	GTGTGAATGG	4140
CGGTACAGTT	AAGGGGGGGG	TGGAAAATGG	GCGGGCTGTT	GTTACAGCAC	TGTGGATGTC	4200
ACATCATGSC	GTACCAACGT	AAAAAATAAT	CAGCAGGCCC	GGATACATCG	TTGTGCGCCG	4260

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ACATCAGCCC	GTCCTGCTGG	TTTTGCCGGG	CTCAGCCCCG	ACTGCAGCCG	AAATTACGCT	4320
CACCAAGTGGC	GTGAGCTTTG	GATGTTTCT	TCGCCAGATA	GTCAGCACGT	TCCAGCACCT	4380
GCTGAAAGCC	AGTGTATCA	CCGCGTTCCA	GCCACACCGC	CGGCGTGTCA	GGAAAATGCG	4440
CCAACGTGGC	ATAAGGCCCG	GCATCCACCC	CCAGGGCACT	GCACCAGGCN	TGWTTAATCA	4500
TCCCGGCCAG	TGACCCCGGA	TCGCGGTAAT	CGCCGGCACG	ACACCAGGTA	TCCCGGTTGA	4560
CCAGCAGCAG	GAGGTGATAG	TGTTTTTTGC	CCCTGAGTAC	CCCGAACTCC	CGGGCCCAGG	4620
CGTAATGCAG	GGTGGTGGGA	TGCACGCGTT	TACCTTCACG	NCGTTACGCT	TCTGGTAAGC	4680
GTCGATTCGG	GCTTTCAGGG	CATTGATGAA	GCGGGATATC	ACAGCCGCGT	CCGTAGCTGC	4740
CGGTACATCC	GGGAGACGCA	GATCAACCCG	AAGTGCCGTC	AGGCGGGGAT	GAACATTCAG	4800
TGCGTGCCGC	ACCGTCTCAC	GAATACGTTG	CTGCCAGAAG	GGGTTGTATT	TGTAGGTCAT	4860
GGTTAAATCT	CCGTATGGTT	CATACGGAAT	AGCCACGTCG	TAAAAAATGC	GCAGAGCCCC	4920
TGACGTGGCC	ACCGACAGAA	CACGGCCTCA	GGCGCGTTGT	GATAACCCAG	CTATCGTTTC	4980
CGGACTGACG	GTTGAATTTT	CTGCGTTGTT	TTCTTAATGT	AAAAAACCTG	CTACGGGTAA	5040
GGCTGTGAGG	AGGAAGTGAT	GGTGATACGC	AAAAAGAAGT	GCAGGGACTG	CGGAGAAGCG	5100
ACAGAGCATA	ACACGGTATG	TTGCCACAC	TGCGGTTCTG	TCGATCCCTT	CGGCTATTAC	5160
CGCAATACAG	ACAGAATATT	CACCTCCTG	ATGGTCCTGC	TGGTTGTGGT	TCTGCTGATG	5220
ACGGCTGCGG	TCAGCGTGTA	TGTGCTGTGG	TAGTCGGAGG	GGCAGGGAGC	AGACGATGAC	5280
GTAAAATATC	TCCGGTGCTC	AGATATCACG	GCCGGTCAGA	CCGCAAACCA	ACGGTTAATC	5340
GTAACCGGAT	CAGGCAAATG	TGTGATTAGC	CCCCTGGCGC	TCATACCCGC	ACCGCAGACC	5400
ACCTTAAGTA	CTTCCCGCCC	GACACCATT	CCTGCTCCCG	GATAATTTGT	TGTCGCTATA	5460
CCGCTTAACA	TCACCGATAC	CACACCGGCG	CAGATAGCAC	CGGATTCATT	GTAGAGATGA	5520
CTTAAGGTTC	AGGTAACATA	TTTCCAGACA	GAAGCGGGAA	CACGATCGTA	AAGTTTGTTT	5580
ATGGTCAGTT	CTGCCAGCCG	GTGATCAACC	GCAGAGTTGA	AATTTTCCAG	CTCCGCCGGG	5640
GTGAGTTTAT	ACCGTGCGTG	GGAAATCACT	TTTTCCAGTG	TCTCCCGGGA	TGAACAACGA	5700
CGGAACTGAT	ACAGCCAGTC	TTCTTTGGTT	TTTACTTCCA	TTCGTCTCTC	GTTACTTTAT	5760
GCTGCGGTTA	ACAGGATGCC	GTGAGTATAC	CGCATGCAGA	CACTCTCCCG	CTCCCCCGCT	5820
TGCTGCGATA	CAACTTAACG	TTTCAGGAAT	CCAGTCATCG	CACCGGGAAA	GGCTTTCTGG	5880
TGACAGGAAA	CGTCAGGAAC	AGGAGTTTCT	CAGACTCCCA	CTCATCGGAT	CAGGCTCAGA	5940
CAGGATTATT	AATACGCTCA	GTTTATGTGT	CATATACAGG	GCATCGGGGA	TGAATATATG	6000
GGTATAACTC	AGAGCCTGTA	CTACAGCTTT	CACTGCTGAC	TGATTTTACG	TATCAGCGTT	6060
CATGTATCTG	CACTCTGATA	TAGAATACTT	CTACCGGAGC	TACTCTTACG	TTAGCTCACT	6120
CTCACATCAG	GCAACATCAC	TTATTACGCT	CACTTACCTC	TTACCACTCA	CTACTTCTTT	6180

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ATATTTATAA TATCAATCAG ACAGCCTTAT CCCCCCGGTA ATATCTGTTG CCTTCCCGCC	6240
AGCCACAGGC TTATTCACCA CAACCACCTC CGATAACAAC TCTGCAATTA TCAGAACGCC	6300
TGCTTCTCTC CCTGTCTCA CGAAAACTAT CCCCTCTTTA TCGCGCGTGC GTGCGGAAGC	6360
ATCTTTTCGC AACAAACCAC CGGGATTCCG CTACGGCTCT GCCATCGCAA TCCCCCGTT	6420
TATCTCCGGA CAGCCACATT CCCGATTATT TTTTACGTTT CTCCCCGGTT GTTATGCCGG	6480
TGAAGGTGGT GCGTCGTTTT CATCACCACA CCGGTTGCGA TTAACAACAT CCGGAGGAAC	6540
ATTCTCATGA CCACACCCTT TTTACTGATG GATGACCAGA TGGTCGACAT GGCCTTTATC	6600
ACTCAACTGA CCGGCCTGAG CGATAAGTGG TTTTACAAAC TCATCCAGGA CGGAGCCTTT	6660
CCGGCCCCCA TCAAACTGGG CCGCAGCTCC CGCTGGCTGA AAAGTGAAGT GGAAGCCTGG	6720
CTGCAGGCGC GTATTACACA GTCCCGTCCG TAATTTCTGC CCCTTATCCG TTCACCCGCA	6780
GCAGACGCCT CCCCAGCCTG CCGTTGACAT TCTGCTGCCT GTTTTATCCC CGTGAGGAAT	6840
ATGAAAATGA AACAAACAGTA CCAGACCCGC TACGAATGGC TCCACGAAAG CTACCAGAAA	6900
TGGCTGACCG GCTTCAMCCG GCACGCCGTA TCCTGGGGCG TGTGTCATCC GAATATCTAC	6960
TATTTCCATA ATCTGACGCC CCGGTGGGTG TCATTCAACG GCGAACAGTC GGAGATTGCC	7020
ATTGTTCCCG GCAGTCTGCA CCGGCTGATT TATGGTCATG ACAAACGGGC CATGCCGCCC	7080
CTGGATGATG ATCTGGTGGT GAATTTATGC ACCAGTGAGA ATCTGCTGGT TCATCATCCG	7140
ATGCTGGAAG GCATTCTGCT GTCTGAGTGC ACGCGCCTGC ATAAAAAATC ACTGGCGAAC	7200
AAACTGATCA GTATATTCCG TCAGTTTGAC GGCACGGAGC TCGCTCTCAA ACTGGTCTGG	7260
CTTTGCTGGT TTGATTTAAT GACCGGAAAC TGCCTTGACG ACTGGACGGA GAACCTGNAA	7320
CGGAAATCAG AAAAAGAGCT GGAGAAATGG ATCATTGAGC GCCAGAACCG GAACGCACCG	7380
CTGACGAATC TGATGGATCA GTACGTGCTC CTGGCATTCC GCACAACGGT TGACGATAGC	7440
CGCAACTGAT GTCTGCATGC TGCCSGCTGA AGCCATATTC ACGGGGACAG GACGCCCCCTG	7500
CTTCCGCAAC AATCCGGGGT AATGGCGACG TACGCCTGCA GAGTGTGTTC ATCGTTGTCA	7560
CAGCCGGACA AGGTGAATAC CGTTGATGAT GCGGGGATGA ACCTGCTGGT CCACCGCGCT	7620
GTCCTCAGA CGCGTCAGCG TGTATGGACG CCCCATATTC ATGGTTCTTC CGCCAGAGTG	7680
CACAGAAATG AGGCACGGAA CGTTACCTGA AGGGTGACCG GCACGGACTG CAACTTGTTG	7740
CCATTGATGG CGCACAAGTC ACATACAGCA GAATGTCGTG ACCGCACCTT ACCGGTGAAG	7800
CGAAACGGTG CTGCCCCACT CCACCACCAT CCCGGATAAC GCCATTACGC TGTCTGATAA	7860
GCGCTTTTAC AGCGCAAATC TGGTGCAGAA AAGCGTAAAG CTGACCTGCC GGAGCAGGAT	7920
GTGGGCATGT TCGGGGCTTA CAACCTGATA CGGCATGAGG CACTAAAAGC AGCATCAGAA	7980
ATCAGCCTGA GTTCGCGTTC CGGTTTATCC CGACAGAGAG GACAGTGCCG GGCAACACGG	8040
TGTCACCGGG GAGCATCCCG AAACGACCGG AGCATCTGCG GGATGCTCTG TAAGTGGTGT	8100

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TAAGGTGGGC	GGTTAAGGTA	TCAAAAAAAT	CGTTATCCTG	TGAAAGACAG	TGCGCTCTGC	8160
TGAAGTGAAC	GTCACTGCCG	GGAAGCATCG	GGTTTCGGTA	CCGGACAGTC	GCGGTAACGC	8220
GTTTACCGGC	ATCTGTCTGT	GTGGCAGGGA	TGGCTCATAT	TGTCGGTTAT	ACCAGCGGCA	8280
GGTGCGTCCT	GTTATCTGTA	AAATCAGGGC	GTGCCGGTAC	ACAACGCCTC	GTTGATGCCG	8340
GTCAGTGAAC	GAATCATCCT	CTGACGAAAA	CAACCGTCGA	TACAACGCCG	GCGTAAAAAG	8400
AAAACCGGAA	ACCATCTTGT	GCACGACAGG	TACTCAGGGG	GGTATAACGC	CTGCGCACCA	8460
TCACATCCGG	GAACAGGGCT	GCTCCTCAGT	GTCTTCGTGT	GGCGAAGCAT	CTGCAACCGG	8520
ACGGTACTGC	CCTCAGAGCA	ATCTCCCTGC	TGCAGTGCAC	AGAGTAAGCC	GGAAAGCTGG	8580
TGAATGCCGC	CATGACACAC	TGCGACGTGG	AGAAACAAAC	GACACACTCC	GTCCGCAGTA	8640
ACACTGAAGG	TAGTCCCGCA	AACCTCAGAC	TTCTTCCTGC	ACGTTATCAG	CGGACTGAAC	8700
CCCGGTCAGC	CACTTAAACC	TGCTAATCGT	GTTGCTGCAT	ACCCGCCCCG	CCGGAAGGTG	8760
TTATGAAGCC	CGCCACCGGA	GCGCTTCTGC	AAATATCCGG	GGAGATAAAA	TTTTCGTGAC	8820
AGGATGACGG	TCGTGCTGCA	GACGTAAAGC	CGCAGGAGCG	GACACGACAG	ACAGTGTTCA	8880
CTGTGGCGTC	CTTTGCCGTC	GGTATCGTGC	TCACGCTGAG	GTCCCGGGGG	TACACCTGAC	8940
GACAAATACC	TGCGATTCCC	GGGACGGTCT	GTTCTCCGTA	AAATAAAGAA	AATGCGGGAT	9000
GCCTCCCGGA	CTGCAGAGAA	GAGGGATTGA	CAGACAGTGT	ATATTGCGTA	CGATTACAGG	9060
GGAAAAACAC	AGTAAATATG	GAGGTCAGGT	CCGAAAACAA	CCTACGAAAT	TTCTATGAAA	9120
AACGATTGAA	AAAATCATCA	AATTCAGTTC	GTTTTTCTAT	GGTAATTTTT	AAACACTCCC	9180
GATGATAACC	TGTTGTATGT	GCATGTGGGG	AACGCACCGA	AAACATCAGA	ATCATCTGAA	9240
AAAAACAACG	AACACACCAG	AAAAACAGGA	GCAACCATAA	CGAAGCAACA	TATTGATTTT	9300
AAACAGAATT	TAAGGTTAAC	AGACAAAAAA	CACTTTCAAC	TGAAGGAGAA	ATATACACTG	9360
GCGACAGTGC	AGGGTTTTTC	ATGCAAAAAA	AATGAGCTTT	TATCTCCGGC	GCATACTGAC	9420
CGGGATGCAG	CCATGACAGA	GCAAAAACCA	TTAAATATCA	GGAGGTTAAA	CACACAAAAA	9480
GCTGACATGC	ATCAGGGAGC	AATCCCTCAC	AACAGAGGCT	GAGCGGCAAC	GCTTCCTCAC	9540
AGGACGGCAT	TCCTGAAAGG	ACAGGCAGCC	ACGGCTTTTT	ACTGCCCGTA	TCCGGTATAT	9600
TTATCTGCCG	TGACGTGCAG	AGGATTTTGT	GTTTCCGGAA	ATCAGGAAAA	CAGGAGAACC	9660
GCGGGAGATA	TGATGGAAAA	AGAACCGGAT	GATATCTGCG	CAGACTGTCC	GAATATTGAT	9720
GCAATAAAAC	GGCACAAACA	ACAGGCCGGA	GCCATCAGGG	AATACACTGA	GTGGTTAAAA	9780
AAACAACCGC	GTGCTTCTTA	CTTTTTTCTC	TTCCGGTTGT	ACGCATACCT	TCAGAATGAA	9840
GTGATATCCC	GAAAACAAAA	ACATTCGCTC	ACCAGCGATA	ACAGCCATCC	CCCGGAATCT	9900
GATGTCACCC	CTCCGGATTT	AACCCTTCCC	CGTCGCTACT	ACTGTGATTA	CGGTTACACG	9960
CCCTACCCCA	TGATGGGCGG	ACAGATGTCT	GTTTTTGCCA	CAACGTCAGA	AACCACCAGT	10020

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TCGACGAATG	CAGTCCCCGG	AAACGCAGTT	ACCGGGAATG	AGACTGAAAA	GCATGAAAAC	10080
GCGGTACCGG	CGACATTCCC	CGTCAGCCGT	TCTGCAATGC	CCCCGGAACC	TCTGCGGTTT	10140
GCCACGGGTT	TTCCATCGCA	ACCACTGCTT	GCCGGTCCCC	GGGAAAAGCC	GATGCGCACC	10200
GTGCATCCTG	ACATCCACAG	CGAAATTATA	TGGTTCTGCT	CCACTTACCT	GCTGAAATCC	10260
GGACCACAGA	TTACGAAGAC	GATTATCAAC	TCAGTATTCT	CTGAATGGGC	CCGCATCAGC	10320
AATGATTACC	CCTCCCCCTT	TTCGTGGGTG	GACAGCAGGG	ACAGTGAACA	GTGTGACTGG	10380
TTATGGAACG	CCATGCAGCT	CCGGTGTGTG	GGAACCCCGC	TGAATCCCCT	TACCCCGGAG	10440
CAGAAATACT	GGTTTGCCTG	CGCCACGTTT	GATAACTGGG	AGGGCTGGAA	TGAGCAACAG	10500
ATACAGTTTT	TACTGAAAAG	TAATCCCAGA	CGAAACAGAG	CGAAGTTTAC	GGTCACCTTC	10560
GGCCCTCCCT	GGATTGAGCA	TAAAGCCATT	CTTCTTGATG	AGCTGAAGAG	TGCCCGGGAG	10620
CAACAAAAAA	GGCGCGATGA	ACGCGCTGAT	GGTTCCGTCC	CGCTGAAACT	GTCCGGAAAA	10680
ATCCACAAAC	ACCTTGAAAG	TATTGCCCGG	AGTCGTGGTA	TCCCCC AAA	AAAAGTGTG	10740
AATGAAATGA	TTGAGCAGGC	GTACCAGGAC	TCAGTGGTGA	ACAGCCGGAA	TAAACCACTG	10800
ATTTAAATA	ATTTGAGACA	GATATTATCT	CCGTGAATCC	CCCSCCACCT	TTCCGGTGCG	10860
CGGGGTTTTG	TCTTTTTTCA	CCGGGAATAC	ATGTATGAAT	CCGTCTGATG	CCATTGAGGC	10920
AATTGAAAAA	CCGCTCTCCT	CCCTGCCTTA	CTCGCTTTCC	CGTCACATCC	TGGAACATCT	10980
GCGCAAACCTC	ACCCGTCACG	AACCCGTGAT	TGGCATTATG	GGTAAAAGCG	GGGCCGGTAA	11040
ATCCTCACTC	TGTAATGCAC	TGTTTCAGGG	GGAGGTCACC	CCGSTCAGTG	ATGTTACAGC	11100
CGGCACCCCG	GAAGTGCGGC	GCTTCCGTCT	GAGTGGCCAT	GGTCACAACA	TGGTTATCAC	11160
TGACCTGCCC	GGGGTGGGCG	AGAGCNGGGA	CAGGGATGCA	GAGTATGAAG	CCCTGTACCG	11220
TGACATTCTG	CCTGAACTGG	ACCTGGTACT	GTGGCTGATT	AAAGCCGATG	ACCGTGCCCT	11280
GTCTGTGGAT	GAGTATTTCT	GGCGACACAT	CCTGCAACGC	GGACATCAGC	AGGTGCTGTT	11340
TGTGGTGACG	CAGGCCGACA	AAACGGAGCC	CTGCCATGAA	TGGGATATGG	CCGGCATTCA	11400
GCCCTCTCCC	GCACAGGCAC	AGAACATTCT	CGAAAAACG	GAGGCGGTAT	TCCGTCTGTT	11460
CCGGCCTGTA	CATCCGGTTG	TGGCCGTATC	GGCCCGCACC	GGCTGGGAAC	TGGATACGCT	11520
GGTCAGTGCA	CTCATGACAG	CGTTCCCGA	CCATGCCGCC	AGTCCCCTGA	TGACCCGACT	11580
GCAGGACGAG	CTGCGCACGG	AGTCTGTCCG	CGCTCAGGCC	CGTGAACAGT	TTACCGGTGC	11640
GGTGGACCGG	ATATTTGACA	CAGCGGAGAG	CGTCTGTGTT	GCCTCTGTTG	TCCGTACGGC	11700
CCTGCGCGCT	GTTCTGTACA	CCGTGGTCTC	TGTTGCCCGC	GCGGTATGGA	ACTGGATCTT	11760
CTTCTGAACC	TGTTGTGGAT	GATGTCCTCC	CTGCCTCTGA	GTCTGCTCAC	AAAAGCGCTG	11820
TTTTCGTTAC	TGTCTCTCTT	GTCCGTGCAA	TAGCTCAATA	ATAGAATAAA	GCGATCGATA	11880
ACTATTTTCAT	CGATCGTTTA	TATCGATCGA	TATGCTAATA	ATAACCTTTA	TTACCAACAT	11940

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GCGCAGATA	GCACAGACAG	ACATTCAGGG	GACGACAGAA	CAACACTTCA	GAAACTCCCCG	12000
TCAGCCGGAG	CTCCGGCACT	GTAACCCTTT	ACCTGCCGGT	ATCCACATCT	GTGGATACCG	12060
GCTTTTTTAT	TCACCCTCAC	TCTGATTAA	GAAATGCTGA	TGAAACGACA	TCTGAATACC	12120
TGCTACAGGT	TGGTATGGAA	TCACATTACG	GGCGCTTTCC	TGCTTGCCCTC	CGAACTGGCC	12180
CGCGCACGGG	GTAACGTGG	CGGTGTGGCG	GTTGCACTGT	CTCTTGCCGC	GGTCACGTCA	12240
CTCCCGGTGC	TGGGTGCTGA	CATCGTTGTG	CACCCGGGTG	AAACAGTGAA	TGGCGGAACA	12300
CTGGTAAAC	ATGACAACCA	GTTTGTATCC	GGAACAGCTG	ATGGCGTGAC	TGTCAGTACC	12360
GGGCTTGAGC	TGGGGCCGGA	CAGTGACGAA	AACACCGGCG	GCAATGGAT	AAAACGGGGT	12420
GGCACAGGCA	GAAACACCAC	TGTCACCGCA	AATGGTCGTC	AGATTGTGCA	GGCAGGAGGA	12480
ACTGCCAGTG	ATACGGTTAT	TCGTGATGGC	GGAGGGCAGA	GCCTTAACGG	ACTGGCGGTG	12540
AACACCACGC	TGGATAACAG	AGGTGAGCAG	TGGGTACACG	GGGGAGGGAA	AGCAGACGGT	12600
ACAATTATTA	ACCAGGATGG	TTACCAGACC	ATAAAACATG	GCGGACTGGC	AACCGGAACC	12660
ATCGTCAACA	CCGGTGCAGA	AGGTGGTCCG	GAGTCTGAAA	ATGTGTCCAG	CGGTCAGATG	12720
GTCGGAGGGA	CGGCTGAATC	CACCACCATC	AACAAAATG	GCCGGCAGGT	TATCTGGTCT	12780
TCGGGGATGG	CACGGGACAC	CCTCATTTGC	GCTGGTGGTG	ACCAGACGGT	ACACGGAGAG	12840
GCACATAACA	CCCGACTGGA	GGGAGGTAAC	CAGTATGTAC	ACAACGGTGG	CACGGCAACA	12900
GAGACGCTGA	TAAACCGTGA	TGGCTGGCAG	GTGATTAAGG	AAGGAGGAAC	TGCCGCGCAT	12960
ACCACCATCA	ACCAGAAAGG	AAAGCTGCAG	GTGAATGCCG	GCGGTAAAGC	GTCTGATGTC	13020
ACCCAGAACA	CGGGCGGAGC	ACTGGTTACC	AGCACTGCTG	CAACCGTCAC	CGGCACAAAC	13080
CGCCTGGGAG	CATTCTCTGT	TGTGGAGGGT	AAAGCTGATA	ATGTCGTAAT	GGAAAATGGC	13140
GGCCGTCTGG	ATGTGCTGAC	CGGACACACA	GCCACCAGAA	CCCGTGTGGA	TGATGGCGGA	13200
ACGCTGGATG	TCCGCAACGG	TGGCACCGCC	ACCACCGTAT	CCATGGGGGA	TGGCGGTATA	13260
CTGCTGGCCG	ATTCCGGTGC	CGCTGTCAGT	GGTACCCGGA	GCGACGGAAC	GGCATTCCGT	13320
ATCGGGGGCG	GTCAGGCGGA	TGCCCTGATG	CTGGGAAAAG	GCAATTTCATT	CACGCTGAAC	13380
GCCGGTGATA	CGGCCACGGA	TACCACGGTA	AATGGCGGAC	TGTTACCCGC	CAGAGGGGGC	13440
ACGCTGGCGG	GCACCACCAC	ACTGAATAAC	GGTGCCACGC	TTACCCCTTC	CGGGAAAACG	13500
GTGAATAACG	ATACCCTGAC	CATCCGTGAA	GGTGATGCAC	TCCTGCAGGG	AGGCGCTCTT	13560
ACCGGTAACG	GCAGGGTGGA	AAAATCAGGA	AGTGGCACAC	TCACTGTCAG	CAACACCACA	13620
CTCACCAGAA	AAACCGTCAA	CCTGAATGAA	GGCACGCTGA	CGCTGAACGA	CAGTACCGTC	13680
ACCACGGATA	TCATCGCTCA	TCGCGGCACG	GCCCTGAAGC	TGACCGGCAG	CACCGTGCTG	13740
AACGGTGCCA	TTGACCCAC	GAATGTCACC	CTCGCCTCCG	GTGCCATCTG	GAATATCCCC	13800
GATAACGCCC	CGGTTCACTC	AGTAGTGGAT	GACCTCAGCC	ATGCCGGACA	GATTCATTTT	13860

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ACCTCCGCC	GCACAGGGAA	GTTCGTACCG	GCAACTCTGC	AGGTGAAAAA	CCTGAACGGA	13920
CAGAATGGCA	CCATCAGCCT	GCGTGTACCG	CCGSATATGG	CGCAGAACAA	TGCTGACAGA	13980
CTGGTCATTG	ACGGTGGCAG	GGCAACCGGA	AAAACCATCC	TGAATCTGGT	GAAACGCCGGC	14040
AACAGTGGCT	CGGGGCTGGC	GACCACCCGT	AAGGGGATTC	AGGTGGTTGA	AGCCATTAAC	14100
GGTGCCACCA	CGGAGGAAGG	GGCCTTTGTC	CAGGGGAATA	TGCTGCAGGC	CGGGGCTTTT	14160
AACTACACCC	TCAACCGGGA	CAGTGATGAG	AGCTGGTATC	TGCGCAGTGA	AGAACGTTAT	14220
CGTGCTGAAG	TCCCCCTGTA	TGCCTCCATG	CTGACACAGG	CAATGGACTA	TGACCGGATT	14280
CTGGCAGGCT	CCCGCAGCCA	TCAGACCGGT	GTAAGCGGTG	AAAATAACAG	CGTCCGTCTC	14340
AGCATTCAGG	GCGGTCATCT	CGGGCACGAT	AACAACGGTG	GTATTGCCCG	TGGGGCCACG	14400
CCGGAAAGCA	GCGGCAGCTA	TGGCTTCGTC	CGTCTGGAGG	GTGACCTGCT	CAGAACAGAG	14460
GTTGCCGGTA	TGTCTGTGAC	CGCGGGGGTA	TATGGTGCTG	CTGGCCATTC	TTCCGTTGAT	14520
GTTAAGGATT	ATGACGGTTC	CCGCGCCGGC	ACGGTCCGGG	ATGATGCCGG	CAGGCTGGGC	14580
GGATACCTGA	ATCTGGTACA	CACCTCCTCC	GGCCTGTGGG	CTGACATTGT	GGCACAGGGA	14640
ACCCGCCACA	GTATGAAAGC	GTCATCGGAC	AATAACGACT	TCCGCGCACG	GGGCCGGGGC	14700
TGGCTGGGCT	CACTGGAAAC	CGGTCTGCCC	TTCAGTATCA	CTGACAATCT	GATGCTGGAG	14760
CCACGACTGC	AGTACACCTG	GCAGGGGCTC	TCCCTGGATG	ACGGTAAGGA	CAACGCCGGT	14820
TATGTGAAGT	TCGGGCATGG	CAGTGCACAA	CATGTGCGTG	CCGGTTTCCG	TCTGGGCAGC	14880
CACAACGATA	TGACCTTTGG	TGAAGGCACC	TCATCCCGTG	ACACCCTGCG	TGACAGTGCA	14940
AAACACAGTG	TGCGTGAACT	GCCGGTGAAC	GGGTGSGTAC	AGCCTTCTGT	TATCCGCACC	15000
TTCAGCTCCC	GGGGAGACAT	GAGCATGGGT	ACAGCCGCAG	CCGGCAGTAA	CATGACGTTT	15060
TCACCGTCCC	GGAATGGCAC	GTCACTGGAG	CTGCAGGCCG	GACTGGAAGC	CCGTGTCCGG	15120
GAAAATATCA	CCCTGGGCGT	TCAGGCCGGT	TATGCCCAAC	GCGTCAGCGG	CAGCAGCGCT	15180
GAAGGTTATA	ACGGCCAAGC	CACACTGAAT	GTGACCTTCT	GATAATTCGG	CATTGTCTCT	15240
CTGTGGTCCC	GGTCATCATG	ACCGGGACCC	GGACAGGTGC	AAACGCTTCA	GTGCCACATT	15300
CACTGGCATT	CACAATAACA	TGATATTCAT	CACGGAGTGA	CTATGTTACA	GATACTCGGT	15360
GCGCTGATTC	TGCTGATCGC	AGGATTTGCC	ATTCTTCGCC	TTTTGTTTCA	AGCATTAACC	15420
AGCACAGCGT	CTGCGCTGGC	AGGGTTTATA	TTGCTGTGTC	TGTTCCGGCC	GGCTTTACTG	15480
GCTGGCTATA	TCACTGAACG	CATAACCCGG	TTATTCCATA	TTGCTGGGCT	GGCAGGCGTA	15540
TTTCTGACGA	TTGCCGGAAT	GGTCATCAGC	TTCATGTGGG	GACTTGATGG	TAAACATATC	15600
GCACTGSAGG	CTCATACCTT	TGACTCTGTA	AAATTTATTC	TGACCACCCG	TCTC3CCGCT	15660
GGTCTGCTGG	CTCTTCCCGT	GCAGATAAGA	ACCATTCAGC	AGAACGGGCT	CACACCAGAA	15720
GATATCAGCA	AGGAAATTAA	CGGGTATTAC	TGCTGTTTTT	ATACTGCTTT	TTTCCTTATG	15780

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GCGTGTTCTG	CATACGCACC	ATTGATCGCA	TTGCAGTTCC	ATATTTACCC	CTCACTGATG	15840
TGGTGGGGCG	GGTTGTTGTA	CTGCTGGGCT	GCATTAGTGA	CGCTGCTATG	GGCGGCCAGC	15900
CAGATCCAGG	CGCTGAAAAA	ACTGACCACT	GCCATCAGCC	AGAACTGGA	AGAACAACCG	15960
GTGCTCAACA	GTAAATCGTG	GCTGACCACT	TTGCAAAACG	ATTACAGCCT	TCCTGACTCA	16020
CTGACGGAGC	GCATCTGGCT	CACCTCATT	TCACAACGGA	TTTCCCGGGG	AGAACTGAGG	16080
GAATTTGAAC	TGGCAGACGG	AAACTGGGTA	CTGGACAATG	CCTGGSTATG	AAGAAACATG	16140
GCGGGTTTCA	ACGAAAAGCT	GAGAGAGAGC	CTGTCAATTA	CCCTGATGA	ACTGAAAACC	16200
CTCTTCCGGA	ACCGCCTGAA	TTTATCACCG	GAAGCGAATG	ACGATTTTCT	CGATCGTTGC	16260
CTGGACGGCG	GTGACTGGTA	CCCCTTTTCA	GAAGGCCGCC	GTTTTGTATC	ATTCCACCAC	16320
GTGGATGAGC	TTCGTATCTG	TGCCTCCTGC	GGGCTGACAG	AAGTACATCA	TGCCCCGGAA	16380
AATCATAAGC	CGGATCCGGA	ATGGTACTGC	TCCTCTCTTT	GTCGCGAAAC	AGAAACACTG	16440
TGTCAGGACA	TTTATGAACG	TTCTTACACC	GGTTTTATTT	CCGATGCAAC	GGCGAATGGT	16500
CTGATTCTCA	TGAAACTGCC	GGAAACCTGG	AGTACAAATG	AGAAAATGTT	TGCTTCCGGA	16560
GGGCAGGGAC	ATGGGTTTGC	CGCTGAACGG	GGAAACCATA	TTGTCGACAG	AGTCCGTCTG	16620
AAAAACGCAC	GGATCCTCGG	TGATAATAAT	GCCAAAAATG	GAGCAGACAG	ACTGGTCAGC	16680
GGAACAGAAA	TCCAGACGAA	ATATTGTTCA	ACTGCAGCCC	GTAGCGTCGG	TGCGGCATTC	16740
GACGGACAGA	ACGGACAGTA	TCGTTACATG	GGAAATCATG	GTCCCATGCA	ACTGGAAGTC	16800
CCCGTGATCA	GTATGCCGGC	GCTGTGGAAA	CCATGAAGAA	TAAGATCCGC	GAAGGTAAAG	16860
TACCCGGTGT	AACCGATCCC	GAAGAAGCGT	CCCGGCTGAT	TCGTCGGGGA	CATCTGACTT	16920
ATACCCAGGC	CCGTAATATC	ACCCGGTTCC	GGACCATCGA	ATCGGTCACT	TATGATATTG	16980
CCGAGGGGTC	GGTTGTCAGT	CTGGCGGGCG	GAGGGATCAG	TTTTGCCCTG	ACGGCATCGG	17040
TCTTCTGGCT	CAGCACCGGC	GATCGCGATG	CTGCCCTGCA	GACAGCTGCT	GTCCAGGCAG	17100
GAAAAACCTT	CACCCGCACA	CTGGCTGTCT	ACGTCACAAC	CCAGCAACTT	CACCGGCTCA	17160
GTGTTGTTCA	GGGTATGCTG	AAGCATATTG	ATTTTTCGAC	GGCCAGCCCC	ACTGTCCGGC	17220
AGGCGCTTCA	GAAGGGGACC	GGTGCAGGAA	ATATCAGTGC	CCTGAACAAA	GTGATGAAGG	17280
GGTCGCTGGT	GACATCTCTG	GCACTGGTAG	CTGTCACAAC	CGGCCCTGAC	ATGATCAAAA	17340
TGTTGCGGGG	ACGGATCTCC	GGTGCAGAGT	TCATCAGGAA	TCTTGCCGTG	GCATCTTCCT	17400
GTGTGGCAGG	TGGTGCTGTC	GGGTCAGTGG	CGGGCGGGAT	ATTGTTCACT	CCACTGGGAC	17460
CATTTGGTGC	ACTGACAGGG	CGTGTGGTTG	GCGGTGTTCT	GGGGGGAATG	ATTGCCTCCG	17520
CTGTATCAGG	AAAAATTGCC	GGAGCGCTGG	TTGAAGAAGA	TCGCGTCAAA	ATTCTGGCAA	17580
TGATTCAGGA	GCAGGTGACA	TGGCTTGCCG	GCASTTTTCT	GCTGACCGGA	CATGAGATTG	17640
AAAATCTGAA	CGCGAATCTG	GCCCGTGTTA	TCGATCAGAA	TGCTNCTGGA	GATCATTTTC	17700

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GCCGCCGGTA

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(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

AATAACCAAT AGATGCTTAA GTTTACGATA TGCCTCAACC CGCGTCTGCT CTAAGCTGAT	60
AAGGCCAGTT TTGTAGAGAT CCGCTGCCAA GGTTCCTGC GTTGCACAT CCATGTAACC	120
GGCGGTGATT TCATTCATGG CATCGTTATC TTGACCAGTC AGCTTAGCAC GCTCCTGTTC	180
AAGCTGCTTG GTTAGGGCGT CAACTCGGCT CTGTAATGAG ACTACGGCCG GTGCGGTTTC	240
CTTCATATAG CTGCGCAGTT GTTTTASCTC CCGCTGTTGA CGCACCAGCT CTCCTTCAAT	300
CTGGCTGACC ACTCCCAAGC GTGCGCTGCT GGTAGATTCA GGGCTGAGAA GTTGGTGGCT	360
ATTCTGAAAT GCTAATACTT TAGCTTTTTT ATCCTGTAAG CGTTGATATG CTCTATTTAC	420
TTCTTTTTCA ACAAAGGCCA ATTGTTGAG CGCAACCTGA TGACCTAATT TGTTAATAAA	480
ACGCTCCGAT TCTTTGAGCA TTAACCAAC AACTCGCTGA CCGTATTGGG GATCAAATGT	540
CTGCAACTCA ACGGTAAGTA CTCCTGATAA TTCATCAAGG TGTAACGTCA AATGTTTGCG	600
GTAATAATCA AGAAAATCTT CCCTACTGAC TCCCTTATGC AACC GCGAGA AATAATCTGC	660
ACTATCACTC TGGAAATGTG CTTTAAAGTC AAGTCTTTG TCCAAGTTGG CCAGCATATC	720
CCATGACTTC ATATAATCCT GAACGAGTAA TATATCCTGA TGATTACTAC CACCTATCCC	780
TAACATTGAT AACGCATCAG GCAACATTTT AACTTGATCG GCTTGTTTAA TCATTAATTC	840
AGCCCGGSTC ACATAACGAT CGGAAGCAAT GAAGCCAAA TAGAGCACTG CGATAGAAA	900
GCAGATAACT ACCCAAAGAA AACTGCCTAG CTGTAACTT TTCTTCCACG AGCGGTGTAC	960
AATTTGATAT CCTCTCGAAT CAATCAAAAA TAGTTTGGGA TTATTGCTCA GTTTTCTTAA	1020
CTTTCGCGTA AGGCGAGATA TTGAGGATGA AGAATTCGGA GATGTCATA TCAGTTGCTG	1080
CTCAAAGTGA CTGGTAAATT TTGATGGCAT CATCAATATT ATCAAAAAC TCTAATTTAC	1140
CATCACGTAA CAAGATGCCC ATATCGCATT GTTGTCTAG ATTTTTCATA TCATGCGAAA	1200
CCATAATCAA ACTAGCTGTT TCTCGCTTTT TGTTAAATAC ATCAATACAT TTTTGTTTAA	1260
AACGTGCATC ACCTACTGAG GTAATTTTAT CGGTAAGATA TATATCAAAA TCAAAGCCA	1320
TACTAACAGC AAAAGAAAAT TTTGATTTCA TGCCGCTAGA GTATGTTTTA ATAGGCAGCT	1380
CATAATGTTG TCCAATTTCA GAAACTCTT TAACCCACTC TTCTACGGGG CTTGTATCGC	1440
GTACACCATG AATGCGGCAA ACAAATCGCG TGTTTTCACG ACCAGTCATA CTACCTTGAA	1500

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ATCCCCCAGC TAGTGCTAGA GGCCAAGATA CTCGGCAGAG ACGAGTTACT TTCCCCCTGT	1560
TAGGCGTATC CATCCCTCCT AACAAACGTA ACAAAGTAGA TTTYCCKGCT CCATKGATAC	1620
CTAGAATACC TATATTACGG TCCCTTGGA GCTCAATATT TACATTCCTC AGGACATAAT	1680
TTCGTCCAAA TTTAGTTGGA TAATATTTTG ATACATTATC AAGAATAATC ATTTTCTTA	1740
ACGCTAACTA GCAATCAATT GGCGATGCCG TAATCGGTAA CAACTCATAG CAAAAGTGAG	1800
CAA	1803

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGGACCCAAG GTAAAAACNG GTAAAAA AAAA CMATTGACCG ATTAACTTT ATTTCTCTGC	60
CCGCATTAGT CTGGAGAGAG GATGGATGTC ATTTTAATTT NACTAAAGTC AGTAAAGAAG	120
CAAACAGATA TCTTATTTTT GATCTGGAGC AGCGAAATCC CCGTGTCTC GAACAGTCTG	180
AGTTTGAGGC GTTATATCAG GGGCATATTA TTCTTATTGC TTCCCGTTCT TCTGTTACCG	240
GGAAACTGGC AAAATTTGAC TTTACCTGGT TTATTCCTGC CATTATAAAA TACAGGAAAA	300
TATTTATTGA AACCTTGTT GTATCTGTTT TTTTACAATT ATTTGCATTA ATAACCCCCC	360
TTTTTTTTCA GGTGGTTATG GACAAAGTAT TAGTACACAG GGGGTTTTCA ACCCTTAATG	420
TTATTACTGT CGCATTATCT GTTGTGGTGG TGTGAGAT TATACTCAGC GGTTTAAGAA	480
CTTACATTTT TGCACATAGT ACAAGTCGGA TTGATGTTGA GTTGGGTGCC AAACCTTTCC	540
GGCATTTACT GGCGCTACCG ATCTCTTATT TTGAGAGTCG TCGTGTGGT GATACTGTTG	600
CCAGGGTAAAG AGAATTAGAC CAGATCCGTA ATTCCTGAC AGGACAGGCA TTAACATCTG	660
TTCTGGACTT ATTATTTTCA TTCATATTTT TTGCGGTAAT GTGGTATTAC AGCCCAAAGC	720
TTACTCTGST GATCTTATTT TCGCTGCCCT GTTATGCTGC ATGGTCTGTT TTTATTAGCC	780
CCATTTTGCG ACGTCGCCTT GATGATAAGT TTTACGGAA TCGGATAAT CAATCTTTCC	840
TGGTGGAATC AGTCACGGCG ATTAACACTA TAAAAGCTAT GGCAGTCTCA CCTCAGATGA	900
CGAACATATG GGACAAACAA TTGGCAGGAT ATGTTGCTGC AGGCTTTAAA GTGACAGTAT	960
TAGCCACCAT TGGTCAACAA GGAATACAGT TAATACAAA GACTGTTATG ATCATCAACC	1020
TGTGGGTTGG GGTGCACACC TGGTTATTTT CGGGGATTTA AGTATTGGTC AGTTAATTGC	1080
TTTTAATATG CTTGCAGGTC AGATTGTTGC ACCGGTTATT CGCCTTGAC AAATCTGGCA	1140
GGATTTCCAG CAGGTTGGA TATCAGTTAC CCGCCTTGGT GATGTGCTTA ACTCTCCAAC	1200

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TGAARTTCAT CATGGGAAAC TGGSATTACC GGRAATTAAW GGTGATATCA CTTTTCGTAA 1260
 TATCCGGTTT CGCTATAAGC CTG 1283

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6836 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCAACCTGAC CAACCACTAG AATCAACTCA CGTCCGTCGT TAGGGGGCTC ATATTCTTGT 60
 GTACTCCCCA CATTGTATTT ACTGACTCGT GATGATTGTA ATTGCGCTAA TAATGACTCT 120
 GCGCGTGCTT CTTCTTTTCG ATCTAAAACG TACGTAGTGA GTAAGTGCTC AAGCTTACTC 180
 GGACGGCGGC TATCAAAATA GATTCCAACG GGGTCAATCG AGAGTGATGA AGGTCGACAT 240
 AAATTAGACC CCAATCCGTT GGAGCGGATA AAACCATCTT CAATCCGGAT CACTGATTGC 300
 AGTTCAGGAT AACGGTTTCC CCACACCAAC ACCTGTTCAT CATCTTTTAA CTGTGAGGGC 360
 ACAGTACGAA CAAAACAAAG TTCATCTGCC AAATACGCAC AAAATGTGCG TATAAAAGCA 420
 CGCTTCCACA GAGAAAAACC AACGAGATAA AGACGACGCC AAGGTTTGGG CTCTACCTGC 480
 TGCTGAGCCA AAATCGCTAC AACATCTTCT ACCTCACAAC GTTTTCCCAA TATAGGATCT 540
 AAATAACGCS GATAACGGAT CAACGCCGCC GCACTAAGC GGGGCAATGA AATAGATGAA 600
 ACGCCTTCGG CTGACATTGC TTCTTCACGG CGTATACAAC GTTTACTGTC ATGCGTTAAC 660
 CCCCACCCAG CATAAAATGG CATACCGAAG CAATATACAG GTTTGCCCAA CAGCAACGCT 720
 TCCAAAGCCA ACCTGCGATG AAAGTGTGTA CACCGCATCC ACCATACGAA TTATTCTATG 780
 CGGATGGCAA GTTCACTCAC CACCTCAACA TCAGCCAGTC GAGGATCACG CCCCCTAAA 840
 CGTGCTAACA CGCCGCTTTT TTTGCTAAAG CGTGTATCTG GGTGTGTTTC CAACAATAGA 900
 CGCGCATTAG GGTGATTACG GCGAGCCTCG ACCACCATAG AAACAAAATC AGCTTCGCAA 960
 GCAAGAGCCC CAGAAATTGA CAAGTCTCCC GCTACTTGAT CCACAAGCAA AATACGCGGT 1020
 CTTGGATCAT CCAGTAAACG TGCTAAGTTT GAATGAGCCG TGAGGTGAAT AACTCAGGTT 1080
 GTATATGTGT CCGTAAATCT AAAGAAGGCC CGTCAGTAGC ACGGGACAGA GCCATTAAAT 1140
 GTATGCTCAG TGCTATTGGG TATAGCAGTT AACTTGGTG ATTCTTAAAC GCAAAATATC 1200
 MGAGATCAGA TGCTCCAGCG CGCGCAAAGT AAAGCCGTAT CCAACAGGTT CCAATAATAA 1260
 GCTGTTCTAA TTGACTCGTC TGATGTGCAT CATAATATAT CCCCAGAGGG TCAGCAATAA 1320
 GAGAAACCGC CTTTCCTCCT TTTGCTGGGT GCCCGATATA GCCAATAAAA CCATCTTCAA 1380
 GTTGCCAATA AGATATTCCT AACTCTTGAG CTTTCTGTTT AATCTGCTTA GTATTAGATT 1440

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TTTTTCCCCA	GCCAACTAAA	ACGTCAATTT	TAGAAAAAGC	CTCGTCTCCT	TTCATATAAA	1500
GCAATGGGTG	ACCAAGCATA	GGCTCAATAT	TATTTTYTCT	GGCAAGAATC	CCTTTTCGATC	1560
CCGTATATAA	ATACATGTTG	TCTCTGTGAA	CTGAAGATTC	TCTACAATGG	TGTATAAAGT	1620
GTGATTTAGA	TGAACAGCTC	TGCGCTCTCT	AATGACTTTG	CAATACTATC	TTTTGCTGAA	1680
GTGAGAATGT	CCGCCTTTAA	CTCGGGCCAC	CTAATACCAA	TTGTAGGATC	ATTCCATGCA	1740
ATGCCTCTAT	CACTGGCAGG	GGCATAATAA	TTAGTTGTTT	TATACAAAAA	TTCGGGCCGAT	1800
TCAGTCAGTG	TTACAAAACC	ATGGGCAAAT	CCTTCCGGAA	TCCATAATGT	CGTTTGTTTT	1860
CCCCTGAAAG	ATGAACGCCA	ACCCATTGTC	CGRASCTCGG	TGAGCTTTTG	CGAATATCTA	1920
CCGCAACATC	AAACACTTCA	CCGCTACAC	AACGCACTAA	CTTGCCCTGG	GCATGGGGAG	1980
GTAAGTGATA	GTGCAAGCCA	CGCAGTACCC	CTTTAGAAGA	TTTTGAGTGA	TTATCCTGCA	2040
CAAAGGTAAC	TGGATATCCT	ACAGCCTCTT	CAAACAACCT	GTGATTAAAA	CTCTCAAAGA	2100
AAAAACCACG	CTCATCTCCA	AATACTTTTG	GCTCAAAAAT	AAGCACACCA	GGAATTGCTG	2160
TCTTGATTAC	ATTCATCTAT	ATGCCACACAT	TTAATTAAAT	ATTTTTAGGG	GAAGCATATT	2220
CCCTCCCCCT	TCTCAATTAC	ATCAGCCTTT	ATCAATCATT	TTTAATAAAT	ATTGCCCATTA	2280
GGCGTTTTTT	GCCAACGGAG	CAGCAAGYTC	ACGAACCTGG	TCGGCACTAA	TAAACTTCTG	2340
GCGATAAGCA	ATCTCTTCCG	GACAAGCCAC	TTTCAATCCC	TGACGCGTCT	CGATGGTCTG	2400
AATAAAGTTA	CTCGCTTCAA	TTAGGCTTTC	GTGGGTACCG	GTATCAAGCC	AGGCATAACC	2460
ACGCCCCATC	ATTGCCACCG	ATAGATTGCC	TTGCTCCAGG	TAAATACGGT	TCACATCGGT	2520
GATTTCCAAC	TCACCACGCG	GCGATGGCTT	GAGACCTTG	GCAACGTCCA	CAACGCTGTT	2580
GTCGTAGAAA	TAGAGGCCGG	TGACTGCGTA	STACTCTTAG	GCTCCAGTGG	TTTTTCTTCC	2640
AGTGAAATAG	CGGTACCTTG	ATTATCAAAT	TCGACCACTC	CATAACGTTT	CGGGTCGTGC	2700
ACATGATAGG	CAAATACAGT	AGCACCGGTC	TCTTTGGCCG	CGGCTGCCTC	CAACTGTTTC	2760
TGTAGGTCAT	GACCGTAGAA	GATGTTATCC	CCCAGCACCA	GTGCACACGG	GGCTGAACCA	2820
ATGAATTCTT	CACCTAGAAT	AAAAGCTTGT	GCCAACCCGT	CTGGGCTTGG	CTGAACCTCA	2880
TATTGTAAAT	TCAGTCCCCA	GTGGCTGCCA	TCACCCAGCA	ATCGCTGAAA	GGANGGAGTA	2940
TCTTGTGGAG	TGCTAATGAT	CAAAATATCG	CGAATTCCAG	CCAGCATCAG	GGTGCTCAGC	3000
GGCCGCAGTA	CTGGATCATC	GGCTTGTCAT	AGATGGGCAA	CAACTGCTTG	CTCACCGCCA	3060
TAGTAACCGG	ATAGAGACGT	GTACCAGATC	CACCGGCCAG	AATAATACCT	TTACGTTTAG	3120
TCATGATGCT	TGTTTCTTAT	TTTAAATTA	CATAAGAATA	AAGTGGCTTG	AGCCGCGCCT	3180
TTCTGTTTTA	TCCTCACCTG	TGGTTTACTT	CCCCATGATC	TCAGTCAACA	TCCGCTCAAC	3240
ACCGACTGAC	CAGTCCGGCA	AAACCAGATC	AAATGTACGC	TGGAATTTTT	TAGTATCAAG	3300
TCGGGAATTA	TGAGGGCGTT	TCGCGGGGGT	CGGAAAGGCG	CCTGTGCGCA	CTGCATTAAG	3360

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CTGTGTGACT	GCCAGTTCAA	CTCCTGCGTC	TCTGGCTTTG	TCAAACACCA	ACCGGGCGTA	3420
GTCAAACCAA	GTGGTAGTAC	CGGAGGCAGC	CAAATGGTAC	AGCCCCGCAA	CGTCGGGTTT	3480
GCTCTGTGCA	ACTCGGATTG	CATGSSCGGT	ACAATCGGCC	AGCAACTCAG	CTCCAGTTGG	3540
AGCGCCAAAC	TGATCATTAA	TGACCGATAT	CTCGCGACGC	TCTTTGCCAA	GACGCAGCAT	3600
AGTTTTGGCG	AAGTTGGCAC	CGCGGCGAGC	ATAAACCCAA	CTGGTACGAA	AGATAAGGTG	3660
ACGTGAGCAG	AGTGCCGCAC	CGTGTTCCCC	TGCCAGCTTG	GTTTCGCCAT	AGAGGTTGAG	3720
CGGGGAAATC	ACATCGGTTT	CCACCCAAGG	ACGTTACCCA	CTTCCATCGA	AAACATAGTC	3780
GGTGGAATAA	TGTACTAGCC	ACGCACCTAA	TGCTTCAGCT	TCTTTGGCAA	TAACCGCCAC	3840
ACTAGTTGCA	TTGAGTAACT	CGGCAAATTC	CCGCTCACTC	TCCGCTTTGT	CGACTGCAGT	3900
ATGGGCCGCT	GCGTTAACAA	TCACATCCGG	CTTGACGAGA	CGTACCGTTT	CAGCCACCCC	3960
TGCAGAATTG	CTAAAATCAC	CGCAATAGTC	GGTGGAGTCA	AAATCAACGG	CAGTGATGTG	4020
CCCCAGAGGC	GCCAATGCAC	GCTGCAGCCC	CCATCCACTT	TCTGGCCACA	CCAGACTCGC	4080
CAGCAAAAAA	GTGAGTGCTG	TCAATAACTC	AACCAGCGGA	TAACGCTTGC	TGATTTTCGC	4140
CTGACAGTCG	CGGCAGCGCC	CTTTGAGCAT	CAACCATGAG	AGCAGCGGAA	TATTGTCACG	4200
AACGCGGATG	GTCTGCTGGC	AATGCGGACA	GTGCGAACGC	GGTAGCGCAA	GGCTTATTTT	4260
TGACTGCGCA	CTCGGCATTT	CACCATGAAA	CTCCGCCATT	TGTTGGCGCA	GCATGATGGG	4320
GTAACGCCAA	ATCACCACAT	TCAAAAAACT	GCCGATGATC	AATCCTCCGA	CGGTTGCCAG	4380
TATGGGCATC	GCCGCGGGGT	ATTGCTGAAA	AACATCAAAA	AGCATGGTTA	AAGGTTATTT	4440
GTTGTAACCT	GCCGGATGCG	GGCCTGCGGG	TGTATGCCAT	ACGGCTTTCC	TTCAGGCCCC	4500
ATGCGCCTTA	TTTCATGCCG	GATGCGGCGC	GAGCGCCTTA	TCCGGCATAc	AGGCTTACTC	4560
AGCTGACATC	TTATGCTCGG	TAACCTGATT	AATGGTTTCC	GGCCCTTGCT	GCGGTTTCGG	4620
CAGATTAAGC	GCCGCCAGTG	TCTCGTAAGC	CGACTGGCTC	ACACCGCCCT	CGAAGTTCAT	4680
CTCGCTCGCT	CCCGGCAACT	GGTAAGCATT	CGCGCCCGGA	TTCCATTTCT	TAAAGAACTC	4740
CGAAAGATCC	GTCTGGGCGA	CCCAGGATGC	ACACAGCATC	AGCTTGTCGG	CAGCGTTACC	4800
GTTGGATTCT	GCACAGTAAT	TTCTTTGCGC	AAACTTGGTT	TTGCCAACCT	CATCGCCGCG	4860
TGCTTTACGG	TGCATCAACT	GGAACAGGTT	CCAGCCTTTC	ATCCCTTCAC	GATCGCTGTA	4920
GAACCTTAGGC	AGGTCACCTT	CTGGATACCA	CTGTTTGATA	TCAAAGTTTT	TCTCTGCCCA	4980
CTCTTTCAGC	TGTGCGTACA	TCAGCAGACG	GTCACCCGCA	CCGCCGCGCG	CCCATGCCTG	5040
ACCGTTGCTC	TCCTCCAGAT	ATTCCGGCGC	GACGGTAATG	TCGTCAGCGA	CACGGTTCAT	5100
CTTGCCGAGA	TAGCGATCCT	GCATGTACAG	CGCCAGCACG	TTGTTGCTA	CTTCAGTTGC	5160
GCCAGGAACA	GTCAGCGGCG	TTTCGGCGGC	GTTGTGACCA	ACTTCGTGCC	AGATCAGCCA	5220
GTCGTTCAGC	GGCGTCGTCG	GCAGCGTGGT	GCTGTTGCTC	GAGAAGCTGC	TGTTTCATTAC	5280

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CGGATAACCA GAGTGGGCAT CACCGATGGA GATCTGCACA TCGTTGGTGA AACGATGCTT	5340
GTGGCCCGTC AAGTTTTTAT AGGTAAACAT CCGGTGCTTA CCGTCTTCAT CATTACGACC	5400
GTAGAAGTCA TTCATCGAGC TGGCAAAGST ATCCAGATCT TTAGCGAATT CTGCTACGCC	5460
ACCAGTGAAA TTGCTGGCCT CAASGTTCTT CTTGGGCGTG GTGTAGACGA AAGCGTCTGA	5520
CTCCAGCTCG CCCAACGGCG CAGGGGAGTT CAGAGCGTTT TTCCATGCGC CATCTTTATA	5580
GAACGGCGCT TTCACCACAC CAGTAAAGST GAATTCGGCT GACTCATTCT GTGGGCTGTT	5640
GCCCTTGATA TAAATCAGAC CACCGTAAGG AACCCTAAAC TTCACCTCAC CATTGGCTTT	5700
CAGCTCATAG GTTTTCGTCA CTTTGGCGG ACGGTTTCTG GCGACTTCAT GCTTCTCACG	5760
TCCGGTAAGG TCGTCGGCCA GCGCCACGGT GACAGTCACA GGAAGTATG CAGAAGACTC	5820
AATGGTGACC TCTTCTGAG CCGGAGCCCA CAGGCCAGTA GACTGCATGT TACCCGCAAA	5880
CCATTTGGTC GGATTCGAST ACAGGCTGAT GGTTCAGTA ACCTTCTCAC CTTCTGCCGA	5940
TACCGCTCCC GGATACTTCT CGACATCAAC TTTGATGTTT AGATCCCACC AGGAACGACC	6000
CAGCATCAGG CGCGTCAGCG GTTTTTCAT ATAGTTGAGC GGATAGCTCG GTTTCATCAT	6060
GCCCGCTTTA TTAACGCTCT TCTCGCCGTA GATCATGTTG TTATCGACCA GCGATTTTTT	6120
CAGCTCATCA GAAACACTGC GTGCCGCCAG TATAGGCATC GTTGGCGTAG CAGTTCAGGA	6180
ACTCGGTGAA CGTTTTAAAG CCCAGCTCGT CATCCTTGTC GTTTTCATAG CGATATTCAA	6240
TTTTATTCCA CAGCCAGACC GACATGTTCT GGTACAGACG TTCCAGATCG ACGCTGCTCA	6300
GACGCTCACC TTTGCGACCA TTGGTCCGGA AGTAGAGCTC ATGCTGATAC AGACGCTGAA	6360
TGTTGGTGCC TAAATCCGCA GCCTGCACCA TCGCTTTTGC CGTGTGGCG TTAAGGCTTA	6420
GTTGCGTATA CTGTGGAACA TACATGCCAC CAGTAACCGG AACCCCGTG CCAGGACGAT	6480
ATTCCAGACA GTTGACCTCG TAGTGGTAAG TTGGGTCCTT AACTCCTTT AATCCAGGAA	6540
ACTTCTCAA GATTTTTGCC TTCGCAGCCT TCAGAGAATC CTCTGTTTTA TGATCGGCCT	6600
CATCAATAAA GGCATAACGC GTTTCCTGTT TGCCATCTAC ATCTCCAGC CAGCTGGCAA	6660
CTTCCAGCTT CGGTTTGTCA TCAGGTTTGT TTTCTACCTG ATATTCCAC TTAATTCCC	6720
CTGTCTTACT ATCGATGGTG TACGGCAGCG CACCATCTAC GGCAGGATAA CGTTCATAGA	6780
CCCAAATGCC CGTTGCGCGC TGCTGACGAA CGCGGTTCCG ATACCCTTGC GGATCC	6836

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

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GGAAAAACNC GCCGTATATT AGCCCGCGCG GAAAAAGCCC CGTNACGGGC AAACGCAGCA	60
AGGTTTTTATC CCAGCGCAGG CGCATGGCAG GATTTTTTGAG TAGCCGTTGC CCCAGCACCA	120
GAAGCCCCAG CAATCCCGCC AGCCAGTAA CGCCGCTGGT CTGTAACTG TCGCTCATGG	180
CGATGAGCGT GCGGGTGGAG GCGGGCAGCG CGTGTCCGAG ATGATCAAAC GTTTCGATGA	240
TTTTTGGCAC CACTGCCGTC AGCAAAATAG TGACCACGCC CGTTGCCACC ACCAGCAGTA	300
CCAGCGGGTA GAGCATGGCC TGCAGCAGGC GTGAATTTCC AGNACCTGCC GCTGTTACGG	360
TGTAACCCGC CAGGCGATTG AGCACCACGT CGAGATGTCC GGATTTTTCT CCGGCAGCAA	420
CCATCGAACA AAACAGGGAA TCAAAGACGC GGGGATGTTT GCGCAGGCTG TCCGACAGGK	480
TGTAACYTTC CTGAATCCGC TGCGCAGCGC CATTCCGAGG CTTTTTACAT GCAGTTTTTC	540
ACTTTGCTCA CTGACCGCCT GTAAGCAGGT TTCCAGCGGC ATTGCTGCCT GTACCAGCGT	600
TGCCAGTTGG CGCGTGAACA GCGCAAGATC TGCCGCCGCC ACGCGACGAT GTGCGTGCCG	660
CCGACGCTGC AACATCCCCC CTGACGAAGT ATTCATCCGG GCTTCAATAT GCACGGGGAT	720
AAGCTCTTTA CCGCGCAACA ACTGGCGGGC ATGACGCGCG GAATCCGCCT CAATCATACC	780
TTTGGTTTTG CGACCATTAC GCTCCAGCGC CTGATAGTAA AACAGTGCCA TTACGCCTCC	840
ATGGTTACCC GCAGAACTTC ATCGAGAGAG GTTTCTCCGG CGAGCACTTT CTCAATGCCG	900
TTGCTGCGGA TACCCGAGA GTGTTGTGG ACATAACGTT CCAGCTCCAG CTCCCCGGCC	960
TGACGGTGGA TCAAATCACG CAATGTGGCA TCCACCACGA TCAGCTCATG GATGGCAGTC	1020
CGTCCGCGAA AACCTTTGTG ATTACAGGCG GGACAGCCCT GTGGATGGTA CAGAGTGACG	1080
GTACGGGCGT CGGTAATTCC CAGCAGGCGT TTTTCTTCGT CGGTGGCAGG CGCGGCCTGA	1140
CGGCAGTCGG AGCACAGCGT GCGGACCAGT CGCTGCGCCA TCACGCCCGT CAGACTGGAA	1200
GAGAGCAGGA AAGGCTCCAC GCCCATATCC TGCAAACGTG TGATCGCCCC CACCGCTGTG	1260
TTGGTATGCA GCGTGGAAG TACCAGGTGT CCGGTCAGTG AAGCCTGAAC AGCGATTTCT	1320
GCGGTTTCGG TA	1332

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCCAACGTTT ATCGTATTTT ATTAAAGTCC CTTGCCCGAT GCTATCTCGA GTTACATGAC	60
GAAATCGCTG ATTTGGATGT CATGATTGCG GCAATTGTCG ATGARCTGGC GCCTGAACTG	120
ATTAAACGTA ATGCTATTGG ATACGAAAGC STTCGCAGTT GCTGATCACG GCAGGAGACA	180

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ATCCCCAAGC ATTAAGATCA GAATCAGGTT TTGCGGCACT GTGTGSGTGC AGCCCTGTTC	240
CCGTATCTTC AGGAAAAACG AATCGTTATC GACTTAACCG GGGTGGAGAT CGTGCTGCAA	300
ATAGTGCACT TCACATCATT GCCATCGGAC GTTTGCGAAC TGACGATAAA ACGAAGGAAT	360
ATGTCGCCAG ACGAGTAGCG GAAGGGCATA CAAAAATGGA AGCAATACGC TGCCTGAAGC	420
GCTATATCTC ACGCGAAGTT TATACATTAC TGCCTAATCA AAACAGGCAG CTCAACAGCA	480
TCCCGATAAC GGCTTGACTC TTAGAAGGGC GTCCAGGGCA GCCACTATAC AAGCAGGCAG	540
TTCCGGCAGT TACTGTGGCG TTACCAGATC AAACAGAGTC TGAGTCGACG AGGAAATTGC	600
TGGGATAACA GCCCGATGGA GCGCTTCTTC AGGAGTCTGA AAAACGAGTG GATACCGGTG	660
ACGGGTTACA TGAACCTCAG CGATGCTGCC CATGAAATAA CGGACTATAT CGTTGGGTAT	720
TACAACGCGC TCAGGCCGCA CGAATATAAC GGTGGGTTGC CACCAAATGA ATCGGAAAAC	780
CGATACTGGA AAAACTCTAA AGCGGTGGCC AGTTTTTGTG GACCACTACA TTTAGTGCGA	840
CACGGGAAGC GCGATATGAA CGATACGATA CATCAATGGT TTATTGCGGT GATAACCTGA	900
AGGGTGAGAT TGAGGCTATT TATAATAGTC TTGAGAGGCG TCAGGTTTAG AGCAGGAATG	960
CTGAGTAGCC ATCTTATCGA TTGTTTTCGA GCGTAAGATG GCTGAATGGA ATGGCTATTA	1020
TTGCACAGTC CTTAATTATA ACATTCATAC CGACATGATT ATCTTCTGTC CGGAAGAATC	1080
AGAGGCTGCG GTTTCAGACT GTCTGCCGGT ACATTCCTCT CTCCGTAAA AACCATAACG	1140
GGTTCATTAT CTTCTGTCTGT CAGCAGATTG AATGGCGGTA TATTTTCAGT ACGAATGCCG	1200
GTCAGCCACT GAAAAATACC TGCGAAATGA CGGGCACTGA TTTTCTGCT GACGGACTGA	1260
TGAGACGTGA TGTCACTGGC GGTAATAATC AGGGGAACGC TGTAGCCTCC CTGCACATGA	1320
CCATCATGAT GAACAGGATT AGCACTGTCG CTGACCGACA GACCATGGTC AGAAAAGTAA	1380
AGCATGGCAA AATGACGGGA ATGCCGGCGA AGGATACCAT CAAGCTGCCC GAGAAAGTTA	1440
TCCCAGTTTA CTGATGCTGG CGAGGTAACA GGCAATTTTT CGGGGATACT GCCCCAGGTA	1500
ATGATTCGGC CAGGAGTTAA GCCGGTCACA CGGGTTCGGA TGAGACCCCA TCATGTGCAG	1560
GAATATCACT TCGGAGAGGA TTTATCCGCC AGTGCACGTT CTGTTTCCTG TAACAACAAC	1620
ATGTCATCCG TTTTACGGGA AGCAAAGCTG CCTTTCTTGA GGAAAACGGT ATGCTCCGCA	1680
TCAGAAGCAA TAACAGAGAT GCGTGATCA TGCTCCCCCA GCTTTCCTG ATTGGATATC	1740
CACCATGTGC TGTATCCTGC TTTTGCTGCC AGCGCCACCA CGTTGTTGCC GGAGTCAGGG	1800
TTCTGCTCAT AGTCATAAAT CAGTGTCGG CTGAGGGAAG GTACGGTACT GGCTGCTGCC	1860
GATGTATAGC CGTCAATAAA TAAACCGGGA GCAGTATTCA GCCACGGTGT GGTGCGCACG	1920
GGATAGCCAT ATACCGACAT ATAATCCCTG CGCACACTCT CACCAGTGAC GATAACAATC	1980
GTGTCATACA ACGGTACACC CGGCAGGATT TTCCAGTTGT CAGCCCCGTG CTGATTCACT	2040
TGTTTATAAC GCTGCATTTT ACGCAATGTG TCAGTTGTCC CCACAACAGT TCCTTTAACC	2100

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ATCCGCAACG	GCCAGCTGTT	TACTGAGCAT	AATACGAACA	GTAGCAGTGC	CAGCCAGTTA	2160
CGGTGACCGC	GGTGGTGTGT	TCGCCAGAAA	ATCACCATGA	ATACCAGAAT	CGCGGCACTG	2220
ACCAGAAAAT	GATAAACAGG	AATCATCCCG	GTAAACTCCG	CTGCCTCATC	AGTTGTGGTC	2280
TGCAGCAACG	CAACAATAAA	ACTGTTGTTG	ATTTTACCGT	ACGTCATACC	GGCAGGCGCA	2340
TACAGTGCAC	AACAGAACAG	AAATAACAGC	GCTGTAATGG	ATGTGAGGGT	ATTTCTGTGT	2400
GCAAGAAGCA	GAAGAAAGAA	CAGCAGCAAC	ACATTCCCGG	TGGTATTCTT	CTCAGTGTAT	2460
CCGCATGCAA	TTGTGGTTAT	GACAGAAACA	ACAAAAAAGA	ATAAAAAACAA	TATAATCCTG	2520
AGAGTGTTCG	CCGGACAAAA	CAGTTTTCTG	ATATTCATCG	GAGTATATCG	ACAACATTAT	2580
TATGAAGAGA	ACAGGATAAT	AAAAATCAGA	AGTTATCTGT	GAAACAGATA	ACAGACANCC	2640
CTGCAGTATA	ATATTACTGC	AGGGTGTTC	TTTTTAATTA	CAGAAATACG	TAATTATCTT	2700
AATTGCAGAA	ATATGCGCAA	TTATCGTTCA	GAAGCAGTGT	CGTCAGAAAGT	TATAAGTCAC	2760
ACCAAGCAGG	ATGTCATGAC	TTTTAACATC	AACCTCTGAT	TTATATTTAT	CCCCTTCTGT	2820
ATCCTTGTA	TACAGGGAGG	ATTTACCAGC	ATCCAGATAG	CGATAGCTGA	GGTCAAGAGC	2880
GATATCCGGG	GTTACGTCAT	AGCGAACACC	GGCCCCAATG	CTCCATGCGA	AGTTGTCAGC	2940
AGAGCCTGAG	CGTGATATAG	AATAACGCAC	TCGCTCACCG	TAGCCATAAT	CCCAACTACC	3000
GCTACCTGTT	GATTTCCTGAT	GAATTCTGGC	GTAACCAATT	CCGGCAGACA	CCCATGGCGT	3060
AAATGCACTG	TCGTTTCTGA	AATCATAGTA	CGCATTGAGC	ATCAGGCTGT	TGACTGACAC	3120
CTCATTCTTC	AGGTCACTAT	GTCCCGCGTG	GTCCTTATAG	AGGTTGTATG	TTGTGTCAGC	3180
TTTTCCACGG	GCGTAAAACT	CCAGTTCTGT	ACGCACAGGA	ATACTGAACT	GCGGATGCAA	3240
GTCATAACCA	AACGCTATAC	CTCCACTGAA	TACCGTGTTA	TGGCCATCCC	CCCCCTATAC	3300
TTTGATGTTT	CCTCTTTATT	TTCGGACAGG	AAACTCTGGT	CAGAAAGAGA	TACTGCTGAA	3360
GTACCTGCTT	TACCGGTCAG	ATAAAAACCG	CTTTTACCTT	CCTCAGCACC	CGCATTGCT	3420
GCAANCATAC	AGGCAGCGGT	AACTGCTGAA	ACAGCAAAAA	CTTTTTTCAT	TTCAATTAAC	3480
TCCATTATTT	CACTATTTTT	GTAAATAGCA	CTCCTAATAT	TTTAAAACCA	GTCAAAAGAT	3540
AGTATCAAGC	AAATTATTCA	TGTCTAATGA	ACAGATAAAA	TCGACTATGT	GTCGGCAAGA	3600
CTCTGCTCCA	CCGATATTCC	TCTTATTTCC	GCCTCGATGA	AATACCCCCG	TTACCTTATT	3660
TGTACCCCTT	ATAATGGGAT	GTTGGCCAGC	CAGACCCGGC	ATGATTAGTT	CTCCCTGTCTG	3720
ACTATGCTCC	GGGAGGGATG	TCACCGGGTC	TGGTGAGGCG	CGGATAACCG	CTAATAGGGG	3780
AAGGTCAGGT	ATTTTACACC	GGGACCGTCA	GGGCAAGATA	ACGAAAGCCA	GCTCCCCGCA	3840
TGAACTGACG	CCAGATAGTT	TCTGTCCATT	GCTGCTTTTC	TCATCTTACG	TCTTAACCCT	3900
GCCTTGAATA	CCTTATCTCT	CGTCAAAATA	TTAATAGCGA	TATGCCGTAT	CCCTGAAAAT	3960
AATCCCGCTG	CGTTTCCTCT	TCTTACTTGC	AGTCGTCTTC	ATTCATTACC	ACGTCCAGAC	4020

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GCCATGCAGC TTATTCTCCA CGTGCCAGTG ATTTGGGATC GGTGTGACGA ACTTCTCTGC	4080
GGTTAAATCA GCAGAACTGA TATAATATCT GACCATTATT TGTGACTCTT GCTTTTGTTT	4140
TGCTATTATT GACCGAAAGG AGACTGCCAG GCATATTTTT TCAGCCCTTT CCATTCAAAC	4200
GTGAATTCAA TCAGCTCATC AGGGAACNTCG CCAAACCATTA TGAAGACGGG ATCCTNCTCT	4260
GCCGTGACTC TTGTCACTAA TTGCGTAACA GTCATGCTCN GGGATAATTA AATCTTTCAG	4320
CGGAAATAAA AAGATTATCA GATATGGGGA TGACACCACA GCACCGCTGA GGCCAGTATG	4380
GATAAACCAT GTACCTTATT AACCAAA	4407

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 824 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TTTTTTGCAA GAGAATTTCC CTGAACCTGA AGCTCATCAT CGCCATCTCC GCCGTTCCAGG	60
TAATTATTAC CTGCTCCCCC AATTAACCTTA TCGTTGCCAT CACCGCCATA GAGCTGGTCA	120
TCTCCGTTTC CACCACTCAG TGTGTCATTA CCTTTATCAC CATATAAGCG GTCATTCCCCG	180
TCATTTCCCTT CTATATGGTC ATCACCATCC GCGCCATGGA AGATATCAGC AAATTTACTG	240
CCAAAAAACT TGTCCGCACG CGTGGTCCCA ATAAGTTCTT CCACGGAATA TAAGTTATCA	300
GTCTCTGTTA AATTTTTACC ATTGATATGA GTGAATTCAT AACTCCGATA TTGCGTTTTT	360
TCAGTTCTTT TTCCAACCTGA AACCTCCTGC TCCTTCACAA CTTCCTGTAA AACCTTAACA	420
TCACCACCAA GTACACGTGT TACCGTGTA TTACCCGCTT CGGTTGCTTT TGTGCCATCA	480
ATGGTCAGAT AACCGGTGTC TGTTTTATCA TAATAACAA CATCATGTCC TTTACCTGCG	540
TAGATATTGG CTGAGCCGGC AGATAAAAAG ACCTTATCAT CCCCCTCTCC CAGGTGTGAC	600
TCAATACGAA TTTCCCGATA CTGGTTATTA CCGACTGATG CATGCTGAAT CAGGTTAGAG	660
TAATCATATA CAGACCCCTT GTCCTGNAAC CCCCTTCACC GTCCATTTAT CAACACCCTT	720
GACTAATAAC TCGGTAATAT ATTCATATTT TCCGGACTGC CTCCTTTCAC GAATTTCCCTC	780
ACCGGGAGTT TAACAATGGG CGTAACNAAT TTGCAATAAC GTGG	824

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GNGGCCGCAG TACTGGATCA TCACCGAAGT TTCGCGCGGA AAAGCGTTAG AGAAAGATCT	60
AATGCTTCAT GATGGTGATG GACTTTTCCT GATGGTGAAA TCCAGCGGGA AATGCTCTGG	120
CGTTTCCGTT ATCAACATTC GACAACAAAG CAGCGGACAA TGATGGGACT CGGTGTCTTT	180
TCCACACTTT CACTTGCTGA TACCCGAGGG CTAAGAGTGG ATTATATTTT CTTATTAGCC	240
AACAGAATCG ACCCGCAAAT TCAAGCTAAA GCCGTAGACG AAGAGCAATA TTTGAAAAGG	300
TGGGCACCTA CGTTACCAAT ACTGGCTTAA TGGCTACATA CGGCGGTCAG GGTCAGTTTA	360
CGCTTACAAA ATATAAAACA ATTTGATACA AAATATTCCT CTTATTCTAA ATAAAAGTAT	420
CTTGAAAACC TTCCAACCTGG AAGGTAGATT GAATTTATGC TAAACATAAA GAGGAATTGC	480
TTATGAATTA CGTTATCCGC ACTACCACCG TCGTCTTTAG TCTCATGCTG GGCAGGTTAC	540
GCAACTGCTG	550

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACTAAAGGC CCTGGATGTT TTTTCGCTCAT TAGTAGACAT CTCGCTGATA ACGGCGCTCT	60
ACGCGCACTC ACTTAAAAAT TCATCCGCCG CTTCCGGTGC CATGCCACCA AATTCGGCAA	120
TCACTTCCAG AAGTGCCTGC TCAACGTCTT TCGCCATGCG ATTAGCGTCG CCGCAGACAT	180
AAATGTGGGC ACCATCATTG ATCCAGCGCC ACAGCTCCGC GCCCTGTTTCG CGCAGTTTGT	240
CTTGTCGTA AACTTTTTTCT TTTTGATCGC GCGACCAGGC AAGATCGATA CGTGTCAGCA	300
CGCCATCTTT GACGTAGCGC TGCCAMTCCA MCTGGTACAG GAAGTCTTCC GTAAAGTGCG	360
GATTACCAA GAACAGCCAG TT	382

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TAAATCAGCA GAACTGATAT AATATCTGAC CATTATTTCT GACTCTTGCT TTTGTTCTGC	60
TATTATTGAC CGAAAGGAGA CTGCCAGGCA TATTTTTTCA GCCCTTTCCA TTCAAACGTG	120

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AATTCAATCA GCTCATCAGG AACATCGCAA ACAATATGAA GAUGGATTTT TTCTGTGCCG	180
TGACTCTTGT CACTAATTGC GTAACAGTCA TGCTGTGGAT TATTTAATTC TTTCAGCGAA	240
AATAAAAGAT TATCAGATAT GGGATGACAC ACAGCACCGC TGAGCAAGTA TGTATAACCA	300
TGTACTTATA ACAAAGGAG ACGTAAGAAG GGAACGGGT ATCAGAGGGC CAATCAAAGC	360
AGGTATAATG AACGCCAGTA TAATTGTCCG CAACCCAGAA ATATATTATT GAACTGGTTA	420
TCTCTGCGA ATGCATATAC TGCAACGGCC GTTAAATAG CATTATATCC ATAAAGCCCG	480
GCAGAGATTT TATCAGGAGA AAGCTCAGGA ATACAGAATG ATACCACCAC ACTCAGAAAC	540
GAAGCGACAA CCGTAATCAT CAGTAGTTTC CGGCTCCCTG CAAAGTAGTC CAGCATAACA	600
AGAATACCGC CGACAGCATC AGGAAACATA AAAATCTCCA TAAAGCTACC AGACAATGCC	660
ACCGGATAGT TTTTCAGCAA AACAGAACCT GCACTTCGCC CGAAGGTACT GACATATCAT	720
GAGGCATTAT TCCGGAATGT AATAACCACG TAGCGATAAT AAAGGGGGCG GTCAATACGG	780
GTAACCTCT GAGCACTGAC GACAACAGGG GAGTAAACAA AACAATACCA AGAGTTCCGA	840
CGATAAGTAC AGCAATTCCG GAGACTGACA CAGGGACAAG CATGCCACAG GCTATGCCAT	900
ACAGAACAGC ATTATATCCC CATATACCTT CATTAATCTC CTCATCAGGA TACCGCAAAC	960
ACCAGGCAAA GAACGGAGAA AGTGCTGCAC TGATGGCTGA GAAATACAGT ATTTGGGGT	1020
GCCCCATATT AAAAGAGGCT ATTCCAGTCG CCAAAAAAAAA GAACAAGCCA GAAACAACAT	1080
TGTTCTGTAA TAATACCTGT GAATACCCCT TACTAAAGGC GGTTATCACC TGTTTTACTC	1140
TCATGTAAAA TGTCACACAC ACCTCATACA TAAACCATTC TCCGCTTCTG CGGGACAGTA	1200
CCGCCCCCTGA CTCCACCTCA CAGCGGATTG TGTATTTTAA AACAATCACA GTCTTCTCAT	1260
ATACTTTCCA TTCTGAAGCT TATCTCTTCC TCCGTGATAA GCTTCCGTG CGGGATGTGT	1320
TATACGCCCT GTAAGACAGT TATAAAGGAC ATCAATGCCA TAGTTAATGA YTACCGAATT	1380
CCGGTGGATA GTCAGTACTG GTTTGCCACA AACAGTGCA GTCACACATG ACAGGAGAAG	1440
ATATGAGCCG GATACCGCTG CTCTGAGACT TAACGCTCAT GTAAACTTTC TGTTACAGAT	1500
TCTTCCAGGG ACTAAGAAGA TAACTGANTT ACGTTCGCAT TCCAGTSTTT ATTTCTGCAG	1560
TGACAGCCAT ACCCGAGCTT AATGGAATGT GCTTATCCC GGTTGACAAA TCATTCTCTT	1620
CAACAGAAAC AATGACATTA AAAACGAGTC CCAGTTTCTG GTCTTCTATT GCATCTAAAT	1680
TTATATTTTT TACCTTACCC ACCAGATAAC CATATCGGGT GTAAGGAAAA GCCTCCACTT	1740
TAATGATGGC ATTCTGCCCC ACGTTAATAA AACCAATATC TTTATTTTGT ACCAGAGCAG	1800
TAACCTCCAG CGTGTCATCT TCCGGAACGA TGACCATCAG TGTTTCCGCT GTTGTAACAA	1860
CCCCACCTTC AGTATGAACC TTCAGTTGCT GAACTTTTCC CGAAACAGGG GCCCTGATTA	1920
CTGAAGCCTG TTGACGCTCT TCATTTTCT CTAAGTCCAG AGTTAATAAC TCAATGCTGT	1980
CTGTGTTG TCTTAGCTTG TCTAAAATTT CATTTTAA AAGCTGCGTG ACAAGCTGAT	2040

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ATTCTTCTTT TGCAGACAAT ATCTCACTCT CAATTTGCTC CAGTTGCGAT TTATAAACCC	2100
GTAATTCATT TGCTGCCTCA ACATATTTAT TCTCCTGCTC AAGTACAGCA TGTTTTGCAA	2160
TTGCCTGTTT ATGCAACAGG CTCCTGAAAT CATCCAGACG GCTTTTTTCA ACCCTCGATA	2220
CATTTTCATA ACGGTTTATA CGGGCAAGTA TTGTAAWCG CTCTGCTCTT TTCTTATCCA	2280
GATTCAGTTC TTTTGGATAC TTCTGATTTT GCCATGTGGA AAAGTGTCTT TTTATCAAAG	2340
AAGTTAAACG CAGTACTTCC TCTTCAGATA CATTCTGAAA ATAAGGCTCA TCAGGAAGTT	2400
TCAGTTCAGG AAGTTTATTT AATTCAATTG ACCGGCTCAG AATTTGATAC CGAATTTGTT	2460
CCAGCCTGGC CTGTAACAGT GATGACTGCG TTTTAAACGT ATCAGCTTCA GCTCCAGCG	2520
CTGTAAGCTT TAATAACACA TCCCCTTTCC GGACTGACTC TCCTTCTTTT ACGAYAATTT	2580
CTTTAACTAT CGAGTTTTCA ATAGGTTTAA TTTCTTTNTA CGCCCACTGA GTGTAAATTT	2640
CCCATTTGCA GTGGCAACAA TTTCCACCTG GCCTAAAACA GATAAAATGA AAGCAATAAC	2700
CAGAAACCCG ATAATAAAAT AAGCAACCAG ACGCGGCCGT CTGGATACCG GCGTTTCAAT	2760
TAATTCCAGA TGAGCGGGTA AGAATTCATT TTCGTCCTTT TCACGTACCG GAGTATCTAA	2820
CTGCTTCCGG ATTTTCCATG TTTCCTCCA GACAAGTTTA TAGCGCAACA GGAAGTCGCT	2880
GAACCCCAT T AACCATGTTT TCATATTCTT CTGTTCTTTC TGTTAGTCTG ACTGTAAGT	2940
ATATAAGTAA CTGTATAAAC TTTCCGGTTC AGAAAGCAGC TCCTTATGTT TACCTGTTC	3000
AACAATTTTC CCTTTTCCA TGACAATAAT GCGGTCTGCA TTTTCTACTG TAGACAGACG	3060
ATGAGCAATG ATTATAACCG TTCTGCCCTT ACATATTTTG TGCATATTGC GCATGATGAC	3120
ATGCTCCGAC TCATAATCCA GAGCACTGGT TGCTTCATCA AAGATGAGTA TTTTAGGGTT	3180
GTTCAACGAG GCCCTTGCAA TTGCGATGCG TTGACGTTGA CCTCCGGATA ATCCTGCCCC	3240
CTGTTCCCCG ACAATGGTGT TATACCCCTC ACGCAATTCA GAAATAAAAT CATGAGCACC	3300
TGSTAATTTT GCTGCATAAA TAACTTTTTC GACGGACATG CCAGGATTAG CCAGTGAAT	3360
ATTATCAATA ATACTGCGAT TAAGCAGCAC ATTGTCCTGC AACACAACCC CCACCTGACG	3420
ACGTAACCAG TTAGGATCGG CCAACGCAAG ATCATGTCCA TCAATTAAGA CCTGGCCATT	3480
TTCAGGAATA TAAAAACGTT GAATTAATTT AGTTAATGTG CTTTTCTCTG AACCAGAACG	3540
TCCGACAATA CCAATAACCT CCCCCTGCTT AATACT	3576

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

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TCAGCCCCGGT GAGCGGGTTT GACAATTCGG CACTCACCAT TGGGCTAAGG GTTATCAGGT	60
GGGGTTAAGG AAATGGCAAA ACCTACCCCC GTCCAAACTC CAGTGGCTGC ACATTCACCA	120
TCCCTGGCTT CTCACCTGCG CTGACATCAA TTTGTGTGAC CCGCAGCGCA TATTTTTCAT	180
CCAGTGCTTT TAACCAGTTC AGCAGGTGAT TAAACACCAAC AGGTTCTATC CAGACCTGGA	240
TATTCTCCCC GCGCTCGGCA ATCGSTTTGA TGACCAACCA GTGCGCGGAA GCTGTCACTG	300
ATGACCCGCG ATACCTGTGC TGGCGTTGTC GTGCGGGATT TTGCGCGCCG AATAATATCC	360
GGCGCGGCGC TCTTCAGTCG CGCGTTCATC GCCACCAAGT GCTGCAACAT CGTCTCCTGT	420
TGCTCAATCC GTTCGCTCAA CGGCTGCCAG ATGAGAAGCT AATATCCGEC GCTAAACAGG	480
AACACTACCG CTGCCAGTAA CATGCCTTTT TCACGCGGCG AACGCCCCGC CAGGTGTTGT	540
GTCAGCCAGT GTTCGCCACG GCTTAACTGG CGTTACGCGC ATTGCTGAAA ATAGTGAATA	600
AATTTATCGC GTAACATGTT ATTTCTCTCG CAACGTTACG CCGCGGAAA CCGCATCACC	660
CTCTTTCTGT AACGCGTCTT GTTGACAAAC ATAATCTGCC GCCAGTGCGC TACGAGTTTA	720
TCGAAGCTGG CAAAGTTCGC AGCCCGTAGC TGGAGGTGAA GCGTCTGGCG TTTTGTATCA	780
AAGGTGAAAC ACGCATTTGC ATGTCGGTAA GTGACGCTGA TTTCAGGGTA CTGGCGATCG	840
CTGACAATTC TGCGAGCAGC CGGGTATCGT CGGTCTGTGG GCGATATTTT TTCAGCGCCA	900
TCGTACCTG AGAGCGTAAA TTCACAATCC GCTTCTGCTC CGGGAATAGC GTTAAGAACT	960
GTTTCTCCGC CTGGGTGCGG CTTTGCGCCA CCTGTTGCTT GACGCTCCAT AACGTCACGC	1020
CCCGTTCCAC TACCAGCGCA ACCAGAATCA ACAATATCGG CAGAATCATC ACCCGCCAGC	1080
GCGCCCACTG TTTTCGGTAG CTGACACGAG GCTGCCACGG CCCTGTTAGC AGGTTCCCTT	1140
CCGGTTGCGC ATAAGTGGTA ATGGCGGGCA GAGCGTAAAG GTCAGCGTTC GGCGTCTGCA	1200
CCAGCCCATG CAGACAGTTC TTCCGGTGCA ATGCCGACCA CGGTTAGTGA AAGCGGTAAA	1260
TCCTGCTCAT TGAGCTGTGC TCGGAACATG ACCGGAGCCA GCGCCCGCCC GGCGCTCCAT	1320
CCCCGGCATT CATCGATGCG GMAGATAACC CGTTGCGCAT CGCCAGCCAT AAACCCACAA	1380
GGAATGGACA TCCAGTCCGG CGCGACGATA GCGCGSGTGA TGCCGTTTGC CTGCAACCAC	1440
TGCGCAATGT TGCGCATATG CTGCTGGTGA ATCAGAGCTA CGGTTGCCAG TTGCTGGTCG	1500
ATTTTCAACG GGGCGAAATG CAGTTCATCG ATATCCTGGT TCAGCTCTTC TTCCAGCAAG	1560
GCGGGCAGAA TCGTCGGTAT CTGCTTGCGG GGCACATCAG GCASTTCAAC CTGCCAGACG	1620
CTGATCCATT CGCCGGGAAT GTAGAGTCGA ATCGCATCAG TTTGCAGCCA TTGCTGGAGA	1680
CATTCATCAG CAACGTCAGG CCAGATGCCG CACTCCAGCT CGGCGGTACG ACGCTGCCAA	1740
CGGATGGGAG CGGAAMGNCA AAGCGGGAAA AAAATCTCAA GCATGGAACT CACTCACTTT	1800
CTCCTGTCTG ATGCCAGAGA ACAGAAAAGT GTTGTGGGTC CATGCGGACA ATTAACGAAT	1860
TCATCGTCAG TTCAATCTCA TTCACGGTGA TATCTGAACG CAGCAGAAAT TAATTGCTGT	1920

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CCACGCTCAG GACGGTTTTT AGCTGTTTTT TAGTACGCTC ATCGACGTCA GCAAGTAACG	1980
GCTGTGCAAG AAACGTATCG ACATCTTCCC AGCCCTTCGC ATGACGTTGT TGTAATAACG	2040
CTCGCGCCTG AACAGGGCTT AACCACGGGT CAAACAGCGC CTCAGAATC ACACTTTGCG	2100
TGACGTCTAA GSTATTGATG TTGATTTGCT GCGGGTTCAT CGGCAGCGCA CAGACCAGCG	2160
GTTCAGTTT TTSATAAAGC CCGGCGTCCA TTCCCTGCAC CAGGCGCATC TCGCTGATAT	2220
CAGCCAGCGG TTGATTAGCG GCGTAAACG GCACCGAAGG GCGGAGATAC TCGCTGTCTT	2280
CACGGCCCAg ACGCGTCTGC ACGCTGCGGT CTTCGTCAAT AAACCTCCAC AGGCTTTTCGG	2340
CTATCAGTTC GSCCCGATAA GCAGGCACAT CCAGGCGCGT GATCAGGGCA ATCAGTTGTT	2400
GTACCGCGAG CGSACGCGAC GCGGTGTCG GCTGAGCGAG GGCATTCAGG TTAAAGCAAG	2460
CCTGTGCGTC ACGCAGAGTG ACGGCGATTT GCCCTGCGGC AGTGGGAAAA AACGCGGGCC	2520
GGAAGCCCN ACGTGCGCCAG ATGCACGCGC TTTTCATTTT TCAGGCTCAG ACTGAGTGCG	2580
CTCAACGCCA GGCTTTCCGC ACTGGCGCTG TACCACAGCG CCTGCTGGTA CTCCTGCTGG	2640
TGCGCGTTCT CCCAAGTTGT TTCTGCATCC GCCCGGAAA GGTGATGGTC ACCAGCATCA	2700
TAACCGCCAG CAATACCAGC ACCACGACCA GTGCCATTCC GCSTTTTGGT GGTGAGGTGA	2760
TCATGATAAT TCGGGCCCGC GTAACAACCA GATGCTTCA ATTTGCCCC ATTGTGGCGA	2820
ATGCAGGGTT ATGCGTACTG CCACGGGGAT CGCCTGCACT GATGACCAGC TCTCCTGCCA	2880
GCGCGTGCCG TCGTAGAACT GCAAACGGAG CGAATCCGCC GGGATTAATT TTTGCGTTGT	2940
TGGCTTCACG CTGCCTGCCG CATCGGTCAG TGGCCAGGCT AACCGTTCTGA GATAACCACC	3000
ATGAATGCGG TAACCGACGG TGAGCAGATT ACTGCGCGGC AGACGCATCA ACGGATTAAC	3060
CACGCCGCCA CGTACAAAAC GCATCCCTTC ACTCTCAGAC GCCAGCACGC CAGCGCCCCG	3120
CAGTAACGCT RGTTCACGCT GGCCCTGATC GCCTCTTACC GAGCGCGGCA TCATTTGTGT	3180
CAGATCGTGG CTCAGAAAAC TCATCGTTTG CTGCATGAGG TTTAGTTTTT GATCGTGTCC	3240
GGCGACGGCG CTATTCACGC GTGTAACCCG TTTGTACCT GCTGCGCCAT CATTGCCAGT	3300
GAGGCAAAAA TGGCTATTGC CACCAGCATT TCCAGTAACG TGAAACCAGC GCGAGTCCTT	3360
CTCACTGTTG GTCTCCACG GCGCTAAACC ANGCGCGTCG TGAAGTAATC ACTGACGAAA	3420
AGTCNTCATG AAGACTGACT TCAATATCCA CNGCATGGAG CAGCGCATTA NCGGTATTCA	3480
GTGGTGTGGG TTCGCCAGAA CCAAGCGGCT TTCTGCCAT AATCGCTCTC GGCCCTGGGT	3540
G	3541

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1234 base pairs
 - (E) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTACTGGACA TCTTTGATGA ACAAGCTCCT CAGTGTAAT TGTACGTCTC TGATCGTAAT	60
CTTCCTGAGG GCGTTGAACA TCTATCCGCT GAATTTATAC CCTATACTCC TGAGTCGGCA	120
GATTTTCTGA TTCAACGTTT TTTCTCTGAA ACTATCCATA TTGAAAGTGC AATTGTTGTT	180
ACAGCACTTA AAATTGCCAA TCAGATTGCT CTATCTCAAA ATGAGACCAA GAATGTGTAT	240
CTGCTTGAT TTGATTTTAC GATAAAGGGG GGGTTCAC TA GCAAGATCCC CTGCGCAGCC	300
TTGCATGCCG AACCAGAATA TCAAGAGCGA ATTATCAGTA GTCAAGAACA GCTATTGCAG	360
ATGCTCCTTG CAGAAAAAAC ACGCCTGAAT ATCAATATCA ATCATGTTGG TAATAAGCCT	420
TACAGCGTAT ATTCTGTTGA TGCATTTAAT CAAGTGTTCC CTGCCCCCCA TCGTGGAGTC	480
GTGCTGCCCA CACATGCCCA GATTTCCTACT ACATCATCAC AAAATGGGGT GAAGGTGATC	540
GCAGAGATTA CTAATAATCA CTTTGGTGAT ATGGACCGAT TGAAGTCAAT GATTGTAGCG	600
GCCAAGCAGG CAGGGGCTGA CTATATCAAA CTGCAGAAGC GTGATGTTGA AAGTTTCTAT	660
AGCAGGGAGA AGCTGGAGTC ACCGTACAAC TCTCCTTTTG GCACCACCTT TAGGGACTAT	720
CGGCATGGCA TTGAAC TCA TGAAGAGCAA TTTTCCTTTG TCGACTCTTT CTGTAAAGAG	780
ATTGGTATCG GCTGGTTTGC TTCTATTTTA GATATGCCCT CGTATGAGTT CATTGGGCAA	840
TTTGAACCAG ATATGATCAA GCTACCATCA ACTATATCTG AACATAAAGA TTATTTGGCT	900
GCTGTTGCTT CTGATTTTAC TAAAGATGTA GTAATTTCAA CTGGTTATAC TGATGAGGCC	960
TATGAGCGTT TTAYCCTKGA TAACTTTACC AAGGTTAGAA ATATTTATCT GCTGCAATGC	1020
ACCTCGGCTT ATCCACACACC GAATGAAGAT ACCCAGCTAG GTGTGATAAG ACATTATTAT	1080
AATTTGGCGA AAAAGGATCC ACGTATTATT CCTGGTTTTT CCAGCCATGA TATTGGTAGC	1140
CTTTGTTCCA TGATGNTGTC GCAGCCGGTG CAAAATGAT TGAAAAGCAT GTTAAATTTG	1200
GCAATGTGGC TTGGTCTCAC TTTGATGAAG TTGC	1234

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ATGGGACCTT TCTTCAATGA TGTTGCCGAG TGGTTAGAGT CATTAGGTCG TAACGCTGTG	60
AATGTTGTAT TCAATGGAGG AGATCGTTTT TACTGCCGTC ATCGACACTA TCTGGCTTAT	120
TACCAAACGC CGAAAGAATT TCCTGGTTGG TTACGAGATA TCCACCGGCA ATTTGACTTT	180

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GATACCATTC TCTGTTTTGG TGA CTGCCGT CCATTGCACA AAGAAGCAAA ACGTTGGGCG	240
AAGTCTAAAG GGATCCGCTT TCTGGCATTG GAAGAAGGAT ATTTACGTCC GCAATTTATT	300
ACTGTTGAAG AGGACGGTGT AAACGCGTAT TCATCGCTGC CGCGCGATCC TGA CTTTTAT	360
CGTAAATTAC CAGATATGCC TGCACCACAT GTTGAGAACT TAAAACCCTC GACGATGAAA	420
CGTATTGGTC ATGCAATGTG GTATTACTG ATGGGATGSC ATTACCGACA TGAATTC ACT	480
CGCTACCGTC ATCACAAATC ATTTTCTCCT TGGTATGAGG CTCGTTGCTG GGGGCGTGCG	540
TACTGGCGTA ACTATTTTAC AAAATAATGC AACGTAATGT ATTGGCTCGG TTAGTGAATG	600
ATCTGGACCA ACGTTACTAT CTTGTTATTT TACAAGTTTA TAATGATAGC CAAATTCGTA	660
ATCACAGTAA TTATAATGAT GTGCGTGATT ATATTAACGA AGTTGTATAT TCATTTTCGC	720
ATAAGGCACC GAAAGAGAGT TATTTGGTGA TCAAACACCA TCCGATGGAT CGCGGTCACA	780
GACTCTATCG ACCATTAATT AAGCGGTTGA GTAAGGAATA TGGCTTAGGC GAGCGAGTCA	840
TATACGTACA CGATCTCCCA ATGCCGGAAT TATTACGCCA TGCAAAAGCG GTTGTGACAA	900
TTAACAGTAC AGTGGGGATC TCTGCACTGA TTCATAACAA ACCACTCAAA GTGATGGGTA	960
ATGCTCTGTA CGACATCAAG GGGTTGACGT ATCAAGGGCA TTTGCACCAA TTCTGGCAGG	1020
CCGATTTTAA ACCAGATATG AAAGTGTTA AGAAGTTTCG TGAATATTTA TTGATGAAGA	1080
CGCAAATTAA TGCTGTTTAT TATGGTGTA AATCAAAAAG CAATAGAAGG TCCGCATTCC	1140
TAAACGGTAG CAGATGATGG TTTTCATGGG CGTTTCAGGT TACTCAATCA GCCAACAACC	1200
GCAGCGAAAA CCCTGCTTTC TCGACCAGTT CAGGCCGGTT TTACCTCCAA TGCTTTCCGT	1260
CAGAACTGAG ATTTTCAGCCA GTTGCCGGAT AAGTGTGTCTG ATTTGCAGCA GTATACTTTT	1320
TCGTACAGCC AGAATGTGGC AGACTGAGGT GGAATAGATA ACGTCCGTAT GCGCGCTCAC	1380
CACCTCCGGG CGGGAGTGTG TGGTATCTGA CATCATCATT TTTCTTTCT GTTTATAAAT	1440
GAAAACGCCA GCCGTGTTCA GGCTGACGTC AGGGAAGTGA AATCGGGTGA GTGATCTTCA	1500
CTGGTTCTGG TGCAAAAGTT ACTGTTGGCG CAGGGTACGG ATACCCTCCC TGGCCTGTTC	1560
GATACAGGGC AACAGTGCTG CCGAATCTGT TTTATCCTCA TCGTTGTCGA AGATAATTCC	1620
CGATTCGCAG TCGATATTGT CCTGCAGCCA CGTAATCAGA ATATCCAGCG CTGTTTCCGT	1680
GGTTAATGAT TTCATGTTGT GAATTTCCGG ATTACCAGTC GAAAGTGGGT AAACCTGGCA	1740
GACATCTGGC ACTGGCATCC AGATGAATGA GACTGACACC ATAACGCCGG ATGAGTGTGA	1800
CGACCAGACG ACGGAACGTA ACAGATAACC GGTACCGGTA AAATGAATCC ATTCTGATTC	1860
ACCAAAGTCA CTGGTCTGGT GTAACAGCGA GTACAGCCAG GCGTTGTCT TTTCCGTGAT	1920
ATGTGCGGTA CTGCAGCGTA TCCCGGAAA AGTCGTAAAC GGTGTGGAG TGCAGGTTGA	1980
CTGTTGGTCA GATTCATCCA CCACGCGGAG TGAATAACCG TTTTCAGCGA CCTTGTTAAT	2040
CAGTTCAGCG AGATTAATAC CATCGACGTC AACGACAATG CGCCCATAT TCAGTGCCTG	2100

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TACGTTAACG CTGTGGGCTT CCGGCGTCAG GGAAAGTTTC ATTGTTTCAC CTCCGGGTGC	2160
TTACCCAGGA TAATATTATT TACCGCTCTG TAATTGTCGC GGGTCATCAG GCCGCTCGCC	2220
CTGCGAGCCC GGAGGATATC GATGCTGTTT ATTAAGTGAG AGCGGTACA GGCGCTGAAT	2280
CCCGGCTGGT CGGTACGCAC CAGCGCGTAT TTTTCCACGA GAAAGTTCAC CGCATCACAC	2340
AGTGAAATGC CTGCCTCAAT ATGCTGCTCG ATCACACGTT CATCGGCAAA CGGTGTGTCA	2400
TTCAGTGTGA GGCGGTAGTG CTGGTCCAGC AGTCGGGACA GAAGTATCTG CCAGATTTC	2460
ACAGGAGACG GGCGAGAACT GGCCGCTGC CCGGTAATA CAGGTAATGT TTTCATACTG	2520
AAGATTTTCC TGATATGCAG ATATAAAAT GGGAAAGTGG CGTGGTGAAA ACACCAGGCC	2580
GTAGCAGAAG GCTATTCTGG AGAGTTAATT TTTTATTTCG GCGTCGGAT AAACAGCCAG	2640
ATAAACGTAA CCACAACCTG TGAGGGTATC GGCTTTGCAG GTCAGCCCTT TTGCATACAG	2700
CGTGACGGTA TGCTGATGGC GGGGATTCAG TTCACCGCTG GTGAGCATGA GTTCCAGTTG	2760
TTTCATCAGC AGCGGAAAGG CCTGGTCCAG GTGGTACGCA TCTGCATTGC TGTATAGGCC	2820
TCTGATACCG GCGCGGTCCG CAAGGTAATG CAACCGGTTA CCCTCCTGCA CCAGACGTGC	2880
CCCGAAACAG GGCGTCACGG TGCAGGGCAG CCCCCACCAG GGGCGGTCGT GATTGTCGTC	2940
GGGAAGTGTT GTCCCGGGGA GTGTGTCTGA CACGATAAAA TCCCTACAGA AAATCGGCTA	3000
AGAATGCTCC GGTATTGGCG ATAATTCTGC TCATCAGAAT TCCCACTCAG TTCAGGGTGA	3060
CGCTCATCAG CCGGACATAC GGGCCAAAAC TGTCTTACG GCGTTCAGCA AACACGGCCA	3120
GCACACCGGG AATATCCTGT ACTTCACGAC CGGTATACGC CTCAGCACTG CCGTGCCAGC	3180
GGTACTTACC GGTGCAGAAC GGAAATAGAC GGGATGCAGG ATGCTGTTGG TGAATACGCA	3240
TGGCTTCACC ACGGGTGATG ATTTTCATAA TGGGATACCT CTGAAGACAG AAGATAAAAG	3300
TGAAAACAGG TGTGATGTGG TTGTGACGGT GACGGGTAA AGCAGACCGT GTTCCGCAAA	3360
GGAGAAAACC TGAATGCCAC CAACTATCAG ATGGTCCGGT ACCCGGATAT CCACCAGGGC	3420
CAGTGCCTGT ACCAGACGTT CCGTGATAAG GCGGTCTGCC TTAAGGGGG TGACTTCACC	3480
GGACGGGTGA TTGTGTGCCA GTACCACGGC GGCGGCATTG TGGTACAGG CGCGTTTAAT	3540
CACTTCCCGG GGATGGACTT CCGTGCGGTT GATGGTGCCG GTGAAGAGGG TTTCACCGGC	3600
AATCAGCTGA TTCTGGTTGT TCAGATACAG TACCCGGAAC TCTTCACGCT CCAGTCCCGC	3660
CATCTTCAGA ATCAGCCATT CCGTGCCGC ACGGGTGGAG GTGAAGGCCA CGCCGGGTTC	3720
ATGAAGATGG CCGTCCAGGG TTTTCAGGGC CCGCAGAATG AGACTGCGCT CGCCGGGCGT	3780
CATCTCTCCG GGCAGAAAGG AAAGTTGTTG CATTGTGCTT CTCTCCATTC AGTCGATGAT	3840
GCGCATAATG GCGCTGCATT CCGGATGCTG CAGGGCGTAA TCCCGCAACC GGTAATAATG	3900
GATCGTCATG GCATAAACT CCGTACGACA GGCATGATGA CTGTACGTCA TCAGACAGGC	3960
GGCAATGCCG GCGGCTTCCG GGCTCATTTT AGCGCGGTTA CCGTTCATGG CATTGAACAG	4020

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TACCCAGTTT	TCGTCATCAT	CGTCATCCGG	TTCGGGTGCC	ATAAATGCCC	CGCCGTTGTT	4080
CAGGGTGTAC	AGATTCCAGA	TACCACCGCA	GTAGTCTTCG	CACAGACGGT	CCATCCAGCC	4140
GAAGACACGG	GGCTCCAGGG	TACCCCACTG	TGGAATGAGG	CCAAAGTGCT	GCGGCCAGAA	4200
GCTGATGCGC	TGTTTCATCAG	GGACTATGGT	GSCAACCAGC	TGAGGCTGGT	CATTCCCTGA	4260
TGCAGCGGTT	ACGGAAACAG	AAGGAGTGGT	GGAATTATGC	AAGACGGTTG	TCATGAGATT	4320
ATTCTTATA	AAAAGTAAAT	GAATGGAAGA	AACCCCGGGG	GAAGGGACAG	ACGTGAGTCA	4380
GAAGTGCCT	TTCAGGGAAA	CGGCATCAGC	GCATACTCTC	CAGCAGCGTT	TCAGCCATCA	4440
CCCACAATGC	GCGGTTGAGC	TTAATGTCGG	TGTCGATGCT	GTGAATGGCA	CGGGTATGGA	4500
TACGTTTTCC	TCTGGCACTG	CGACCGGAAA	TTCCGCCTTT	CAGCATATTC	TCCTGAATGG	4560
TCTGATAAGC	ACTCCACAGG	TCCTTACCGT	AATCCTCCCG	GCGTCGTGGT	GTCAGAATGT	4620
CGGCGGTGGT	GACGGGCTGA	TGTTCTGTCAC	CATAACGGTA	AGTCAGTGCC	GCCTGTGCCA	4680
GCGCCTGGCG	TGCCGGTGGC	GGCAGAATCA	GCGACTGCAT	GGCATCACGC	TTTTCTCTAA	4740
TCCGGTCAAA	AACCCCCACC	ACCTCGTAAG	CCCCTTCAAT	AACTTTCTCC	ACCACATTTT	4800
CCCGGTGCGG	AACACGCACT	TCCCCCAGAG	ACTGACCACA	GACGCATCCG	TTCTGGCAGA	4860
CGAACCTGAA	GTAACCCGGC	AGCATCTGGT	AGCTGGAGGT	ACCGTCATGA	GAGTTGAGCA	4920
GAATAATTTT	AGGGACATGT	TCTCCGTTTA	TCTCTCCGGC	CCGCCGCAGA	CGCAGCATGT	4980
GTTTGGTGTA	TTCCCGGCGG	TCCGGGTCAC	GTACGCGGGT	CTGGCAGGCG	AAGAATGGCT	5040
GAAAGCCTTC	CCGCTGCAGG	CTTTCCAGTA	CGGTGATGGT	GGGGATGTAC	GTATAGCGTT	5100
CACTGCGGGA	GGTATGCCGG	TCTTCACCGA	AAATACCCGG	TACATGGTGC	ATCAGTTCTT	5160
CGTGTGTCAG	CGGACGGTCA	CGGCGTATCT	GGTTCGCATA	ACCAAACGA	CTGGCTAGTC	5220
GCATAATTTG	CTCCTTATCG	GTGGTTAAGA	TTTACTGGTG	TAATAAATGA	AAAAGCCACG	5280
TCTCCCGGAG	AAGACGCGGC	CTGACAGATG	AAATGAATGA	CGTTTATTGT	CTGAGAAGCC	5340
CTTAAGTGGC	GAGCTGAGTA	TTAAGCTGTG	TTCCGGCATC	ACCAGCGCAA	CTGACCTTCA	5400
GCATTACGGA	TAACCAGCCG	GGAATATGTT	CCCTGGTCAT	CTTCAGTAAA	CACATTGCGG	5460
TAAGCTGTTA	TGACAGCAAC	CGCCTGCCCG	TATGAGAAAG	ATCCTTCAGC	CAGGACATAC	5520
TCTGTGTGTA	ACCCGGCATA	TCTGGTTTCT	CCTGATAAAT	AGCCTCTGCC	ATACGTTGTG	5580
GCAGAGGCTG	AAGCATGAAA	CTGACTTCAG	GGATCAGTTA	ACATTTTTTC	CGGAAACGGT	5640
AATCAGCAGT	GGATGGTAGT	CCTGGGGATC	GAAAACCGAT	AACGGCAGAC	TGACACGATG	5700
GCCGTTACTT	TCTTCAGTTG	CTTTAATGAT	TTCGGTTGTG	GCGACATTTT	CCACGCACTC	5760
CGTTTCCAGA	AATGCGTCTG	TGTTTCGCGT	GGCATTACTG	TCACCAAAGG	CTTCCGTTTC	5820
CATTTTTCTG	GTCACCAGCG	TCTGACCATA	TTTGTCTTTG	AGTTGCAGAG	TGATGGTGAG	5880
GGGGCCAAAT	CCTTCATCGT	TTCCGCCATT	ATCCAGCCGG	AACTGGTAAG	CACAAATATT	5940

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TCCCGGGAGC CATATCGTAT CTGTATTGCG TATACTGATG TAACGTTGAT CCTGTGCCCC	6000
GAGTGGGGCA GACCACGTTA ACCCCAGAAT GAAGGCGGTA ATCATGCAGG TTTTGAACAG	6060
GTGAATCATG GTATTTACCT CTCTGAGTCA TGACGATTAC ACTGACAAAT CAGGTGATAA	6120
AACGTAAAAG GCGCAGAATA GCCGTTATGC CGGTAACTCC GGGGGTAATG TTTCTTCCAG	6180
TCCGTTAACC ATATTGCCGA GATGGGATGC ATCATATTCC ATGACGGGGC GTTGCCCTGAT	6240
GATACTGACC ACCAGTGGTT TGATTAACAT GTTGGTCGCG GCCCGTTGTT GTATACCGGC	6300
GGCGAAAATG ATC	6313

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGTTGGCCGC TTGCGCAGAT AAAAGCGCGG ATATTCAGAC GCCAGCACCG GCTGCAAATA	60
CGTCTATTTT AGCAACACAA CAACCAGCTA TCCAGCAACC GAATGTCTCC GGTACCGTCT	120
GGATCCGTCA GAAAGTCGCA CTGCCGCCTG ATGCTGTGCT GACCGTGACA CTTTCTGACG	180
CGTCGTTAGC CGATGCACCG TCAAAAGTGT GGCGCAGAAA GCGGTGCGTA CTGAAGGTAA	240
ACAGTCACCA TTCAGCTTTG TTCTGTCATT TAACCCGGCA GATGTTGAGC CGAACGCGCG	300
TATTCTGTTG AGTGCGGCGA TTACCGTGAA TGACAACTG GTATTTATCA CCGATACCGT	360
TCAGCCGGTG ATCAACCAGG GCGGAACTAA AGCCGACCTG ACATTGGTGC CGGTACAGCA	420
AACCGCCGTG CC	432

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GGGCTGATTA CGATTTTATC AATCTGTCTA TAGAACATGA ACTGAATGAA GGAATAGCTG	60
GCAGAGAGAG GTTATGCCGG ACTGGCGGAT AACCGGAACC GGTGGCAGA GGTGGTTACC	120
CGTAAATTGC AGGACAGCTT TTATATGAAC TTTCTGGGA TGCGCTGAAC ACGGCATACA	180
GTGAACACCC AGAGTGGTTT TCCGGGCTTG TCTCCGGGGA TGAGAATTAA AAAGTGGATT	240
ATGCTGCTAT AGCGCGGCGT GATTTCCTGC AGGGATTTC ATTTATAAGA ATACGCCGCT	300

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TCGGGGAATC TCCGGTTCTC CTGAGAGTTA CGATTGTTTT TTTACTCAA TCCACAACAC	360
CTGAACTGGA ACTTGTGTTG CATCCCTGAT TGTTACTCTG CAGGAAACAT CTTTTTTACC	420
ATCAAAGGAT GACTGTTTTT CTTTCTCCCC TCCGTAAAAC ACAACTTCGA TCACATTTCT	480
GACATTTTTT CCAGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTA	540
ATTTACGAC TGACATTCCG CTTACGTAA TTTACACTGA ATACCCACG AGGAGAATAT	600
GCAGCACCGG CAGGATAACT TACTGGCGAG CAGAACGTCG TTGCCTGGTA TGGTTCCGG	660
TCAGTGCACA TTTAAGCTCC GCACTTTCTC TCCGGTGGCA CGCTATTTTT CCCTCCTCCC	720
CTGCCTTTGT ATTCTTTCTG TTTCTGCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG	780
TGCAATTCAG CAGCAACAGC AACAGTTGCT GGATGAAAAC CAGCGCCAGC GTGATGCGCT	840
GAAGCGCAGT GCGCCGCTGA CTGTCATACC GTCTCCGGAA ATGTCTGCCG GTACTGAAGG	900
TCCCTGCTTT ACGGTGTCAC GCATTGTTGT CCGTGGGGCC ACCCGACTGA CGTCTGCAGA	960
AACCGACAGA CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GGCTGACCGC	1020
GGTCACGGAT GCCGTGACGG ACAGCTATAT ACGCCGGGGA TATATCACCA GCCGGGCCTT	1080
TCTGACAGAG CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT	1140
GCAGCAAATC CGGGCGGAAG GCGCTGACCT TCCTGCCCCG ACCCTGAAGA TGGTTTTCCC	1200
GGGAATGGAG GGAAGGTTT TGAACCTGCG GGATATTGAG CAGGGGATGG AGCAGATTAA	1260
TCGTCTGCGT ACGGAGCCGG TACAGATTGA AATATCGCCC GGTGACCGTG AGGGATGGTC	1320
GGTGGTGACA CTGACGGCAT TGCCGGAATG GCCTGTCACA GGGAGTGTGG GCATCGACAA	1380
CAGCGGGCAG AAGAATACCG GTACGGGGCA GTTAAATGGT GTCCTTTCCT TTAATAATCC	1440
TCTGGGGCTG GCTGACAACT GGTGTCAG CGGGGGACGG AGCAGTGAAT TTTCCGTGTC	1500
ACATGATGCG AGGAATTTTG CCGCCGGTGT CAGTCTGCCG TATGGCTATA CCCTGGTGGA	1560
TTACACGTAT TCATGGAGTG ACTATCTCAG CACCATTGAT AACCAGGGCT GGCAGTGGCG	1620
TTCCACGGGA GACCTGCAGA CTCACCGGCT GGGACTGTCG CATGTCCTGT TCCGTAACGG	1680
GGACATGAAG ACAGCACTGA CCGGAGCTGC AGCACCGCAT TATTCACAAT TATCTGGATG	1740
ATGTTCTGCT TCAGGGCAGC AGCCGTAAAC TCACTTCATT TTCTGTCGGG CTGAATCACA	1800
CACACAAGTT TCTGGGGGGT GTCGGAACAC TGAATCCGGT ATTCACACGG GGGATGCCCT	1860
GGTTCGGCGC AGAAAGCGAC CACGGGAAAA GGGGAGACCT GCCCGTAAAT CAGTTCCGGA	1920
AATGGTCGGT GAGTGCCAGT TTTCAGCGCC CCGTCACGGA CAGGGTGTGG TGGCTGACCA	1980
GCGCTTATGC CCACTGGTCA CCGSACCGTC TTCATGGTGT GGAACAACCTG AGCCTCGGGG	2040
GCGAGAGTTC AGTGCGTGSC TTTAAGGAGC AGTATATCTC CGGTAATAAC GGTGGTTATC	2100
TGCGAAATGA GCTGTCCTGG TCTCTGTTCT CCCTGCCATA TGTGGGAACT GTCCGTGCAG	2160
TGACTGCACT GGACGGTGGC TGGCTGCACT CTGACAGAGA TGACCCGTAC TCGTCCGGCA	2220

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CGCTGTGGGG TGCTGCTGCC GGGCTCAGCA CCACCAGTGG CCATGTTTCC GGTTCGTTCA	2280
CTGCCGGACT GCCTCTTGTT TACCCGGACT GGCTTGCCCC TGACCATCTC ACGGTTTACT	2340
GGCGCGTTGC CGTCGCGTTT TAAGGGATTA TTACCATGCA TCAGCCTCCC GTTCGCTTCA	2400
CTTACCGCCT GCTGAGTTAC CTTATCAGTA CGATTATCGC CGGGCAGCCG TTGTTACCGG	2460
CTGTGGGGGC CGTCATCACC CCACAAAACG GGGCCGGAAT GGATAAAGCG GCAAATGGTG	2520
TGCCGGTCGT GAACATTGCC ACGCCGAACG GGGCCGGGAT TTCGCATAAC CGGTTTACGG	2580
ATTACAACGT CGGGAAGGAA GGGCTGATTC TCAATAATGC CACCGGTAAG CTTAATCCGA	2640
CGCAGCTTGG TGGACTGATA CAGAATAACC CGAACCTGAA AGCGGGCGGG GAAGCGAAGG	2700
GTATCATCAA CGAAGTGACC GCGGTAACC GTTCACTGCT GCAGGGCTAT ACGGAAGTGG	2760
CCGGCAAAGC GGCGAATGTG ATGGTTGCCA ACCCGTATGG TATCACCCTGT GACGGCTGTG	2820
GTTTTATCAA CACGCCGCAC GCGACGCTCA CCACAGGCAG ACCTGTGATG AATGCCGACG	2880
GCAGCCTGCA GCGGCTGGAG GTGACTGAAG GCAGTATCAC CATCAATGGC GCGGGCCTGG	2940
ACGGCACCCG GAGCGATGCC GTATCCATTA TTGCCCGTGC AACGGAAGTG AATGCCGCGC	3000
TTCATGCGAA GGATTTAACT GTCCTGTCAG GCGCTAACCG GATAACTGCA GATGGTCGCG	3060
TCAGTGCCCT GAAGGGCGAA GGTGATGTGC CGAAAGTTGC CGTTGATACC GGCGCGCTCG	3120
GTGGAATGTA CGCCAGGCGT ATTCATCTGA CCTCCACTGA AAGTGGTGTC GGGGTTAATC	3180
TTGGTAACCT TTATGCCCGC GATGGCGATA TCACCCTGGA TGCCAGCGGC AGACTGACTG	3240
TCAACAACAG TCTCGCCACG GGGGCCGTCA CTGCAAAGG TCAGGGCGTC ACCTTAACCG	3300
GCGACCATAA AGCGGGAGGT AACCTGAGCG TCACAGCCGG AGCGATATCG TTCTCAGCAA	3360
TGGAACGCTT AACAGCGACA AGGACCTCAG CCTNGACCGC CGGCGGCAGA AATTCCTCA	3420
ACAGAATGAA AAAGTACTG CCGGCCGGGA TGTAACGCTT GCCGCGAAAA AACATCACAC	3480
AGGGTTACCG GCCA	3494

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GNCCCAAGCT TAGGTTGCGG GCCGCAGTAC TGGATCTATT GCCAGCTTCA CCGCCAGACT	60
GTCAGTCAGT ACATCACCGT ATTTCTGCTG GCAGGTTGCC GGGCGGCTGC ACAGTCACTG	120
ATCAGTTGCT TCTGCTGTGC CGTACTCAAC TCTTCGTACT TTTTGATAAT ACCGCCGCAG	180
TCACCGCCTT TCGCCTGACA GGAATTCATT TCAGCAGAGC AGGCATCTAT CTGCTTATTG	240

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CTCAGGTAGT TATTCTCAAC AACAAACCACA GGGGATTAGA AGCCTTTTATAG CCTGAAATAT	300
TTTGCGAGAG CACATCCAAT ACCAATAAAT GAGCCAATCA CACATCCGAT AAATAAAACA	360
TGCCGAATCT CTTTCAAACCT AATATTTTAA TTACCTGTTA TCAACCACTC CACCAAAGAA	420
AAAAACACAT CAATACATAG GAATGACACC ACTATAGAAA GAAATGCGAT TATAAAAATA	480
ATAACAATT CTGATAAGTG CTGAGAATTG CCGCTCATTT TTTCACCTCC GGAATGTAAG	540
ACTCAATCTT TTTACCTTCA TACTCAGAAG CAAAAGAAGC CGACACATCC CCAGCTATAC	600
CAGGAATCCT ACTGGGTGTC ATTTCTTTTG ATAGCCCCAA TTCTCCTTTA ATATCGGTAT	660
ATTTTTGAAG TGTTGGATTA AATTTGGGGT CCCAGCCGTC TTTTAACCAG TTAGCACCAC	720
TATTAATGCC CCATGAAAGG CCTTTACCAA TGCCATATCC AATAGCAGAA CCAGCACCAT	780
TGATCAACGC ACCAGATGTT GGGGCTTTTC CTTCGAGCCA GTTTCCTAAT GCTCCTCCAG	840
TTGCATTCCA GCCAACTGTG CCTACAACCTC CATTCCCTGC ACTAATCACA TTAACCCAAC	900
CACCGATAAT CGCTGTTGTA GGATCTATAG TTCCATCCGT CAGATAGCTA ACACCTGCAT	960
TAGCTCCTGC CCCTAATCCC CACATGGCCT GAGCACCGCC AGTAAGAGAG CTACACTACC	1020
AGTGGCCAAC GCTCCGGCAT ACGCTTTATT GACTGCTTCT CCTCGCTTAC AGGCTTCACC	1080
GCCTGGGGCA TCGTTACAGG AAAGTACATC TGCGCCATGC GTCTGAGCAG CTTTGCTCTG	1140
CTCGGACTCT GTGCCACCAA CCAGGTTATT CTCAGCAATG TTCTTCCCGA CACCAGCCCC	1200
AGCAGCCGCG CCAGCCACAT CGCCACTGGC AATGCCGCCA GCCATACCCG CTGACAGCGT	1260
TGCCAGCGTG CTTACGGTTT GCTTCTGATC TTCTGTCAGT TTCGACGGAT CTACGTCCGG	1320
ATAGAGGCTT TTCGCAATGG CTGACGAGAT CACTTCACCA GTACCCGCAC CAATTGCGCC	1380
TGCTGCCGCA CTGTTGCCCT GAAGGGCTGC TGTCACACCA CCGAGAATGG CATGGGCAAT	1440
GGCTTTTGCC GCTGTATTGT CATCAATACC CGCGTGATGA CCGATGATGT TCGCCAGCTC	1500
CGGCGCCGAA GCTCCGGCCA GAGCACCTGC TAAATTACCC CCCGCCAGCC CCTGAAGTGC	1560
AGCCGTTGCA GCCTGGATAC CGCGCTGCAT ATCGCTGCCG GTACCATACT TTTCTGTTC	1620
CTTTTTGTAT TCCGGCGTAT CACGCAGTTT TGCCAGATAT GCCTGCCGCT GTTCTTCCGT	1680
CGCATCCGCC GGAACAGGCC CATATTTATC CTGCGCAGCT TCAACGCATT CAGTTCCCCC	1740
TGCGTCCGCG CAATATCCGC CACCTGACTG CCTATGTCAC TGATAAGCCC CACTGTCTGC	1800
AGACGCCTCT GCTCCTTCTC CTTGTCAAAT ATCGGGCTGA TACTGTCAAT AGCGTGCGCA	1860
GGGTCACGGC TCAGGTTTCG CAGATTCTGC TTCTGATTGC CCCTGTCCCG GATGGTGATA	1920
GTGCCTTCTG CCACTGCGGC CTGAGTCGTT CCTTCCGCAT GTCCGCTGTG ACCTCCGGCG	1980
GATATCATGC CACCCGGCAT GTTACCCTGA AATTTATCCC CGAAGCTGCC ACCACCGCTC	2040
AGACTGATTC CACTGTGACT GACTTTATAA TCCGCTTCGT TGTGAAGGTC ACTGAACCCC	2100
AGCGTTCCGG TATCCAGGTG GTTTTTATCC GGTGTGGCAG TGGAGGCAAT CACCGCACCA	2160

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TCCAGTTGGG	TATGTTTACC	CACTGTGATG	TCGAAGCCGC	CGTCACCGGC	AAACATTCCG	2220
STTTGTTTAC	CAACGGAGTC	AAAGGCGCTC	TTCATCTTAT	CCCGGGAGGC	AGCGATGTAA	2280
CCTGAGCCGG	TCATGGAGCC	AAAGGTAAAA	CTGCCGCCGG	CAGCCACGCT	GGTCTGTTTA	2340
CTGTCTGACT	TACTGGTGTC	CTGCTGGCTG	CTTATCAGCA	GGTCGTGGCC	CACATCGGCG	2400
ATAATCCTGT	TGCCGTTGAC	CTGAGCACCG	TTCAGTACCG	TATCCCGACC	ACTGTTGATG	2460
GTGACGGTTT	TACCGCTGTC	TGTTGTGGTT	TCAGTCCACT	CAGTACCGTT	ACCTTTCTCG	2520
CTGCCCTTTT	CCGCATTAAAC	GCTGGCAAAG	ACACTGATAC	CGGCACCTTT	ACCTGCACCG	2580
ATACTGACAC	CCACGCCACC	GCCACTGCTG	CTGTTCCCTGC	CCGTTGTTTT	TTGTGTGTTT	2640
GCCGCGCCAC	TCAACAGAAC	ATCATTCGCA	GCATCCAGGT	TTGTGTTACC	ACCGGCCTTA	2700
AGCTGGCTTC	CGGCAATCAC	AATATCTCCG	CGGTTATCGC	CCCTGTTTTT	ACCGGTTGCG	2760
ACAACAGACA	GATTATTCCC	GGCATTGAGC	GTAAGTCCGG	ATACTGTGTC	ACTTTCAGAA	2820
TGTTGTTGTG	ATTTTCGATTT	CTGGGTGGTG	AGCGACAGGC	TGACTCCCGT	CGCATTCCGGG	2880
TCACCGGTTG	CGGAGGCCAT	TGCCGCAGCC	TGTCCGGCCT	GCACACCAGA	CAGCGCTGTC	2940
TTTGTAGCCT	GCAGGGTTTT	CAGACGGCTG	TCAGTGTCTC	CCTTCGTCTC	CTGTGCACTG	3000
GTGACCGCAT	TATTGATGGC	ACTGCCCACT	GTGCCCGAAA	GGGCAACCGT	CAGCCCGCTT	3060
TTCTTCTGCT	CAAATTTTTT	GTCCACAGTA	CGACGGTCAT	GCCCCGGGTC	AACCACCACA	3120
CTGTCACCGG	TAATGCTGAT	ATCCCGGTTT	GCAATCACAT	CCGAACCGCT	GATATGAGCC	3180
TGTTTGCCCG	CGGTAATACT	GACATTACCG	GCAGTGGAGC	CGATGGTACT	GGCACTCTGA	3240
CTCTGCGTTG	TCCCGGCCTC	GCGGCGGTCG	TGCGTTGTCT	TACTGCTGCC	AATGGTGAAG	3300
CCAATACCGC	CGGTACCCAT	CAGACCGGAT	TTCTTCGTTT	CCTTAAAGCG	CCAGGACGTA	3360
TCTGTACTGG	TGGCAGCAAG	AACATCAACA	TGGTTACCCG	CCGCCAGTGA	CACATCCCGG	3420
TCAGCCACCA	CATCCGAACC	CTCTACCGTC	AGGTTATCAC	CGGCGTTAAC	GGTCACGCGG	3480
TTCCCCGACA	GCAGGGAACC	TGYTTCACGG	GAGGCACTGT	CCTCACTGAT	GGTGTGGGTG	3540
GTTTTCTTAC	TGAGAAAACC	TCCGCTTTTT	TTCTTCGTTT	CCAGATAGTG	ATAGTCACTT	3600
TCTGTCGCCG	TGGTCAGGGC	AACATCACGA	CCGGCATTCA	CGCTGATATT	GCCGGTTGCG	3660
GTAACGGATG	ACGCAACAGC	GGTGATATCC	CGTCTGCGG	TGACGGTGGT	GTCACCACCK	3720
CTGGCGATTT	CCGTTCCCTG	CTGACGGACT	GTCTCGTTAA	TCTCTTTCTT	TTTCTTCGAC	3780
GTATAGCTGT	CGCCTGCGCC	GGCAGACTCT	GCCACCAGGT	TCACATCACG	TCCGCCCCGG	3840
ATGACCACGT	TATTTTCCGC	AGCCATACCG	GCAGCCTGAC	TGGCAATATC	ACGACCGGCA	3900
ACAAGGAGGA	GGTTATCGCC	CGCCGTCACC	GTGGACACAG	CTGCGTGGCT	TTCATGACTT	3960
TCTGACCTGC	CGTTGCGACT	GTTTTTGCTT	TCCCTGACTG	CATTCAGACT	CAGGTGCTTA	4020
CCTGCAGAAA	GCAGGGCGCT	GTGCCCGGCA	GAAACAGAGG	ATGCTGTGAC	ATCCAGATTA	4080

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TGGCCTGCAG	CCATCGCCAG	GTTACCGCCG	GCGCTGATGC	TGCTGCCCTG	TGAGGTGGTG	4140
GATGATGAAC	TGTTGTCATC	AGTGTGCCAG	AAACCGGACT	GACTTTTGCT	CCCGCTTATC	4200
AGGTTTACGG	CAATGTTGAT	GTCATTACCC	GCAGACATTC	CAAGGTCTCC	ACCGGACGAG	4260
ACCGTTGCCC	CGGTAATATC	AATGTTTTTC	CCTGCATCCA	GTGAAAGTGA	ATCAGTGCCT	4320
TTAATGGTCG	CAACCGGACC	GGTGTCCGTA	CCGCTGAGAT	GCACACCACC	ATATCGGCTG	4380
TCACTGCCCG	CATTCCATTG	CTGACGCCGG	GTGATATTGC	TGATGTTGCC	ACTCACGCTT	4440
TCCAGTTGTA	CGGTTTTACC	GCTGATGACT	GAGCTGATAT	TGCTGATATC	CCCGATGGCG	4500
CTCAGGTCCA	GGCTACCGCC	CGCGCTTATC	AGCCCTGCAT	TCAGGTTGTC	GATATAGCCG	4560
GTACTGTGGA	GCGAAAGGTC	GTTCTGTGCG	TTGATGCTGC	CGCCGCTGTT	GGTGATATTG	4620
CCGTCCGCAA	GCTGCACGTT	GTTCCCGCTG	ATAACGCTGC	CGTTATGCAG	GGTGATATCT	4680
TCCGGCGACA	GATACAGTTT	CGGGACCATG	ACTGTCTGTC	CGTTGATGGT	GACTGACTCC	4740
CACCACAGCA	TGCTGCCGTC	AAGCTGAGCA	ATCTGTTTCA	CTGTCAGCGC	CACACCAAAC	4800
TCTAATCCCA	GTCTTTTCTG	TTGTCTGGCC	GCGTTATCCA	TCAGATACCG	CATCTGTTCC	4860
GTGTCTGAAC	CCAGTCCGTT	GAGATAACGT	GAACCCGTCC	GGCTCAGCAC	CGCGTTACTG	4920
ACATACCGGG	TATCAAAGAC	CGCATCCCCC	AGGAAACGAT	AATCTTTTTT	CGGTTTCAGC	4980
CCGAGGCGGT	CAAGAAAATA	CGATGAGCCC	AGAAACTGTT	TTTCATCGGT	ATACGACGGA	5040
GCCGTTTCAC	GTGGCGCCTG	ACCCGGTTTC	GCTCCAAGAA	GCTCATAACG	TCCGGCAAAC	5100
AAATGGCTGT	CCACCTGTCC	GAGACCATCC	AGTTTCGGGT	TCACCGTAAT	CAGATACGGA	5160
CTGTCCGGGT	CCGTGGACGG	AACCAGGTAT	CCATTGTTGC	CGGAAGGCAG	TGGCCAGTCA	5220
TCACTGATAC	CGGTCTGACC	GGTCAGTGGC	GAACCTCCGG	CAATATTTTT	CAGGGCACCT	5280
GCCAGTTCAT	CGTGCCATTG	CGGAGAGCCA	ACCACCACCG	GCTCATACTG	CTGCAGCGCT	5340
GTCTGTGTCA	GACTGTCTCC	GCCGGTCTGC	TGACTTAACG	TATTCAGTAC	AGGTGCAGAG	5400
ACCACCGGAC	TGACACTACC	TGCATGTGCA	GTGGTTGTTC	CGTTATTGAT	ACTGCTGGTA	5460
AAACGGGTCT	TAACATCCCC	GCCCGCCTGA	ATAACGGAAT	AATACGTCTT	ACCGGGCGTG	5520
TAATCTTTTT	CCCGGCCATC	CAGTGAAAAT	CTGATGGTAT	TGTTTTCAAA	TTCCGGTGAC	5580
AGCAGGGGCA	GTTTATCCAG	AGAGCCTGTT	GCATAGCTAC	CGTAAAACGT	TTTCGGGTG	5640
TAGCGGTATA	CCAGATATTC	ATTCTCTGTC	CCCGTCTGCC	AGCTCTGATT	GCTTAACTCT	5700
CTGCCCCGAG	GTGCGATATC	CCCATTCGCC	AGGATAAATG	ACGCCCCGTT	TTCCAGTCGT	5760
TCAGCCTCAG	CAGAAAGATT	ACGCCCTGAC	GCAATGCGGC	CTGCCGGATT	ATCAGCACCG	5820
GTTACTGTTG	TGATGTTCTG	GCTGCTGAGA	AAGCGCTGTG	TGGCACTGTC	AGCAAACGGA	5880
GCGTAATAAT	AAAGCGTATC	CATTGTGATA	TTGCATGCCC	CGTGCCCGTT	GCAGGGCGTA	5940
CCGTGCTGAT	TTTCAACTTC	ACGGGTGAAA	TAGCCATAGC	TGCCGTCAGG	AAGAAGGGAA	6000

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AGGGGAATAT	CAACCAGAGC	ATTTCCCAT	CCCTGAATGG	ATGAGGGGTT	AGTCCGGGTT	6060	
GTTGTTGTGG	CAGAAAATCC	CTCCCGCTGG	TTCAGAAAGAT	GCCCGGTTCT	TACAACAATA	6120	
TCGCCCTGAT	GCGTCTCAAT	ATTCCCGGAA	GTATTGATAA	TCTCTGTGTT	TGCACCGCCG	6180	
GAAGCATCCT	TCTGTACCCA	CAGACTGTTG	CCGSCCAGGA	TATCACCATG	CTGGTTATGC	6240	
AGACGGTCTG	TAAACAGCTT	CAGGTTATTC	CCCGCATAAA	TCAGCGCACT	GTTCAGCAGG	6300	
GTACCGGCCA	CATTCAATTGT	CAGACTGCCT	GCCGTGCCGG	TAAAACCACT	GATGGTGATA	6360	
TCACTCCGGC	TGTTTCAGACT	CACATCGCCA	CCGGCCTGAA	GTGAACCCGG	TGCGTTAAGG	6420	
AAAAGACGCT	GTGCGCTGAA	AACACTGTTG	CCTTTACCGG	CAGTCAGCGT	TCCATTGTTG	6480	
GTGAATGCCT	CTCCGGCACC	GAGCACCATG	GCATCACCTT	GCATGACACC	GCCGTTGGTG	6540	
ATGGCATT	TTT GCGACGTGAC	GGAAAGGGTT	TTCCCTGCGG	CCAGGGTACC	GTAATTCGTG	6600	
AGGGCAGCAA	TCAGTTTCAG	TGTGACATCA	CCGGTGGCCA	CCACCTGCCC	CTGACCACTG	6660	
AAGTCCTGAG	CGTCAAGCAG	CAGGTTGCCT	GCACTGTACA	GCCGCCCTGT	ACCATTTTGC	6720	
AGCAGTGAAC	TGCCCTTGAC	GCCAAGCCCG	GAGGTTCCCA	GCAGGGTACC	GCTGTTGCTG	6780	
AATGTGTGGT	AATTCACCAG	CAGGTCCGCA	CCCTGAAGCG	TACCGGTATT	ATTCAGCGTG	6840	
GTTCTTTTAA	CGTCGGCACT	GCCGGTGGCA	AGTACGCGTC	CGCCGTTGAC	AGTATTCACC	6900	
ACATCCAGCA	GCAGGGTGGC	AGCCTGTACC	AGTCCGCTGC	CGGTGTTCGC	CAGCACCTGC	6960	
GCCGTCAGCG	TGAGGTTACT	GCCGGAGAGG	ATTTTGCCGT	CGTTCTGCAG	ACGGTCAGTG	7020	
GCGTTCAGGG	AAACCCCGCC	ACCACCCTGT	ATCGTGCCCT	GGTTACTCAG	GGTCGCAGTA	7080	
CTGACATTCA	GTGCATTCCG	GCTCATCAGA	ACACCACCGG	AACGGTTGTT	CACGCCACCG	7140	
GAGGCGGCCA	GCGTCAGCGT	TTCGCCCTGC	AGATGCCCGC	CGTTTGTGAG	TTGTCTGCC	7200	
GTGATGGTGG	TGGCATTTCC	CTGTAATTGC	CCGTGTTT	TGACACTGTC	TGCCTTCAGC	7260	
GTCAGCACAC	CTGCACTGAG	CAGTTTTCCG	CTCGCGTGAT	TGTGCAGCGT	CTGATTCACC	7320	
GTGAGCGTGA	GAGCATCCAC	ACCGGTGATG	TCACCCGCAC	TGGTCAGTGA	GTTGCGCTTC	7380	
AGGGTCAGAT	TTTTTGCAAT	CCATTGTCCG	CTGTTGCTTA	AATTCAGTGC	ACTGAGCGCC	7440	
ATTTACCGT	TCGAGGTGAC	TTTGCTGCCT	GCTGTGCTGA	CGAGCTCACC	CGTCAGACGT	7500	
GCAGTCAGGC	TGTCAGCCGC	CTGGATCGCC	CCGCTGTTT	CCAGACTGTC	TGCGGTGATC	7560	
AGCACCCGTT	TGCCCTGCCA	GTGTCCGGAA	CTGGTAATAC	TGCCTGCGGT	GATTGTCAGA	7620	
TCGCCGCTGG	TCAGCAATGA	ACCTCCGTTA	TTCATCAGCG	CAGGTTGAGG	GSATGCCATA	7680	
CGGGCGGCAA	GCGTCAGCGC	GGCTATCCCG	GTGAGCGTGC	CACTGTTGGT	GACACTGTTT	7740	
TGGCGAATCG	TGACATGGTT	ACCCTGGACA	GTGCCGCTGT	TATCCAGTGA	GTTTCCATCA	7800	
AGGGAGAGCG	TGCCGGCCGA	AAGCAGACTG	CCCCGGTTGT	CCATGGTGGC	TGCTTTCAGC	7860	
GTGGTGTAC	CCTGGCTCAT	GATATCGCCG	GTA	CTGCTGCTCA	ACTGACCGGT	TGCCGAAGCA	7920

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GTAAGGTTAC CGGTTGCCAG CACCGAACCA CTGTTGCCCC AGTTGTCCCG CYTGACGGT	7980
GAGATTCTGT CCCTGCGTGG TCCTGCGGTA TGCAGTGTTT TACCCCGGAG GGTGAGGTGG	8040
CCCGCCGTCA GCCAGCGCCC GTTACTACCC TGTGAGAGGG TGTCGCCAGC AAGGCCAGT	8100
GCACCGGGCG CCGTCAACAG GCCGTACCA TCCAGCGTGG TCGCCCTGAC GCTCAGCGTG	8160
TCAGCGATGA TTTTCCCGG ATTCCTGAGG GAGACAGCAT TTAACATTAA ACCATTATCA	8220
CCGGTGATAA GCCCGCTGTT GCGGATGTCC GGTATATCCA GCGTCAGGTC TGCAGCACTG	8280
TACAGCGTGC CGTTCTGCTG ATTATCAAGC CTCTGTGTGT TAACGGTAAG TGAGGCCTCC	8340
CCCTGCAACA GACCGCTGTT GGTGAGGGTC TGTGACTGTG TATTCAGGGC GGAACCAACA	8400
AGTACGCCGC TGCTGGTCAG TTCCGSCGCA CTGAGGCTGA GCGACGGGGC ACTGCTTTTC	8460
CCGCTGTGGG TGAGCTTTTC ACTGSCGTC ACCACCATGG TCTGTTGTGC TGCCTGCGTA	8520
CCTGCAAGAC GTGCATCTCT GGCCTTGATG CTGAGATTTT TACCGCTCTG AAGCTGTGCG	8580
CCCGCTGCGG TACTCAGTTT GTCTSCCTGA ACCCGGAGGG TGTCACCGGC ACTGTTTTCC	8640
CCGTCCAGCG CCACTGTTGT CACATTCAGC GTCATCGCAG CATCGCTGTG GGTGACCGAT	8700
TTTTTACCGG AGCTCAGCGC CTGCGCACTG ACCGTCAGCC CTTTGCCGCC GGACAGCACA	8760
CCGTTCTGTG TCACATCCTG CGCCTTCAGC ACCAGTACAT CATCGCTCAC CAGCGAACCT	8820
GTAAGGTTAC GTTTCCCACT GGCCGTGATA TCCACTTTGC CCTTCGCGCC AGTGCGGCCG	8880
CTCTGGGTAA AGTCGCGGGT ATTCACGGTC AGGGGACCGC CACTGAGCAG GGAGCCACTG	8940
TTGCTGAGCG TTGTACTGCC GAGCGTCAGG GAAGCCCCCT GAACAGCACC ACTGTTATTC	9000
AGCGTGCCGG CATCGAGTCC CGCATGACCT TTCGCCAGCA ATATTCCGTC CTGTGTCAGC	9060
GTGGTGGCGC TGGCCGTGAG ATTCTGCCCC GCGGTTATCT GTCCCTGTGT TGTCAGCGTG	9120
TCAGTGGCGA CAGTCACGAT ATCGCGGGCC GCGTTAATCT GGCTGGCGGT ATCCTGTGTG	9180
ATGTTTTTTCG CGGCAAGCGT TACATCCCGG CCGGCAGTCA GTTTTTCATT CTGTTGAGTG	9240
ATTCTGCCGC CGGCGGTCAG GCTGAGGTCC TTGTCGCTGT TAAGCGTTCC ATTGCTGAGA	9300
ACGATAATCG CTCCGGGCT	9319

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 551 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ATGAGGCGAT TAAAGCAACA TTGGGCAGTG ATAATGCCCC CACCCAGCCA CCTAACGCAG	60
CGAAGAGTAA TACATCGCCC ATGCCTAATG CTTCTTTACG CAGAACTATT CCGGCTATCC	120

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AGCGSAGGGA GTAAAAAGTG ATAAATCCCA CCAGTACGCC GGTAACTGCG TCTTG TAGCG	180
TTAACGGACT CTGTTGCGCC CATGCTGCAA TCAGCCCGGT CCACAATACG CCTGAGTAA	240
AAACATCGGG CAGCCATTGG TTGTCGAGST CAATGACGCT CGGCGCAATC AGCCAGGCGG	300
ATAATATCAT CACCGCCAGC CCCCATCCAC TTTCTGGCCA CACCAGACTC GCCAGCAAAA	360
AAGTGAGTGC TGTCAATAAC TCAACCAGCG GATAACGTTG CTGATTTTCG CCTGACAGTC	420
GCGGCAGCCC TTTGAGCATC AACCATGAGA GCAGCGGAAT ATTGTACGA ACGCGGATGG	480
TCTGCTGGCA ATGCGGGACA GTTGC GAACC GGGTTAGCCA AGGGCTTTAT TTTTGGACT	540
GCGGCACTCG G	551

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CATTTACCAA ACCCCGTTTC AATATCTTAT CTATTGCCCA TCTCATATTA AATATAACCG	60
ATAATTTGGT GGATACTAAT AGTAATTACC TTGTTATTGA AAATATAATT ATTGTTATTT	120
TTAGCCTCAT TAATTAAATT GAAAAATCCT CTCTAATTTT TGTCAGATTA GGGCTGTAGA	180
AAGGATCGAG TTCAAGATGT TTACCCCATT TGCTTTTCAT AAAGTCCACT TCCCTGGCAA	240
ATCTGGCTAG TTTCTCCGGT GAATCTTCGG CTCCTCGACT AATCGATTCA TAGTGGTAAA	300
GCTCGGCATA AGGTGTCCAG AGATTACGAT ACCCCGCTTC GNGTACTTTC AGACAGAAGT	360
CCACATCATT AAAAGCAACA TGCAGATTCT CTTCATCCAA CCCGGCAACT TCCTCATAAA	420
TATCTTTGCG AATAAGCAGG CAAGCCGCCG TGACGGCCGA GAGAGTTTGT GTCAACAACA	480
AACGGCTGAA ATAGCCCGGA TGGTGGCGAG GATAATGTTT ATGGGAGTGT CCAGCTACAC	540
CACCAATACC GAGAATCACT CCGCCATGTT GTAAAAGTAT CATTACTGTN ATAGG	595

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TGGCAGTTGA ACAGATTTTC ACATCAGCAA CAGATTAGCG AACGGGACTT GGCATTAGCC	60
GAGCGTTTTA GTGAANGTTT AGCTCTAACA CGTCTATTAG AAGAGCGCAC GCAGNATTAT	120

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CACTGAACTA GAGATTGAAA AACAAATTGCT TACCACCAAG TTGTCTGGCG TAGAGCAGCA	180
GTTAAGGGCT GAGCAAGAGT CGCTTCAGCA GGCCAGTCT GCATTGCTCT CAGCAGCAAA	240
AGAAAAGCAA CATCAACTTG ATGAGTTGGA ATCGGTGCTC AATGAGCGGT ACAGTGAGAT	300
TGCAACCTTA ACCCGTTGSC TGGAAGAACG TGATCAGGCA CTCCTTAGTG CAGCAAGTGA	360
ACAACAACAG ACCAATGANA CCATATAGAG CTCAGCCAG	399

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ATACTCTGCT TGTGAGCAG CCATTACGTC GCTTTGTGAC GCAATATTAG ACTCGTGCAC	60
TGCTATTAGT TGAGTCAGTT CATCACATTG TTTAGAAGCC GCAGCCAAAG CAAGAGTTTG	120
CTCATCTATG CTTTGCTGCA ATGTTTGTTG CACAAGTTGC CCTTCTTCCA GCTGTTGCTG	180
TAGATTTGCA CTTACCTTTT TCAGTGCATC ATATTCCAAG CCTAACGTAT CGTGCTGTGC	240
TTCCAGTAAT CCATAAGCAT GCTGCAACTG GTTTTTAGTT TGCTGCTCAC CGTCAAGCTG	300
TTGCTGCAAT GCATTAGCCT GCTGTTGCAA CAAGTTCACC ATATTGTCTC GCTCGGCCAG	360
TGTACGAACC TGTGTATCCT GGATATGTAG CGCTTGTTCC AACTGAAGCT GTAATTCGGT	420
AATTTGCCGC GAATGTTTCG TCAATGCTCT GTTGCTCTTG CTGAGCGCGA GAGTAAGGTG	480
AGATGCACGC TGTGTTTCTT CACTCAATTG TAACGTCAGG GTATTGACCT GTTGCTCCAG	540
TTGATGGCGA GCTTGCTCCT GGCTCGTGAT GCGACTCTGT TGCTGCTCTA GTTGATGCAG	600
AGCTGTATGC AACTCATCGT TGGCTTGAT TCGCTCCTGC GACCATACAC TCAAGTTTGT	660
TTGGGCCTCA TTGAGCTGTT CTTGCAATAA TGCCACCTCA GATGTCAGCG AATTGATATG	720
TTGCTGGGCA AAAGATAGCT CATCAGATTG CACTTGAGCA TGTGCAAGCT GCTTTTCCAT	780
TTCTAATATG CTGTTATGTT GTGCAGTAAT GCGCTCGGCA AGACGCCCCC TTTCCAATGC	840
CTGCTGTTCT ACCAATAGCT GCCGTTTCAGC CTGAATGTCA TCTTGTTGTG TAGACAAGT	900
ACGTTTTTAAC TGGGAATTCT CCCAACTCTC GCTACAAGAT TTNCCCAAAC GACAAAAGAT	960
GTCTTGGAAT TGTNTGGGTT ACACGAGCAT TTTCTGAGGA TTTTATACCA ATN	1013

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GATATCCACA TCGAGACGTT TGAAAAGAGT CTGGTGATCC GTTTTCGTGT TGACGGCACA	60
TTACATGAAA TGCTGCGTCC GGGGCGCAAA CTGGCTCGC TGCTGGTGTC GCGTATCAAG	120
GTGATGGCGC GGCTGGACAT TGCCGAAAAG CGCTGCGC AGSATGGACG TATTGCGCTG	180
TTGCTGGGCG GCCGGGCGAT TGACGTGCGT GTATCAACCA TGCTTCCGC CTGGGGGGAA	240
CGGGTGGTGC TCGACTGCT GGACAAAAC CAGGCTCGCC TGACGCTGGA GCGTCTGGGT	300
TTAAGTCTCG AACTGACTGC GCAGTTGCGC CACTGTTACA CAAACCGCAC GGCATTTTTT	360
TGGTGACGGG GCCGACCGGT TCCGGCAAAA GCACACGCT GTACGCTGGA TTGCAGGAGC	420
TGAACAACCA CTCGCGTAAC ATTCTACGG TTGAAGACCC TATCGAATAC ATGATTGAAG	480
GGATCGGTCA GACGCAGGTT AACACCCGCG TCGGCATGAC ATTCGCCCCT GGCCTGCGCG	540
CAATTTTGCG TCAGGACCCG GATGTGGTGA TGGTCSGTGA AATCCGCGAT ACCGAAACCG	600
CAGAAATCGC TGTTCAAGCT TCAACTGGAC CGGACACCTG GGNACTTCN ACGCTGGNAT	660
ACCAAAAAAA AGGGGTGGGG GGATTATAC	689

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCAGCAGAA CCGAGATCTT CCATCAGCTG GCGGGCCTCG GAAGANTCCC GCTGCCAGAC	60
CGCATTCAGC CGCTGTTCAA ATTGGGCTC GTCGATTTC CTCAGCGTAA AGGGCGCGTT	120
CAGCCCCCGT TGCAGCTCCT GCAAAACAGA GAGCGACAAC GGATGCACAT GGAGGATCTC	180
CAGCGACGCT TCGCACCATG CCACCAGGCT AAACCGACGG CTGAAACTAT AGGGCAGACG	240
CACGGTGTTA GCGGTGGTTT CCTGTGCTAC AGGCACCATT AACGCGTTCT CCCGGCATT	300
AGGAACGCAC GAACTTCTGG CGGTAAGGCC TGATTTTGG CAGGCAATAT CGCTGCGCAG	360
TGTGCGGCAT CAGGCTTAAG CCCTGCTCAT CGCGTAGAT TTGCTCGGCG CGCATGTAGT	420
TATATTTGCG CTGCGACACA CCGTCTGCC CCATACGTC ACGCAGAATG GTCGGGCGGA	480
TAAACACCAT CAGGTTACGT TTTTCTTTT TATCGCGCT CGATTTAAAC AGGTTACCAA	540
TCAACGGGAT ATCGCCAGC AGCGGCACTT CTGCGCAGC TTTCTCCCGC CTGGTCGTCC	600
ATCAGACCGC CAAGCACAAT TAGCTACCA TCGTTAGCCA ACACGGTGGT TTTCAAGTTG	660
CGCTACCAA ACACCACGTC GAGGCTGGTC TGTCCTTCCA CCTTCGACAC TTCCTGCTCA	720

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ATCACCATCT GTACCGCGTT TCCTTCGTTA ATCTGCGGCG TGACTTTCAG CATGATGCCG      780
ACTTTTTTCC TCTCTACCGT GTTGAAAGGA TTGCTGTTAT TGGAGCCAAC GGTAGATCCA      840
GTTAATACCG GAACGTCCTG GCCCACCATG AAGAAGGCTT CCTGGTTGTC CAGCGTGGTG      900
ATGCTCGGCG TGGAGAGCAC GTTCGAGCTG GAGTCCTTTT TGACCGCCTG TACCAGCGCC      960
ATCCAGTCGC CTTTCAMCAC GCCAACCGCC GTACCGCTAA AGCCAGAAAG AAGCTGAGCA     1020
AGCGTGGAGA GATCGCCGTT AGTATCCGGA TTTATGGTGG TAGCGCCGTT TTCACTGATC     1080
ACCGTGGAGC CTTTCTGCGG TTTTGCTTGA GAAATCGTGC GCCCAGCGTA CCAATAGGGA     1140
TCTGCGTACC GTTAGCAAA C GCAATTAATC CGGCATCTTT CGACGCCAC TGCACGCCGA     1200
AATTGATAAT TCACCTTCGG CAACTTCCAC GATCAACGCC TCGACATGTA CCTGAGCACG     1260
GCGAATATCC AGTTGTTCAA T                                     1281

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(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

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CAATATTAGC GCACGGCACC AAAGGTGATG AATGAGCAGG CTGRAATATT ATTTTCCCGC      60
GGTGCAGAAA TCCTTGTTCT TGGTTGTACA GAAATTCGGG TTATTCTGGC GCAACGTAA      120
AGAGCAGCCT TCCCGCTATA TTGACTCAGC GCGTCACTCG TTCGTGCCGG AATAAAATGG      180
TACGAAAATC GTGTCGGTAA ACATTATCTT TTAACCCAAT AATCATTTAA ATCGCAGCCA      240
GAAAGTTATT CGCTTTTAAC TGAATTATAT TTATAACGGA GAACATTATG GTTTGGCTGG      300
AAATTATCGT AGTACTTGGT GCAATAKTTT TTGGTATTCG CCAGGGGGGA ATCGGTATTG      360
GTTTATGTGG CGGCTTGGG CTTGCCATTC TGACTCTGGG ACTTGGTCTG CCTATGGGGG      420
G                                     421

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(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1018 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

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GTTAACAATG GCGTAACAAA TTTCAATAAC GTAGAAGATT TGCTGTCAGA AAGGTCAATA      60
TTTCCTTTCA ATGGGTCAAA GACTTGCTTC TGGAATTCAT CCGGTTTTTT CTCCAGACGT     120

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TTTCCTTCTT CATAASTGTT AATATAACTT TTACCACTGA GTGTTTTGKC YCCATTTCTG	180
GTGACACCCAG CTAACTCACG TATCAGCGTA TCCCMATGTT GCTGGGTAAT GAGGACTGAT	240
CTTTCAACAG AATACTCTTT ATTATACTGA GATAATATTT TAAAGTTATC TTCTAAAAAT	300
GCAGCATGGC GGGCATCATA TCCCATTTTC AAAGTAATTT TTGCCGTGTT TTTTCTCCCA	360
TTCAGCAATA ACATCGGCCA TTTTACTGGC GACATGTTCA AACATTGCCT GTTTTGAAGC	420
CTCAAGGATG CCTGAAATTA TCCCCGTAAC AGCCCCTACC AGCGCGCTTA CCGGTGCACC	480
AACCAGAGAT GTCGTTGCAG CAGCACTAAT ACCTGAAGAT ACTGAAGCCA GAACAGTGCT	540
TATCGTTGTT AACGATGCAT CAATAGCTCC TGTTTCTTTG TGGAAAGCAG CAAGTAAACT	600
GTCACCATCG TATCCAAGTT TTTTGAATCG TTGTGAATAC TCCTCTATTT TATTGGCAGC	660
TTTAAACTTA TCGGCAATGG ACAGGAATGA GAGGGGACTA ATTGCCAGTG TCACAACAGA	720
AGCAATTAAA CCGGCAGCAG CAGCAGATGT AGATAACCCC TGTGCTGCAC GCTGTGCGAY	780
NAATATATTG AGAAATACCT TTTCCAACAT TACCCAGTAC TTTCGTTGTT AATTCAACAC	840
CTGCTGCAGC TTTAGTTCCG GTATCTGCAT CTGCATTGCT CAGAATGAAA CTTGCTGAAA	900
TCGCAGATAA AATACCCGAT ACAGTATCTA ACCCTGCACC GATATTATCA AGGTTAGGTA	960
AATTCTGTAA CTTATTACCA ACACCGTTCTN GGNCCTGTTGG TATTGGGATA ATACACTT	1018

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGCAATGTTT AAATCGATAT TGTGCAGCAC CTGGGTTGGG CCAAAGTGCT TGGAGACGTT	60
TTTAAATTCA ATCAGAGGAT TTTCATCCTT CTTTCCAGAC GACGCAGAAT AAAGCTCAGC	120
ACCAGGGTAA TAATCAGATA GAACACCGCC ACGGCGCTCC AGATCTCAAG GGCGCGGAAG	180
TTACCGGCAA TAATTTCTTG CCCCTGACGG GTCAGTTCCG CCACGCCGAT CACAATAAAC	240
AGCGAGGTGT CTTTAATGCT GATGATCCAC TGTTTACCCA GCGGCGGCAG CATACGACGC	300
GTGCCAGCGG TAAAATGACG TAGCGAATGG TTTCCMACG TGAAAGACCG AGCGCCAGTC	360
CTGCTTCACG AAAACCTTTG TGGATAGACA GCACCGCACC	400

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CGTGTTCCCC	TGGCCNGCTT	GGTTTCGCCA	TAGACGTTGA	GCGGGGAAAT	CACATCGGTT	60
TCCACCCAAG	GACG TTCACC	ACTTCCATCG	AAAACATAGT	CGGTGGAATA	ATGTACTAGC	120
CACGCACCTA	ATGCTTCAGC	TTCTTTGGCA	ATAACCGCCA	CACTAGTTGC	ATTGAGTAAC	180
TCGGCAAATT	CCCGCTCACT	CTCCGCTTTG	TCGACTGCAG	TATGGGCCCG	TGCGTTAACA	240
ATCACATCCG	GCTTGACGAG	ACGTACCGTT	TCAGCCACCC	CTGCAGAATT	GCTAAAAATCA	300
CCGCAATAGT	CGGTGGAGTC	AAAATCAACG	GCAGTGATGT	GCCCCAGAGG	CGCCAATGCA	360
CGCTGCAGCT	CCCATCCTAC	CTGACCATTT	TTGCCAAACA	ACAGAATATG	CATCAGGTAC	420
GCTCCCTATA	GTTTTGTTCA	ATCCAGGATT	GGTAGGCACC	ACTCTTGACG	TTGTTAATCC	480
ATTGTTGATT	ATCCAGATAC	CACTGCACGG	TCTTGCGAAT	ACCAGACTCA	AAAGTCTCCT	540
CTGGCTGCCA	ATCCAACGCA	GCGCTCATCT	TGCAAGCATC	AATCGCATAT	CGGCGATCGT	600
GTCCGGGGCG	ATCCGCCACA	TAAGTAATTT	GATCGCGATA	AGAGCCAGCT	TTCGGTACCA	660
TCTCGTCAAG	CAGATCACAA	ATAGTATGTA	CTACATCCAG	GTTCTGCTTC	TCGTTGTGAC	720
CGCCTATGTT	ATAAGTCTCC	CCGACCAAGC	CAGTGGTCA	TACCTTG TAG	AGTGCTCGTG	780
CATGATCTTC	CACATACAAC	CAGTCACGAA	TTTGGTCACC	TTTACCATAA	ACCGGCAGCG	840
GCTTGCCATC	CAGCGCATTG	AGGATCACTA	GCGGGATCAG	CTTCTCGGGA	AAGTGSTAAG	900
GGCCATAGTT	GTTGGAGCAG	TTAGTGACAA	TGGTTGGCAG	GCCGTACGTA	CGGTACCAAG	960
CACGCACCAG	ATGATCGCTG	GAAGCCTTGG	AGGCAGAATA	GGGACTGCTA	GGAGCGTAGG	1020
AGGTAGTTTC	GGTAAAGAGC	GGCAATGCTT	CACCGGAGGC	TACTTCATCC	GGATGGGGCA	1080
GATCGCCATA	TACTTCATCG	G TAGAAATAT	GGTGGAAGCG	AAAGGCCGCC	TTGCTCAACT	1140
CGCCCAGACT	GCTCCAATAG	GCGCGAGCCG	CTTCCAGCAA	TGTATAGGTG	CCTACGATAT	1200
TGGTTTCGAT	AAAGTCGGCT	GGCCCTGTGA	TAGAACGATC	AACATGGCTT	TCAGCAGCCA	1260
GATGCATCAC	GGCATCTGGC	TGGTGCAGAG	CAAACACCCG	ATCCA ACTCA	GCACGATTAC	1320
AGATATCAAC	TTGTTCAAAC	GAATAACGCT	CACTTGACGA	TACACTGGCC	AAAGATTCCA	1380
AATTGCCAGC	ATAGGTGAGT	TTATCCAGAT	TGATAACGGA	GTCTCCAGTA	TCACTAATGA	1440
TATGACGCAC	CACGGCAGAG	CCGANAAAAC	CAGCACCGCC	AGTAACGAGA	ATCTTCATAT	1500
ATTTGCTCT	CTTATTTTAC	AATTAATAGC	TATTA AAAAT	AACTTGTTG	ACTCCGATAT	1560
ATTAGAAATA	TCGGGATACC	GAAC TAAATA	TTTTTATATG	CTTTTGCCAA	GCAGACTCTA	1620
TATCCACCCT	GTATCACTAT	GCTTTCTGGC	ATACAATATC	CCATCATTGA	CACAATGATA	1680
AACATATAAA	TAAAGAAAAT	TTTAAATCAT	ATAACCAAAT	TACTTTCATT	TATTATCAAT	1740
AAGTATTTTG	ATAAGAATAC	CTATACCACA	GGGAGCCCCC	TGAAACATAA	TATTAGCGAA	1800

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GAATGATAAC TGATAGTTAC CATCTTAGAG ATAAAACTT ATTTGTGTGG CGGGATG 1857

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGCTCTTTCG TGATAAATAA AATACAGCAT ATCCTATATA GCTTACAATC ATTAAATGAA	60
GTCGCCAATA TTTATATGTT TTATCAATAT CAGCTTGACT CATTGTTATT TCTTTGTCAG	120
GAGACTCTGA AAATATGGAC ATATATAACC TCTTTTATTA TGAAATATTT TCAATAATAA	180
TAATCCGTTA GTAATCCTAT CATAGGGTAA TGTCTCATCA TGTTAAAATG ATCACATTTA	240
TAATCATGTC AAAAAGAACA ACAGAAAAAA TCATATAAAA TCAATTAAAT ATAATTGCCA	300
CATATTGTTG TTATTWAAAC ATTGGTGGTG AATTTAAAGC GAGAACAGTT TGTAACAGTG	360
ACTCCTTGCA GACTAAGTTA GAGTCTCCTT CTAAAATTAG ACGGWKTTCT ATTGATGGAT	420
AATAGTAAGC GCACCGTGAA KGACGTGGGG TAAAATTAG TTTACAGATT GAGTGACATT	480
CCAGGGCAAC AACTCTTTCA CGCGGTTGGC AGGCCAGGTG TTGATTACAC TGATCACGTG	540
GCGTACATTA CCGGACTCGA TTCCGTTAAG TTTGCAGCTA CCGATCAGGC TGTACATCAC	600
TGCCGCACTC TCGCCTCCAC CATCAGAGCC GAAGAACATG TAGTTACGCC GCCCCAGTGC	660
AATACCCGGA GGCGTTTTCA CACAGGTTAT TGTCGATCTC CACCCAGCCA TTGCGGCAGT	720
ATTCGTTTCA AGCGTCCCAT TGCTTCAGCA GATAGGTGAA CGCTTTCGCT GTATCCGAGT	780
GGCGCGACAG TGCTCATCTG CCCCTGGAGC CACTCATACA ACGACTGCAT TAGCGGTACC	840
GTTCTGGCTT TTCTGACCGC CAGTCGCTCT TCTGCCGGAC TGCCGCGGAT CTCAGCCTCG	900
ATAGCGTACA GTTACCGAT ACGCTGCAGG GCTTCCGTGG TGATGTCAGG TGGCGCTCTT	960
GCATGCACAT CGTGGATTTT TCTCCGGGCA TGGGCCATAC AAGCCGCTTC GGTTACCTGA	1020
CCGCTTTCGT AAAGAGCATT GTAACCCGCA TATGCATCGG CCTGCAGGAT ACCTCTGTAG	1080
TCCGCCAGAT GTTGCTGTGG GTGGATGCCT TTGCGGTCGG GAGAGTAT	1128

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

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GTTTGCTTAC GAACCGTGAA ATATGACGGT CCCATATAAC TGCCTGATAC TTGTATATCA	60
TATACTTGTG CATGCATGTC ATCATTAAAA AGTACTTTGT CACCGTCTTT AAGTTGAAGA	120
CGTGTA AAAAT CTTTATACGG CAAGTAGACG GAAAACGGGC GCTTTCCCTG TCGCCAATCA	180
CACCGACATG ACTGACTTTT GCGAGAGGAA GTGCATAATT CACCAATTCA GAGCCTAATG	240
CATTGCGCTG GGTAAGCTCA AATCGGAATG GGTTCGAAC CTTTCCCGCA ACATTGATCA	300
TTGGACCTTG TTGCTCAACT GAAAATCACA TCTTGATCTT TTAATGCCAG CTTCGGGAGT	360
TTCCCATACC GTATGAAATC ATAAAGATCA ATTTGCKGTG NTTACTGCTA TTTTGTGCGT	420
GAACACCTTA ATTTTTCGCG	439

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TATTCGTAAT TAGTTATAAA CAGATGATGT AAACACCACT TGACTAGAGT CAATCTTATA	60
CTGGCAACAT CTATGATTAA TTTGTGTGGT TATAATTTTA AATATCTTAT ATTTATGGGC	120
TATTATTGAT ATCTGTCAGA GTATCAATAA TAGAAGGTAA TTGTTTTACA TACTATCAAC	180
TTTTGGATAA CGTTTTAAAA TGCACCTTGC ACATCGTATT TTATTATTTT CACTAATCTT	240
TTTTATAACG GCCTGCGCAC ATGATCCAAA ACAAGTTGAA GCCTCTCGTC CATTGGTAAC	300
AGCGATTAAT TCTTCTTATT CTCTTATTCC TGAAGATTTG CAGGCACCAT TAAATAACCA	360
AGATCAAGGC ACGACATTCA ACAAAAATGG CGTAATTTAT ACTATTGAGG AAAGGTATAT	420
ATCGGCTTTA GGTTCCTCAAT GCATAAAGTT AAGTTATGCG ATGAATAAAA ATTATTCAAA	480
GCGAAGTGTT GTATGTAAAG AGAATAACAA GTGGTATCAA GTACCTCAGT TGGAACAAAC	540
ATCAGTTAGC ACTTTGCTTA TTGAAGAATA AAGTTGAAGG TAGACGGTTA GAAAATAATG	600
AAAATTTTCGC AACTTAGCAC TCTTCTCTTT CTTATTTCTG CATCAGCATT CGCCGCAATA	660
GAGCAAAATC AATCTAATGG TTCACATTTA GATTATGATC TTGCTGCCTC GACAGGAGAG	720
TCTCGGAAAA TGCTAGCAGA CATCACTGGA CAGCCTAATA CAACCTCCAC AACAGGAAGC	780
TTCACACAAC AGAATCGTAA TGGGATGTTG CTTCCAGGAG AGTCAGATGT ACGAAAATTA	840
CTGCCGCAAT CTGAAGCAGG CTTACCTCCT CCGTATGGTG CTAATTTATT TGCCGGAGGC	900
TATGAA	906

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGGCCTGAT ATATGCCGTT ATTACAAAAA GAGGATCAAC CACACTGCCT TTTGGACCGT	60
GTTTAAGTCT GGGCGGTATA GCAACACTTT ATCTACAGGC ATTGTTTTAA TGATAACCAC	120
GTCATTATCA AAGTGACATT TTAACCTTTA TTAATAACCT TAGAGATTAT TTACCATGTC	180
GATAAAACAA ATGCCAGGGA GGGTATTAAT ATCGCTATTG TTGAGCGTTA CAGGATTATT	240
AAGTGGCTGT GCCAGCCATA ATGAAAATGC CAGTTTACTG GCGAAAAAAC AGGCGCAAAA	300
TATCAGCCAA AACCTGCCGA TTAAATCTGC GGGATATACC TTAGTGCTGG CGCAAAGTAG	360
TGGCACGACG GTAAAAATGA CCATTATCAG CGAATCGGGT ACTCAGACCA CGCAGACACC	420
TGACGCCTTT TTAACCAGCT ATCAACGACA AATGTGCGCT GACCCAACGG TGAAATTAAT	480
GATCACCGAG GGAATTAATT ACAGCATAAC GATTAATGAT ACACGTACAG GTAACCGTA	540
TCAGCGGAAA CTGGATCGTA CCACCTGTGG AATAGTCAA GCATAACGTC GGGTAGATAT	600
AAATTGGCGC GGTTGTTTT TCGTGACGCA CGAATTTATC TCATTCAATG GCTGACAAAA	660
ATTCGTCACA CTCTTAACCA GAGACAATCT CTTAATACAG ACAAAGAGCA TCTGCGCAAA	720
ATTGCACGCG GGATGTTCTG GCTGATGCTG CTTATTATTT CTGCAAAAGT GGC GCATTCA	780
CTCTGGCGCT ATTTCTCCTT TTCTGCGGAA TATACGGCGG TTTCCCATC GGCGAATAAA	840
CCGCTCCGTG CGRATGCAA AGCGTTCGAT AAAAATGACG TGCAATTAAT CAGCCAGCAA	900
AACTGGTTTT GCAAATATCA GCCCGTCGCC ACGCCGGTAA AACAACCCGA ACCTGCACCT	960
GTGGCCGAAA CGCGTCTTTR TGTGGTGTG CGTGGGATCG CCTTTGGTGC CAGACCCGGC	1020
GCGGTTATTG AAGAAGGTGG TAAACAGCAG GTCTATTTGC AGGGTGAACG CTTGGCTCGC	1080
ACAACGCAGT GATTGAGGAA ATCAACCGCG ACCATGTGAT NTGCGCTATC AGGGAAAAAT	1140
AGAGCGCCTG AGCCTGGCTG AAGAGGAGCG TTCCACCGTT GCCGCGACCA AAAAAAAGC	1200
TGTCAGTGAC GAAGCAAAGC AAGCTGTTGC TGAACCTGCT GTCAGTGCGC CAGTTGAGAT	1260
CCCNGCTGCC GTGCGTCAGG CACTGGCGAA AGATCCGCAG AAAATTTTTA ACTATATCCA	1320
GCTTACGCCT GTGCGTAAGG AAGGGATTGT CGGTTATGCA GTGAAACCGG GGGCAGATCG	1380
TTCTCTGTTT GATGC	1395

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```
CACTTGAATA AAAC TGACAC CGTTTACCTC CATAATAGTG AGCATAGCCG CCATTGCGGC      60
CTGATCGGCG AACCGGAAAT CGCAACCTGC GAACGACAAC CGAACCGGCA AGCGTGCGGG      120
AAGGACGGAT ACCGGACTCT TTCGCCACTT CAGCAATCAC CGGCAGCGTG GAAAAACAA      180
TAAACCCAGT ACCGGCCATA ATGGTCATAG ACCAGGTGAT AATCGGCGCG ATTATGTTGA      240
TATATTTTCG GTTACGCCGC ATAAATTAC CAGCGACGGT ACCAGATAAT CCATTCCCCT      300
GCGGCCTGTA AGGCTGAGGC CGCCACAACA ACGGTCATAA TAATCAGGAT CACGTCGACT      360
GGCGGCGACC CCATAGGCAG                                     380
```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

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CTTTACGGTT TAATAGGGGA ANGCCGACTG GATGNAAAAA TGGAATCTGG AGCCCAGAAT      60
AAATCTGAAT TTAATGTGGA CTGGATATGC TCCAATAACC CCGGCAGGGA GTCATCTGTG      120
CGAAGATATT TGC GTTATGC TGTAATATAA TAATTCAATG TATTTAGGA ACAGTAATAT      180
ACTACAGTTT CTACTTTCTT GTATTTAATA AATTGTTCCG CATCGCTAAA AGCAGGTCTT      240
TCAGAAGCCA CAAGAATTCT GTGGTCCCAG TATTTTTAGT TATCCTATTT TTATATCTAA      300
CTTGTAATAC TTACAGCATT TTCATTCATC CTAATGGAAG GCTGTAATAA TCTTTGAGCT      360
TAGAAACATC AAAATTATGC ATCTCATTAA TTTTGTGAGT CACACGACCT CTGGTAAAAA      420
TAAACCCCC AGAAATATGC CATTTCTAGG GGGGGCGTAA GAATCAATAT ATTTTAGTGT      480
TGTTACATTT AGCTCTTAGC TCTTAGCTCT TAGCTCTTAG CTCTTAGCTC TTAGCGTTTG      540
TAGTTTCATC GCAATGAGTA AAAGGACAAC AAGAATAAGT GATAACGTTA AGAGAAGAGC      600
ATAGAAACCA TTCCAGTGGT ATATTTCTAT TATTTTAGAC AATGGATAGC CAGCCGCGGA      660
CGCACCAAGA TATGCGAATA AACTAACAAA ACCAGTAGAA GCACCAGATG CATATTTATG      720
TGAGTTTTCA GCAGCTGCCA TTGCGATCAG AAATTGTGGC CCAAAGATAA AGAAGCCAGT      780
GATGAAAAAT AATAACGAAA AACATATTT ACTATCAATA GAAACCAACC ATAGACATGC      840
AGAAGCAATG ATTATACCAA TTGTATAAAT AACATTCATT TGAGAGCGAT TGCCCTTAAA      900
CAGAATATCT GATCCCCATC CAGCTACGAT AGCACCAAAA AAGCCTCCAA CCTCAAACAT      960
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CATTACTGTT GCATTTGCTG TTAGCAAGTC ATATT

995

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TAAAAGCGAC TCCATGTGAA ATTTCTGTTT GTCGTTTTTT CCCC GTTGTA GCGGCTCTGC	60
TCCTGGCTTC CCTGATAGTC AGCCCGCAGG CGCCAGGGCC CCAGATTCCC CCCACAGTC	120
CCGTTATAAC TGAAGTGATG AGAGTCTCCT CCCTGATAAT TACGGGAAAC CGTCCC GTTG	180
AGGTTATAAT CCAGCATCAG TCCGGGAATG CCGTCGTCCC AGCGTGAGGG AGGCAGCCAG	240
GTGGCATCAG AATACTCAAG CCAGGCCTGC GGCATATTGA TGC GTAATAC GCCCGCTCCG	300
GTATCAGGAC GAATATCCAC TCCCGGCAAC CCATGAAAAT CCGCACACTG ACCATCATGC	360
CAGTAAACAA CTTTATCCAG AGATTCTGCT GTTAACCCCA TCAGTCTGAC CATATCTGAT	420
GTCAGACAGC TCGGGCAATT TTTTCTCTGC CTTATCTCCT GACAACGCAG GTTCAACAAA	480
TGAMATCTGT AACGATGCGG GAGAAATACT TTGCCCCGTTA ACAATCACAT CCAGAAGATA	540
TTGCCCCGGC AGAACATAGC CGGCTTCTGA AAAACGGGTG AAGTCAATAT TTTTCTTGTC	600
CGTGCGTCA AGTACATCTG TATTAACTC AACGGCACTG GCTGCGTTAC AAAACAGAGA	660
CAACAATATC ACACAGGTAA TATTGTTGAC TGCAAAAAGGT ATTCTGTCTT TCATTCCACG	720
CATCACCAGA TTCACAAAAA AGATAAATAA CCGGACATCT CACCGGAGTG ACTCACTCAT	780
AATCGACCCG GAATCCCAGC ACAGCAAAT AATTTC	817

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTTTGTCAG AGCGTTCCT CTCTGGCTGG ATGATTTCCG CTCGGGAAAT GCAGGCTTAA	60
TGTGGGGACT GTCGGGGATG TTTGAACGGG TAAAAATAAG TCATGAGTTT TTTATTATG	120
TCCTGAAAAA CGGGTGTGCA ATGCCACTTC TCCGTGCTGT GGCAGACACT GTTGCTGTC	180
ACAACAGAGG CGTGATACTC GAAGGTGTTG AAAATGAAGC GTTGTTCCGT ATTGCCAGAG	240
ACATGAATGT CCAGGGCTGT CAGGGATGGC TCTACAGGCG TGTGGGGGTT GATGAATTAT	300

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CCGCGCTTAT TCAGCAGTAT GAATAATCCT TTTTCACAGA CTGGTCAGCT GTCAACATTT	360
ATGTTTTTTT ATCTGCGGGA ATTTATCCGT CTGCCTGTCG GGACTIONCT GTCATACAGA	420
AATCAGGCCA GAATAAATTG TTGTGGAAAG GTGAGATTTA CCGGATGACT GATGTGCTCT	480
TGTGCACAGG TATACAGGCA GTGTGTTTCC AGTATATGGA AAATGATTAA ATGAATAACA	540
CAGACTTATT AGAAAAAATC ATCAGGCATC AACAAAACAA AGATCCTGCA TATCCTTTCC	600
GGGAACATCT TTTGATGCAA CTCTGTATCC GTGTAAACAA AAAAATACAG AACAGTACAT	660
CTGAGTTTTT TGGTGCATAT GGTATAAATC ACTCAGTATA TATGGTTCT	709

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TCATCAAGGG ACGGGGCATA TCTGGATGCG ACAGGGCAAA CCAACCACTG AGAATCCAAC	60
CTGCCAAAGC CTGACCAGGA AGTCCGACGT TAAAGAAACC AGCTCGACTG GCAACGGCAA	120
AACCAAGACC AATCAAGACC AGAGGACCCA TAGCACGGAA GATTTCTCCA ATCCCACGCA	180
GACTGCCAAA GGCTGTATAG AACAATTCTT CGTAGCCCCA AATAGCATCA TAACCGAAGA	240
TCCACATGAC AATGGCTCCG AGTAAAATTC CTAGGAATAC AGAAATCAAG GGAACCGAAA	300
TTTGTGTGTA TTTTITAGAC ATCACTCTTC TCCTTTCCCA AGTTYCCACC AGCCATCAAG	360
ACACCAAGTT CTTGTTTATT GGTGTTTCT GGTGATACAA TACCTTGAAT CTTACCATCG	420
TGGATAACGG CAATACGGTC TGAGACGTTT AAAATCTCAT CCAATTCAAA GCTGACNACA	480
AGGAC	485

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

AGCAGAATAG GCAACATCAC CACCCCGACA AACAGCGAGA AGAGAATGAC GCCAGCCGCC	60
AGGAACACCA GCTCATAGCG CGCCGGGAAG ACGTTACCAT CCGGCAAGAG CAGCGGGATA	120
GAGAGCACAC CGGCCAGAGT GATCGCCCA CGCACCCCGG CGAAAGACGC GATCAGGATT	180
TCTCGTGTGG TCCACGAACC AAACTCCATC GGCTTCTTCT TCAGGAAGCG GTTGCTGAAC	240

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TTTTTCATCG TCCACAGCCA GCCGAAACGG ACCAGCATCA GCGCCGCATA TATCAGAATA	300
ATATTGGTAA AAGCATCCA GATTTGACG TTAGGGTCGA TTTCTTGCTG GCCATCAGCG	360
GACGTCTTCC AGRATTACCC GGCAGCTGCA GACCTTAACA GCAGGGAACA CCATGGCCGT	420
TTTAAGGACA ATTTNAGCA TCGGCCANG TGCTGTTTT	459

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 908 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTAATAGCAC TAATACTGTC CTGCTCTATT CCGCTGACAT TTTCAGTCAG CTGCTGTATG	60
GGATGGGTTA CCCAAAACCA GACCAGCATA CCTGACAAGA GACCGCATAT CACTACCAGA	120
AACAGCGACC AGTACAGTGC ATTCCATAGT GCCTTTGTCC AGGCTGTATC AGTAAGAGCA	180
TTAAGTTCCT CTCCCTGTAA AATAATATAC AGATATCCTT TCGGTTTCATC ACTCTGGTAA	240
AGCGGTGCGG TACTGAAAAC TTTTGTCTTA TTTACACTTC GGGGATCATC ACCATATACG	300
GGCCAGACAC TGCCGGAGAG AAATTTTTTC AACGGTGCAA TATTGATATA CCGGCGTTTG	360
AGATGACCCG GAGGGCGGCC TCCACAAGCA GTCGCCCTTC CGGTGAAACC ATATACAGCT	420
CCCACTGGG ATTAAGCGTC ATCAGACGCT CAAACAGACT CGTTAATGTC CGGTGTTACC	480
AGACAAAACA AGCATCGCAA GACGCCACAA ACGGTGCGCT TACTTAAATA AGCCGGTTAC	540
AGGTGAAAAA TCACGTCCTG ATATTCAAAT GTTTTTTCAG GTCATATTTT AGCAGGACAC	600
TACCAGCACC TAACAGCAGC ACATCTTTTA TAACAAAACCT GTCAACTTTC CCCAGTTGTG	660
GTAACAGGCT GAGCGTGGTT ATTCCTGTAA CAATAACGAT AATATCTCCC AGTACACCAG	720
CAGCAGGCCT GAAGAAACCG ATAATCAATG CCAGAAATGT GATAGTTTCC ACTATGCCGA	780
GGAAATAGCT CCCTCCATGA ATACCAAATA TAATATACAG GATATTCAGC CAGGTGGGAT	840
ATATCAGGGG CTTGAGAGCC ATAACCTCAA AATCAAACCA TTTATAAGTC CAAAAAGCA	900
TAAATATT	908

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1057 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

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CGGGCTAACC CAATATGCTT TATTAACCCG GGATAATTAC CCTGTTGCAT ATTGTAGTTG	60
GGCTAATTTA AGTTTAGAAA ATGAAATNAA ATATCTTAAT GATGTTACTT CATTAGTCGC	120
AGAAGACTGG ACTTCTGGTG ATCGTAAATG GTTCATTGAC TGGATTGCTC CTTTCGGGGA	180
TAACGGTGCC CTGTACAAAT ATATGCGAAA AAAATTCCTT GATGAACTAT TCAGAGCCAT	240
CAGGGTGGAT CCCAAAACTC ATGTTGGTAA AGTATCAGAA TTTCACGGAG GTAAAAATTGA	300
TAAACAGTTA GCGAATAAAA TTTTAAACA ATATCACCAC GAGTTAATAA CTGAAGTAAA	360
AAACAAGTCA GATTTCAATT TTTCATTAAC AGGTTAAGAG GTAATTAAAT GCCAACAATA	420
ACCGCTGCAC AAATTAATAAG CACACTGCAG TCTGCAAAGC AATCCGCTGC AAATAAATTG	480
CACTCAGCAG GACAAAGCAC GAAAGATGCA TTAATAAAAG CAGCAGAGCA AACCCGCAAT	540
GCGGAAAACA GACTCATTTT ACTTATCCCT AAAGATTATA AAGGGCAGGG TTCAAGCCTT	600
AATGACCTTG TCAGGACGGC AGATGAACTG GGAATTGAAG TCCAGTATGA TGAAAAGAAT	660
GGCACGGCAA TTAATAAACA GGTATTCGGC ACAGCAGAGA AACTCATTGG CCTCACCGAA	720
CGGGGAGTGA CTATCTTTGC ACCACAATTA GACAAATTAC TGCAAAAGTA TCAAAAAGCG	780
GGTAATAAAT TAGGCGGCAG TGCTGAAAAT ATAGGTGATA ACTTAGGAAA GGCAGGCAGT	840
GTACTGTCAA CGTTTCAAAA TTTTCTGGGT ACTGCACTTT CCTCAATGAA AATAGACGAA	900
CTGATAAAGA AACAAAAATC TGGTGGCAAT GTCAGTTCTT CTGAACTGGG CAAAAGCGAG	960
TATTGAGCTA ATCAACCAAC TCGTGGGACA CAGCTGGCCA GCCTTTAATA ATAATGTTNA	1020
ACTCATTTTC TCAACAACTC AATAAGCTGG GGAAGTG	1057

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TACCGGGCCCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT TCCTGCAGCC	60
CGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAGC TTTTGTTCCT	120
TTTAGTGAGG GTTAATTTTC AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA	180
ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCT	240
GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC	300
AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG	360
GTTTGCGTAT TGGGCGCTCT TCCGCTTCTT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC	420
GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG	480

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GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA	540
AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCT GACGAGCATC ACAAAAATCG	600
ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC	660
TGGAAGCTCC CTCGTGCGCT CTCCTGTTTC CGACCCTGCC GCTTTACCGG ATANCTGTNC	720
GGCTTTCTCC CTTCGGGAAG CGTGGCGCTT TC	752

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTTGGGTAAT NGACCTCATA TCCCTCCGCC AAAAAAGGAT CTACATGCGA TTTTGCGAAG	60
CCAGCGTTGA TTGTAGGCGA GAGAATGGTT CTGTTGTTTT GGTACATTTT AGTTGTCATG	120
GATTTACAA ATGTAGCATG ACCTTTCACC TGTCCAAGAG ACTGCAACAC CATCTGTCCA	180
AAACAATAAA TAGGAATCAA ACAGGCTACC AACATCAACA AGTATCCCAA TAAGGCTCGT	240
AGTTTAGTCC TTGACATGAC GCCCCTCCAA TTGCTTTTCT AGTCCTTTGA CAATCCGTCG	300
ATTACGATAC ACGCGATACA GCAAGAGAAG GATGACCGCC ATCGCTCCTA GTAATAACCA	360
CAACCAGAAT TGCCACGCT CTCTACCGC TCGATTCCGC TCTGCAATTG GTGCCGTATA	420
CGGAATCCGC TTCCACGTA CCAACAGACG ATGACTGTTA ATCCTATACG GTGTACNAGT	480
CAACCA	486

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTACGCNTTC AACCAGGTCT TCTGGTTTAC CAACGCCCAT CAGGTAACGC GGTGTGTCTG	60
CCGGAATTTG CCGGCATACA TGCTCCAGAA TGCGGTGCAT ATCTGCTTTC GGCTCACCCA	120
CAGCCAGACC GCGACAGCG TACCATCAAA ACCGATATCT ACCAGACCTT TAACAGAAAT	180
ATCACGTAAA TCTTCGTAAA CGCTGCCCTG GATGATACCA AACAGCGCAT TTTTGTTTCC	240
GAGACTGTCA AAACGCTCAC GGCTACGTCG CCCAACGCAG AGACATCTCC ATGGAGCGTT	300
TTGCGTAATC CCA	313

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(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CGGAAATCCC AGTAATTCCA TCCTCANATA TTCCACTCAN CCTCACTGTA ACAAAGTTTC	60
TTCGAATAAT AAAAATCATG CTTTCTGTTA TCAACGGAAA GGTATTTTAA TTCTCTGTGT	120
TTGCTTTATT TGTGAAATTT AGTGAATTTG CTTTTTGTTG GCTTTATNTG ATGTGTGTCA	180
CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA AAATGCATTT AGACGATCTT	240
TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA GTGCATTCTT TTTGTTGGTG	300
TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC GTTTAAATCA ATATTTACAA	360
CATAAAAMMC TAAATTTAAC TTATTGCGTG AAGAGTATTT CCGGGCCGGA AGCATATATC	420
CAGGGGCCCC ACAGAAGGGG GAAACATGGC GCATCATGAA GTCATCAGTC GGTCAAGGAAA	480
TGCGTTTTTG CTGAATATAC GCGAGAGCGT ACTGTTGCCC GGCTCTATGT CTGAAATGCA	540
TTTTTTTTTA CTGATAGGTA TTTCTTCTAT TCACAGTGAC AGGGTCATTC TGGCTATGAA	600
GGACTATCTG GTAGGTGGGC ATCCCGTAAG GAGGTCTGCG AGAAATACCA GATGAATAAT	660
GGGTATTTCA GTACAACACT GGGGAGACTT ATACGGCTGA ATGCTCTTGC AGCAAGGCTT	720
GCACCTTATT ATACAGATGA GTCGTCGGCA TTTGACTAAA TTATGGCATT CCGGAGTTTC	780
TGGAAGATAA AAAAAGAAGC CCTTATCAGA AAGCAGACAG GTTATATCAG TATTCTGTCTG	840
ATAAATAACC TGCCCTGAAA ATACGAGAAT ATTATTTGTA TTGATCTGGT TATTAAAGGT	900
AATCGGGTCA TTTTAAATTG CCAGATATCT CTGGTGTGTT CAGTAATGAA AAAGAGGTTG	960
TTATTTATGA TTAAGTCGGT TATTGCCGGT GCGGTRCTAT GGCAGTGGTG TCTTTTGGTG	1020
TAAATGCTGC TCCAATATT CCACAGGGGC AGGGTAAAGT AACTTTTAAAC GGAAGTGTG	1080
TTGATGCTCC ATGCAGCATT TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC	1140
TTTCAAAAAG CTTCTTGAG GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT	1200
TGGTTAATTG TGATATTACT GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA	1260
AGCTGGCTTT TACTGGCCCG ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG	1320
GTACGGGCAC AGCTATCGTA GTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG	1380
AAGTGATGCT AATACCCTGA AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTAA	1440
GAAGTCGTCA GCCGTTGGTG CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT	1500
CAACCTGACT TATCAGTAAT ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG	1560

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TTTATTTCTC AGGGTATTTA TCATGAGACT GCGATTCTCT GTTCCACTTT TCT 1613

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

NTAGTCCATG GCCCCATGGA GCGAANTCCA AAGTGTGGAT ATTGTCGTTT TAATTCATCC	60
CAAAAGCTGA AATACGCCAA AACCCACGTT CCCTAACATT GGTATCATGC ATAATGACCA	120
CAGCCNTTCA GAAAGCTTTG GCAACCAGCT TTCAAATCA TGGGTACCGC TTCAAACGTA	180
TGCAAACCAT CAATATGAAG CAGATCAATG CTACCTTG TG AAAAATGCTC TAACGCTTGG	240
TCAAATGTAC TGCGAATGAG AGTAGAAAAA CCTGAATAGT GCTGTTGATT ATATTCTGAT	300
ACTTGCCCTGT AAACCTTCTTC GCCATACAGC CCCGCATGTT CATCTCCCCC CCAGGTATCA	360
ACGGCAAAGC AGCATGTTTC TAAATCTAGT TTAGAGACTG CTTGGCAAAA TGAGAAATAA	420
GAACCTCCAT AATGAGTTCC CAGCTCAACA ATATTTCTTG GCCGCAGTGT GTCAACTAAC	480
CAGAAAGCAA AAGGAATGTG TTCTAGCCAA GCAGATTGTG CAAGGTATGT AGGACACCAN	540
AAAAGAGATG GTTTGAAAAT GAAATTCAAT TCCCTGCCAA TATCAGTGAT GGGATATAAC	600
TCACGATTCT CTACTAACTG ACTAATTTTT TGAATATCCA TTGAGGAAAA CTCACATGTA	660
TTTATAGAAT TAAATCAAGA AACCTGAAAA TACCTATAGT GCGGTAACCT ATTAATAAC	720
ATTTAAATAT TAACAATACA CTTGGAAATA TTAGTTAAAA ATAAATCATT ATGATTTCTC	780
ATCAATCCTG GTGCTCACGC AAAGTTGCCA GCCCATAAT AATAAGACCA TAGAACAAGC	840
AAAGTAATAC ACCCACAGTC GCAAGATTAT AGAATCGCCG TGGATATTCG GCATCTTCCG	900
CTAAAGTTGG TTGGGTAATA ACCAATAGAT	930

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 659 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ACGATATCCC CCTCTGCTT TTGAGAGGCA ATCTGCTTTA ATACATGATT CATCACAACA	60
CCTCTTGCTG CGCTTTGATC TTAATTTTAT ATTTTGGGT AGGGAAAAGT AATTGCCCT	120
GATACGGCTC ACCATTTACC AACGTTTCAC AGCTATGTTT CAGAGCTAAA TTAAGACCTG	180

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GTAGAATATC CCAGCAATTC ACCCCTTTGA CATTTCATAA GCACCGGNN	240
AGGGGGGGGCC AACATGTTAT ACATGGAGCA GCCAATGATA CGATATTCAA AGCCCTCTTC	300
CAGTTGCATC AGATCCTGCT TGGTAASGGA GGAAGAGAGG CCACGAATAC GAGAGCGATG	360
ATGTGTAATC GGCATACCTG TGATATGAAG ATCATTCAAT TCAGGTAAGA AGATGCAGGA	420
CTCTTGATGT TTCCCCTCGG TGTAATGCT GATACCAATG CCCCCTCTT TGAGCCCAGA	480
GACAAAGTTT TCTGTGCCAT CAATTGGATC TAGACAATG TAAGAACCTT TGGGATTCCA	540
CTCAATATCT CCTAAAGGGG CTAATTCCTC TGAAATTAGC ACATGCCCTG GTAGATGCTT	600
TCTACAGAGT TCGAAAATA TATCTTGAAC TTTTAGATCC AGTACTGCGG CCGCGATCC	659

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCGGATATA CATCAGGAGA AATTGGAGCA GCAATTGGAT GCGCCATTAA TGCCTGGTTA	60
GGGATCCCCG CATGTGGGCA CGCAAATGGC TCAGAATATG ATCGACCTTC ACCAGATAAA	120
CCAAATCTGA GCGAACCATT TATCCCAAGA CCCACGTATG ACGCTTCACT TCATTCTCTG	180
CATGGCGGAT ACTGAGTAAA TCATCCTGAA TCATTATGTT CAACATCATC AATTCTCCGG	240
ACTTGTGTGC AGATGTCCGG AGAATATTAA CCTTTTCTTC AGAAACAGAW TGATCAAGAA	300
TCACACTCCT TCTTTAAGAG GATTTTATCC AGAAAATGA CTTTCTTCTA TCAAAATMAC	360
AGTATCCTGT TTTATCAGGA ATAATCTTTA CCTCCGGTAT CATTCCCATA ATCAGATATC	420
AGAAAAATGT GCCAGTAATT TTTTACTGAT GACTTCAAAC ATTCACATT CATCACACGT	480
CAGATTACTC CAAAGTTCTT TCAGATATGT GTTCTGCGCC AGAGTGAGTC TCTGAATAAA	540
AAACATACCT TCAGAC	556

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TACCTGTTTG TGGAATTTGA CCCAGAAGTG ATTCATACCA CGACTATCAA CGCGACCCGN	60
GTGTNCAGCC ACTTCGTGCG CTTTGGCGTN CGCAGCGATA GTCCCATCGG CGGTTATTCA	120

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TCAGCTATCG GTATATAAAC CGAAAGACAT TGTCGATTCC GGCAACCCCT TATCCGGGTG	180
ATAAGGTGAT TATTACCGAA GCGCGTTCGA AGGCTTTCAG GCCATTTTCA CCGAACCCGA	240
TGGTGAGGCT CGCTCCATGC TATTGCTTAA TCTTATTAAT AAAGAGATTA AGCACAGTGT	300
GAAGAATACC GAGTTCCGCA AACTCTAAAA CGCAATCCCA AACAGTGTTT TGACATTAGC	360
ATCCGTGGTG GCAGCCAGCC ATGCGGCATC TTCTCCACGC CAGTGCGCAA TACGTTGCAA	420
AATATGGGGC AGATGGGCTG GCTCGTTGCG CCGGGATGAN GGCTTTGGCG TGAGATCGCG	480
AGGGAGCAGA TACGGNGCAT CAG	503

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTTAACATCA AAATTACCTG CAGCTGAAAT GATTTTGCTG ATTCATTAA TTAATGGATT	60
AAGATTACCC TGACTTCCAT AGGCTAATGC ATCATTCCCA TACACATAAC TTGCCTTATT	120
ATTACTCTGT TGATACTNAA GTGCCTTTTT AAGGGAATCT GGTGTGATTA CCCTGCCGTC	180
TTTATCAAAA ATCTGCTCTA TCTGGTGATT AGAGATATCA CCTGACTCTT TTTCAAACCA	240
GTTTTTAAAT GTAATACCAT TTTTGTGGCC AATGGAAAGA ACATTACCTT CAGCTTTATA	300
CATGATGAGG TCATTACCTT CTCGCCTGAA GGCCACATCC CGGAAATCAA TATCAGCCAA	360
ACTGAGTTTA TCGTCTTTCC CCCCATCATC GTCAATAATA TGATGGCCAT ATCCTGAAAG	420
ATAACGATAA ATA	433

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCTCTGTT CCCGTTCTG TTCATCACCA TCGCCTGTGG TGCGGTATCT GGCTTCCACG	60
CGTGATCTC TTCCGGTACG ACGCCAAAAC TGCTGGCTAA TGAAACCGAC GCGCGTTTCA	120
TCGGCTACGG CGCAATGCTG ATGGAGTCCT TCGTGGCGAT TATGGCGCTG GTTGCTGCGT	180
CCATCATCGA ACCGGGTCTT TACTTCGCGA TGAACACCCC GCCTGCTGGC CTTGGCATCA	240
CCATGCCTAA CCTGCATGAA ATGGGGTGGC GAGAACGCGN CGGATTCATC ATGGCGCANT	300

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GA

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(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTAATAAG CCAAATACTA CATCACGTAA TACTTGCAAA GAAGTGCGTG GAGTTTGACT	60
AATAATGGGT TTCTCCATTA ATACTTACCC AAATAATCGG CTCATTATAG CAACGAGCCT	120
CCGATTAAAA TTAAATAAC TCAATCATTT AATAGCAACG TTAGCAGCTA CAGCGATTTG	180
ATAAATAATT TGTGTGATAT CTTTAAATGA TTGCATGGTT TTGCTATCAA CCTGAGGTAG	240
AACCAATATC TGATCCCCCG GTTGTACTTT ACCTTGCCCT TTAAATTCTA CAAGACCATT	300
TGCATGTACA ATAGCAATTC GCTTGTCGTT AGCTCGCTCA GTAAAACCTC CGGCCCATGC	360
AACATAATCA TCCAAATTAG CATCGGCATT ATATACTACT GCTTGTGGCA TCAACACTTC	420
ACCCCCCACT TGAATAAGAT CAGTCTTATT TGGGAATAACT ATTTGATCGC CTTGTTCTAA	480
TTGGATAWTG GCAATAACAC CTTTATCTGC AACTACTACT TTACCAAGCG GTKGAACTTT	540
ACGAGCCTTT YCAACAACT GCATCACTAA CTCTGCTTCT TTAGCACGTA TATTCGCCTC	600
ACCATCAGAT CGCGCGGGTG TGGTAAANTT CATACGTTCC AAGCGGTTTA GAGATT	656

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATATGTTATC TGGATCCAGA TAAAGAGCGT TCTTGACCCG CTATATCCAG ACAGGTCAGT	60
TACACCCTGT CCGGAAAAAC TGATCGGAAT AACAACAGTA TATTTTCTAA TACACTGGCA	120
AATGGTGCCG GCGGTGTGGG GATTAGCTT CTGGATAGCG CTGGTAATGC GGTGCTGCT	180
GGACAGAAGA AATATCTGGG ACAGGTAGGA CCATCAACAT CTCTCAATAT TGGATTAAGG	240
GCATCTTATG CACTGACCAA TGGACAGACT CCACCTACTC CCGGACGAGT TCAGGCGTTA	300
GTTGATGTTA CCTTCGAGTA TAATTAGGAA TGTCGGGGAT GGGCTATCCC CGATATTATT	360
GCAGGATTAG TCTGTGATAC AGATATACAG CCCATATGAA CAACTGTTTG CATATATAAA	420
AATGATGATA ATTTTA	436

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(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (E) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AATAATTAAA TTTGGAGGGA TCAGTTTTCT GATAATGTTT	60
TGTTATTAAA ACATTATCCC	
ATGGGGCGTA GTTATATCAA TTAGCAGGAT CTTATGAGTT	120
AACTAACATC AGTTTGAAT	
TTTTAATGGG GGTAATTTAT CTTTTACTAA AAATATTTTA	180
ACTATTAATA TAGCATCATG	
GTTGTTACGG TTTGTTTTAA TTCTATTTTA TAATGTGCTA	240
TATATTGTAT TTTGTGCTT	
AGATAAATAT GTTTTTTCAT TACTTTAGTG ATGTTAATAT	300
TTTGCGTGTA GTAAAAATCA	
TTGTTATAAC AAATGTCACG GTTGCTATAC TTTGCTGAAC	360
TGTTTATCGG TCATTTTGAT	
TCAATCACTG GTTCTATATT TTTTAATAAC CGTTCGTAG	420
CGATTAATAT ATTGCTCTCC	
AGAGGATACA CTATATGAAA TATATTAAAA GTCATTAATT	480
TTNATTCAAT GTTGTTTAGA	
GTTATGTTCA GTGTTTGGNA ATAGGATGTG TTTCTAAACC	540
GTCTTGGGTT CTATAATAAA	
TTCTATTCTT ANAGGTTT	559

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (E) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CATGTCCCTT CCTGAATACT GGGGAGAAGA GCACGTATGG	60
TGGGACGGCA GGGCTGCTTT	
TCATGGTGAG GTTGTCAGAC CTGCCTGTAC TCTGGCGATG	120
GAAGACGCCT GGCAGATTAT	
TGATATGGGG GAAACCCCGG TACGGATTTA CAGAATGGTT	180
TCTCCGGACC TGAAAGAAAA	
TTCAGCCTCC GGCTCAGGAA TTGTGAATTT AACAGTCAGG	240
GTGGGAACCT TTTCTCTGAT	
TCCCGGATAA GGGTGACTTT CGATGGCGTC CGGGGTGAAA	300
CGCCGGATAA GTTTAATTTA	
TCCGGTCAGG CAAAAGGCAT TAATCTGCAG ATAGCTGATG	360
TCAGGGGAAA TATTGCCCGG	
GCAGGAAAAG TAATGCCTGC AATACCATTG ACGGGTAATG	420
AAGAAGCGCT GGATTACACC	
CTCAGAATTG TGAGAACGGA AAAAACTTG AAGCCGAAA	480
TTATTTTGCT GTCTGGGATT	
A	481

(2) INFORMATION FOR SEQ ID NO: 122:

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(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

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CCATATAGTG ACTTCATTGA ACAAATGTA AATGGAATCT TGCTGGAGAA TGACCCACAT      60
ATATGGATAA AAGCTCTTTC ATTACTTGTT AGTGCAGATC ATAAACGTAG CGAGTTGGCG      120
TTCAATGCTA AAAAATATGC TTGTAAATTT GTAGGTGTCG AGTAAAAGA TATTTTTATT      180
TAATTGGTGC TATTGAATGT TTAAAAATCG AACTGATTGG TGTTTTAATA TTAATCATAG      240
GTTATGATGC AAAAATATAT TAGGCATTGC CTGCTTCAAT TAACTTGAGA GTGTAAGTTG      300
AATTGAAATA TGGTTATATG ATAAAGCAAT ATATGTTAAT ACATATGTCA ACCGAAAATG      360
CCATTATGTG TTTTTTACTT TATCTGTAAC GACACAATAT ATAAAATAAG GCTAATAATC      420
AAAACGCTTT TTAATTTGAT TGTTTTGAAT CAAGTGACTA AGAAATTCTC TTGCTGCAAA      480
TAACTCCCTT AGTGATTTTT TTTGAGTCTA TTTTATTCTC TGGGCATGGT CATGC          535

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(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

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CCGGCCCCAT AATGATGGTT TTATTAAGGT TAGCGCCGAC GGTTCGATG AACGATTTCA      60
GGTCGGTATC TTTAAAATTA GCGGTGAAAG TGGCTTCTTC CGCCCAGACC GGTGAACTGC      120
ATAATGCCGC TGCCAGCACC AGCGGCAGTA AACGCTTTTT TGTTTTGAGG CCAGTTGTCT      180
TCTTACGCCA GACCGACAAC GTCATATCAC GCCAAAACAC GATGAATGAT TCTCCTGGAT      240
TAAATGCGGT TAGCGCAGCG CGATGGAAAT GTCGTGGCGC GCACCCTTGC GTAAAACCGT      300
AAGTTGAATG GAATCCATTG AAGGTAAGTG CCGCATCAGA GCAATCATTG CTCGTGGATC      360
AGTGAAATCC TGCTGATTTA GCGCAAATGC GATATCGCCT TCCTTAAAC CG              412

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(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TAGCCTGTTT	ASCGTATATT	TGGGATGAGA	AGCCAAAGTG	GCTTTGGTGG	TGTCCCAGCC	60
CAGGTTTTTA	TTACTGCTGG	TTATTTACCT	TTCATGTTTT	TCAATAAAGT	TGTGACTCAG	120
TTGAAATCTG	CTGTCAATGC	TAATATGGGA	CTTTTTTGTT	ATAGACAAGT	GA CTCCTTTT	180
GCAACTTTTA	TAGCACGTTT	TATGCTAGAA	ACAATGGTGG	GCATGATTGT	CGGTATAATC	240
CTAGTACTAG	GATTATTGTG	GTTTGGCTTT	GATGCAATAC	CTGCGGATCC	ATTGCAAGTG	300
ATCCTTGGTT	ATTCTCTTCT	GATGCTGTTT	TCTTTTTCTC	TTGGTATTGT	ATTTTGTGTT	360
ATTTGTAATT	KRGC GARAGA	GGCAGATAAA	TTTCTTAGCT	TGTTAATGAT	GCCTTTGATG	420
TTTATCTCTT	GTGTTATGTT	TCCTCTTGCT	ACTATTCCCC	CTCAATATCA	GCATTGGGTT	480
TTTATGGAAT	CCACTTGTGC	ATGCTGTAGA	ACTAATCCGA	AGGGCATGGG	ATATCTGGGT	540
TATCGTAGTC	CTGATGTAAG	TTGGGCGTAT	CTGTCTG			576

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

TTACCAAGCA	GGATCTGATG	CAACTGGAAG	AAGGCTTTGA	ATATCGTATC	ATTGGCTGCT	60
CCATGTATAA	CATGTTGGCC	GCCGTACGCG	GTGCCTATGA	CAGCTTTGAA	AATGTCAAAG	120
GGGTGAATTG	CT					132

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GATTAGGGGT	CACTCAGGAT	TATAAAAAAG	CGGCAGAATA	CTATAAAAAA	GGTGATAAAA	60
ATAATGATAT	TACAGCACAA	TACCGTCTGG	CAAACTTTA	TGAACAAGGT	AACGGTGTA	120
AACGTGATTA	TCAACAAGCG	ATAAACCTTT	ACCTTAAACA	TATCAACAGA	ATGGATCACA	180
TCACTGCCCC	CAGTTTTGTG	GCTCTGGGTG	ATATCTATTC	TCTGGGATTS	GGGGTAGAGA	240
AAAACCCACA	ACTGGCTGAA	AAATGGTATC	AAAAAGCGAT	AGATGCAGCT	AATACACAAC	300
ATAACCAGGA	AATAAATCAT	TAAACGACAA	CACTTAATAC	CATATTGTGA	AGATGTTTCA	360

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ACATGGCGGA ATTCCCCTAT TCTTTGTTGG CGCTTACAAC AGACTATATT CCGCCATATC 420
 TGTCTTTATT GTGTATAAAC CATCGATACT GATGTTTGAT AGTGCTAAAT AATCATTGGC 480
 GCAATCACAA AGCCTAATGC CACTCCAGCA ATAATTCCCC CCAACCCAGG CAGCATAAAT 540
 GG 542

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GAACCACTTA GCGGCAGCTA TCGGGAATCG CCTGCTGAAA GACGGTCAGA CAGTGATTGT 60
 GATTACCGTG GCTGATGTTA TGAGTGCCCT GCACGCCAGC TATGACGATG GGCAGTCAGG 120
 CGAAAAATTT TTGCGGGAAC TGTGCGAAGT GGATCTGCTG GTTCTTGATG AAATTGGCAT 180
 TCAGGSCGAG ACGAAAAACG AAGCAGGTGG TACTGCACCA GATTGTTGAT CGCCGGACAG 240
 CGTCGATGCG CACGTGGGGA TRCTGACAAA CCTGAACTAT GAGGCCATGA AAACATTGCT 300
 CGGCGARCGG ATTATGGATC RCATGACCAT GAACGGCGGG CGATGGGTGA ATTTTAACTG 360
 GGAGACTGGC GTCCGAATGT CG 382

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGTCCCGCAC CCGGAAATGG TCAGCGAACC AATCAGCAGG GTCATCGCTA GAAATCATCC 60
 TTAGCGAAAG CTAAGGATTT TTTTATCTG AATTCTAGCC AGATCCCCGC TGATTTATGC 120
 TGGTTA 126

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

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ACCCCCAGCC TAGCTGGGGG TTTTCTGTGC AAAAAAATC CCGGCATAAT GGCCGGGATT 60
 TGGGAGCTTT CCCACTATTT CTTGATTCCT AAACGGAACA TATCAGTTGG GAATAAAGGT 120
 TGTATTATCA CTTTCATCATT ANAAATGAAT AATTTGGGCG ATAAAGCTGT TACGTCATAG 180
 ATATTTTCAG CGATTAATCT TAGANTTGAC CTAAAACTG GAATACTTGC ATCATCTGCA 240
 AAGACAAACA TGTCATCG 258

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AACCAGCGGT TCGCATCATC TCATCCCACT GACTCTCCGC TTTTGACAGA TCTGCATATC 60
 CTCGGGCCAA CTTATCCAGT ACTCCGTAGT TTGCCGATTT ATTACCCCGC CAGAACACCG 120
 CCTCACCTGC ATCGGCAAGC CGGGGGGAAA ACTGATACCC CAGTAGCCAG AACAGACCGA 180
 AAATAATATC GCTGCTACCC GCAGTGTCTG TCATGATTTT AACTGGATTC AGCCCTGTCT 240
 GCTGCTCAAG AAGTCCTTCC AGTACAAAAA TCGAATCCCG TAATGTACCG GGTACCACAA 300
 TGCCATGGAA CCCAGAGTAC TGATCAGATA CGAATTATAC CAGGTGATGC CTCGTCCAGA 360
 ACCAAAATAT TTTCTGTTAG ATCCTGAGTT GATGGTCTT 399

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AAATAACATC AACATACATT TGA CTGCGG GGGAAACGTT TACGGAGTCT TCATACTGGC 60
 ACTTTTTTAT GCTGCTGACT ACTCTTCGTC ATCGCCATCA ACATGCGCAC GAATCAGCGC 120
 CATAAACGGT TTGCCAAAGC GTTCCAGCTT GCGCATCCCA ACGCCGTTAA CGCTGAGCAT 180
 TTCGCTGGCG GTGATCGGCA TCTGTTTCAAG CATCTCAATC AAGGTTGCGT CGTTAAACAC 240
 CACGTACGGC GGGACATTAC TTTTCATCGGC TATCGATTTA CGCAGTTTGC GTAATTNGGC 300
 GAACAGTTTG CGATCATAGT TGNCGCCGAN CGATNTCTGC ATCGCTTTTCG GTTTGAGCGC 360
 CACGATACGC GGCACGGCAA TTGCAAAGAG GATTGCGCGC GCAGCACCGG GCGCGCGGCC 420
 TCTGTCAAGT GTAGGGCAGA ATGCTGGGCA ATATTTTGCG TCACCAGGCC GAGGTGAATC 480

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AGCTGGCGGA TCACGCTCAC CCAATGTTCA TGGCTTTTAT CACGGCCCAT GCCATAGACT	540
TTCAGTTTGT CATGACCATA GTCGCGGATA CGCTGGTTAT TAGCACCACG AATCACTTCC	600
ACCACATAAC CCATCCCAAA CCGCTGATTC ACACGACCAA TGGTGGAAAG GGCAATCTGA	660
GCATCGGTTG AACCGTCGTA CTGTTTCGGC GGATCGAGGC AGATATCGCA GTTCNCCGCA	720
CGGCTCCTGA CGCCTTCGC CAAAA	745

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

AGAATGGCGG CTTCTTGCCC CCCTTGCCC CGGTCCTGAC TAGCATGGCT GGAGTCCAGT	60
GTCCAGGCCA CGACCATGCT CATCATGGAA GCAGCTTTTG TAGTACANTC GCAGCTTATT	120
TTCCTGGAAC GAAATGTCTG GCATCGTGGT GCATAACATA ACCCCCAATG CCCAGCAGAT	180
GCACAGAAGG TTCTAGAATC GCCCACTGAT ATCCCATACA AAATTTACCA AAACGTGTTC	240
GTATTTCTCG TATAAATAAT GTCTCTATGG TGACGTTCTA GACTTCAAAC CCACTTTTTG	300
AATTTGATGA TGTGCTCCTA ATCTCTTCAG GAATGTAACG CCCTTGGTTT ACAGCTACCA	360
ATACACTGGA GGTATACTTA TCTGCAACTG GATGAACTAG ATGTACTTGA GCAAACATTT	420
CATAAGCTCG ACGACAGTT	439

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CTGGAAAGCG ACGTTGATGG ATTAATGCAG TCGGTAAAAC TGAACGCTGC TCAGGCAAGG	60
CAGCAACTTC CTGATGACGC GACGCTGCGC CACCAANTCA TGGAACGTTT GATCATGGAT	120
CAAMTCATCC TGCAGATGGG GCAGAAAATG GGAGTGAAAA TCTCCGATGA GCAGCTGGAT	180
CAGGCGATTG CTAACATCGC GAAACAGNAC AACATGACGC TGGATCAGAT GCGCACCGTC	240
TGGCTTACGA TGGACTGAAC TACAACACCT ATCGTAACCA GATCCGCAA GAGATGATTA	300
TCTCTGAAGT GCGTAACAAC GAGGTGCGTC GTCGNATCAC CATCCTGCCG	350

(2) INFORMATION FOR SEQ ID NO: 134:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCCCAAGATT GCTAACAAAT GCGCGTTGTT CATGCCGGAT GCGGCGTGAC CGCCTTATCC	60
GGCCTACGAA ACCGCAAGAA TTCAATATAT TGCAGGAGCG GTGTAGGCCT GATAAGCGTA	120
GCGAWTCAGG CAGTTTTGCG TTTGCCCGCA ACCTTAGGGG ACATTTAGCG ACCCCATTTA	180
TTTCTCACTT TTCCGCCTCA TCATCGCGCG TTAATTTCTT TCATGAATCA CGCTTTACAA	240
TATCCAGCGC GCGCANAACG GTACTGGCAG GGATCTGAAT TTTCTCCAG CAGCACAATC	300
AAATCGACAG CCAGTTTGAC ATCGTCAAGG GGCATTTTCC CAGTGACATA ATCTCTCCAT	360
TGCTAAGCGG GTTAAAACGC GCTAACCTGT TTCGATTTTT	400

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CTATCCTTAT GACCACCCAA CTACNTCATT TACACCCAAA CCAGCGATCT GAATAAAGAA	60
GCGATTGCCC AGTTACGACT GGGCGGAAAA TGCGCGTAAG GATGAAGTAA AGTTTCAGTT	120
GAGCCTGGCA TTTCCCTGTG GCGTGGGATT TTAGGCCCCGA ACTCGGTGTT GGGTGCGTCT	180
TATACGCAAA AATCCTGGTG GCAACTGTCC AATAGCGAAG AGTCTTCACC GTTTCGTGAA	240
ACCAACTACG AACCGCAATT GTTCCTCGGT TTTGCCACCG ATTACCGTTT TGCAGGTTGG	300
ACTGCGCGAT GTGGAGATGG GGTATAACCA CGACTCTAAA CGGGCGTTCC GACCCGACCT	360
CCCGCAGCTG GAACCGCCTT TATACTCGCC TGATGGCAGA AAACGGTAAC TGGCTGGTAG	420
AAGTGAAGCC GNGGTATGTG GTGGGTAATA CTGACGATAA CCC	463

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 584 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

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TTGGTCAGCC GTACCTGAAT GGGGGCTGAT GCCCGGCTGG TTAATGGCAG GTGGTCTGAT      60
CGCCTGGTTT GTCGGTTGGC GCAAAACACG CTGATTTTTT CATCGCTCAA GGGGGGCCGT      120
GTAACGTATA ATGCGGCTTT GTTTAATCAT CATCTACCAC AGAGGAACAT STATGGGTGG      180
TATCAGTATT TGGCAGTTAT TGATTATTGC CGTCATCGTT GTACTGCTTT TTGGCACCAA      240
AAAGCTCGGC TCCATCGGTT CCGATCTTGG TCGTCGATC AAAGGCTTTA AAAAAGCAAT      300
GAGCGATGAT GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC      360
TATCGCCGAT AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACBCGAAGCC      420
TACGNTAAAG AGCAGGTGTA ATCCGTGTTT GATATCGGTT TTAGCGNACT GCTATTGGTG      480
TTCATCATCG GCCTCGTCGT TCTGGGGSCG CAACGACTGC CTGTGGCGGT AAAAACGGTA      540
GCGGGCTGGA TTCGCGCGTT GCGTTCCTG GCGACAACGG TGCA                          584

```

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

GCAGGCAGGA GGAAGTCCCC AGTGATACGG TTATTCGTGA TGGCGGAGGG CAGAGCCTTA      60
ACGGACTGGC GTTGAACACC ACGCTGGATA ACAGAGTTGA GCATTGGNTA CACGGGGGAG      120
GGAAAGCAGA CGTTACAATT ATTAACCAGG ATGTTTACCC AGACCATAAA ACATGGCGGA      180
TTGGCAACCG NAACCATCGT CAACACCGTT GCAGAAGKTG GTCCGGAGTC TGAAAATGTG      240
TCCAGCGGTC AGATGGTCGG AGGGACGGCT GAATCCACCA CCATCAACAA AAATGGCCGG      300
CAGTTATCTG GTCTTCGGGG ATGGCACGGG ACACCCTCAT TTGCGCTGGT GGTGACCAGA      360
CGGTACACGG AGAGGCACAT AACACCCGAC TGGAGGGAGG TTAACCAGTA TGTACACAAC      420
GGTGGCACGG CAACAGAGAC GCTGATAAAC CGTGATGGCT GGCAGGTGAT TAAGGAAGGA      480
GGGAAGTGCC GGCGCATTAC CACCATCAAN CCNGAAAAGG GAAANCT                      527

```

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

GTCAGTCTCT GGGGGAAGTG CGTGTTCGGA CCGGGGAAAT GTGCTGGAGA AAGTTATTGA      60

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```

AGGGGCTTAC GAGGTGGTGG GGTTTTTTGA CCGGATTGAG GAAAAGCGTG ATGCCATGCA      120
GTCGCTGATT CTGCCGCCAC CGGAGGCCAG GCGCTGGCAC AGGCGGCACT GACTTACCGT      180
TATGGTGACG AACMTCARCC CGTCACCACC GCCGACATTC TACACCACG ACCCGGGGAR      240
GATTACGGTA AGGACCTGTG GAGTGGTTAT CAGACCATTC AGGAGAATAT GCTGAAAGGC      300
GGAATTTCCG GTCGCAGTGC CAGAGGAAAA CGTATCCATA CCGGTGCCAT TCACAGCATC      360
GACACCGACA TTAAGCTCAA CCGCGCATTG TGGGTGATGG CTGAAACGCT GCTGGAGAGT      420
ATGCGCTGAT GCCGTTTCCN T                                          441

```

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

CGAGCGAGAT GAACTTCGAG GGCGGTGTGA GCCAGTCGGC TTACGAGACA CTGGCGGCGC      60
TTAATCTGCC GAAACCGCAG CAAGGGCCGG AAACCATTAA TCAGGTTACC GAGCATAAGA      120
TGTCAGCTGA GTAAGCCTGT ATGCCGGATA AGGCGCTCGC GCCNATTCCG ATGAAATAAG      180
GCGCATCGGG CCTGAAGGAA AGCCGTATGN ATACACCCGC AGCCCGCATC CGGCAAGTTA      240
CAACAAATAA CCTTTAACCA TGCTTTTTGA TGTTTTTCAG CAATACCCCG CGGCGATGCC      300
CATACTGGCA ACCGTCGGGA GGGATTGATC ATCGGCAGTT TTTTGAATGT GGTGATTGG      360
GCGTTACCCC ATCATGCTGC GCCAACAAAT GGCGGAGT                          398

```

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

GCCGAACAGA CACAGCAATA TGAACCCTGC CAGCGCAGAC GCTTGCTGAT TAATGCTCTG      60
AACAAAAGGC GAAGAATGGC AAATCCTGCG ATCAGCAAAG TCAGCGCACC GACTATCTGT      120
AACATAGTCA CTCCGTGATG AATATCATGT GTATTGTGAA TGCCAGTGAA TGTGGCACTG      180
AAGCGTTTGC ACCTGTCCGG GTCCCGSTCA TGATGACCGS AACAGAGAGA CAATGCCGAA      240
TTATCAGAAG GTCACATTCA GTGTGGCTTG GCCGTTATAA CCTTCAGCGC TGCTGCCGCT      300
GACGCTGTGG GCATAACCGG CCTGAACGCC CAGGGTGATA TTTTCCCGGA CACGGGCTTC      360

```

-237-

CAGTCCGGCC TGCAGCTCCA GTGACGTGCC ATTCGGGGAC GGTGAGAACG TCATGTTACT 420
GCCGGCTGCG GCTGTACCCA TGCTCATGTC TCCCCGGGAG CTGAAGGTGC GGATAACAGA 480
AGGCTGTACC CACCCGTTCA CCGGCAGTTC ACGCACACTG TGTTTTGCAC TGTCACGCAA 540
GGTGTACGG GATGAGGTGC CTTCANCAAA AGGTCATATT 580

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGCGGACATC CAGCGTCCG CCATCATCCA CACGGGTTCT GGTGGCTGTG TGTCCGGTCA 60
GCACATCCAG ACGGCGGCCA TTTTCCAGTA CGACATTATC AGCTTTACCC TCCACAACAG 120
AGAATGCTCC CAGGCGGTTT GTGCCGGTGA CGGTTGCAGC AGTGCTGGTA ACCAGTGCTC 180
CGCCCGTGTT CTGGGTGACA TCAGACGCTT TACCGCCGGC ATTCACCTGC AGCTTTCCTT 240
TCTGGTTGAT GGTGGTATGC GCGGCAGTTC CTCCTTCCTT AATCAMCTGC CAGCCATCAC 300
GGTTTATCAG CGTCTCTGTT GCCGTGCCAA CGTTGTGTAC ATACTGGTTA MCTCCCTCCA 360
GTCGGGTGTT AWGTGCTCT CCGTGTANCG TCTGGTCANC AACACGCAA ATGANGGTGT 420
CCCGTGCCAT CCCCAGAGAC CAGTAA 446

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGAATACGTT AAGTCAGCAG ACCGGCGGAG ACAGTCTGAC ACAGACAGCG CTGCAGCAGT 60
ATGAGCCGGT GGTGGTTGGC TCTCCGCAAT GGCACGATGA ACTGGCAGGT GCCCTGAATA 120
ATATTGCCGG AGTTCGCCAC TGACCGGTCA GACCGGTATC AGTGATGACT GGCCACTGCC 180
TTCCGTCAAC AATGGATACC TGGTTCCGTC CACGGACCCG GACAGTCCGT ATCTGATTAC 240
GGTGAACCCG AACTGGATR GTCTCGGACA GGTGGACAGC CATTTGTTN CCGGACTGTA 300
TGAGCTTCTT GGAGCGAAAC CGGGTCA 327

-238-

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>5</u> , line <u>8</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection (ATCC)	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 23, 1996	Accession Number 97726
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
DNA plasmid PAI-1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>5</u> , line <u>8</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection (ATCC)	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 23, 1996	Accession Number 97727
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
DNA plasmid PAI-2	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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-240-

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>5</u> , line <u>14</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection (ATCC)	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 23, 1996	Accession Number 98176
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
Escherichia coli, 596	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
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What Is Claimed Is:

1 1. An isolated nucleic acid molecule, comprising a polynucleotide
2 having a nucleotide sequence at least 95% identical to a sequence selected from
3 the group consisting of:

4 (a) a nucleotide sequence of an open reading frame depicted in one of
5 Tables 1 through 4;

6 (b) a nucleotide sequence beginning with the first initiation codon
7 encountered reading 5' to 3' in an open reading frame depicted in one of Tables 1
8 through 4, and ending with the 3' terminal stop codon;

9 (c) a nucleotide sequence beginning with the first initiation codon
10 encounter reading 5' to 3' in an open reading frame depicted in one of Tables 1
11 through 4, and ending with the nucleotide preceeding the 3' terminal stop codon;

12 (d) a nucleotide sequence of (a) excluding codons for amino acids
13 eliminated during processing of the putative protein identified in one of Tables 1
14 through 4; or

15 (e) a nucleotide sequence that is complementary to any of the
16 nucleotide sequences in (a), (b), (c), or (d).

1 2. An isolated nucleic acid molecule of claim 1, wherein said
2 nucleotide sequence is 100% identical to the nucleotide sequence of an open
3 reading frame depicted in Tables 1 through 4, or a complement thereof.

1 3. An isolated nucleic acid molecule, comprising a polynucleotide that
2 hybridizes under stringent hybridization conditions to a nucleic acid molecule of
3 claim 2.

1 4. An isolated nucleic acid molecule, comprising a polynucleotide that
2 encodes the amino acid sequence of an epitope-bearing portion of an *E. coli* J96
3 PAI protein encoded by an open reading frame depicted in one of Tables 1
4 through 4.

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1 5. A method of making a recombinant vector, comprising inserting
2 an isolated nucleic acid molecule of claim 1 into a vector.

1 6. A recombinant vector produced by the method of claim 5.

1 7. A method of making a recombinant host cell, comprising
2 introducing a recombinant vector of claim 6 into a host cell.

1 8. A recombinant host cell produced by the method of claim 7.

1 9. A recombinant method for producing an *E. coli* J96 PAI
2 polypeptide, comprising culturing a recombinant host cell of claim 8 under
3 conditions such that said polypeptide is expressed and recovering said polypeptide.

1 10. An isolated polypeptide of an *E. coli* J96 PAI IV or PAI V protein
2 encoded by a polynucleotide of claim 1.

1 11. An isolated polypeptide of an *E. coli* J96 PAI IV or PAI V protein
2 encoded by a polynucleotide of claim 2.

1 12. An isolated polypeptide comprising an immunogenic epitope of an
2 *E. coli* J96 PAI IV or PAI V protein encoded for by an open reading frame
3 depicted in one of Tables 1, 2, 3 or 4.

1 13. A vaccine, in dosage form, comprising
2 (a) a pharmaceutically acceptable diluent, carrier, or excipient, and
3 (b) an antigen selected from the group consisting of:
4 (i) a polypeptide having an amino acid sequence at least 95% identical to
5 an amino acid sequence encoded by a uropathogenic *E. coli* J96 PAI IV or PAI
6 V open reading frame depicted in Tables 1, 2, 3 or 4, and
7 (ii) a polypeptide comprising an immunogenic epitope of an *E. coli* J96
8 PAI IV or PAI V protein encoded for by an open reading frame depicted in one
9 of Tables 1, 2, 3 or 4;

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10 wherein said antigen is present in an amount effective to elicit protective immune
11 responses in an animal to pathogenic *E. coli*.

1 14. An isolated antibody that binds specifically to a polypeptide of
2 claim 10 or 11.

1 15. An antibody having binding affinity to a polypeptide according to
2 claim 12.

1 16. A method of detecting a pathogenic *E. coli* antigen in a sample,
2 comprising:

- 3 (a) contacting said sample with an antibody according to claim 14 or
4 15 under conditions such that immunocomplexes form, and
5 (b) detecting the presence of said antibody bound to said antigen.

1 17. A diagnostic kit comprising:

- 2 (a) a first container means containing an antibody according to claim
3 14 or 15 and
4 (b) second container means containing a conjugate comprising a
5 binding partner of said antibody and a label.

1 18. A hybridoma which produces an antibody according to claim 14
2 or 15.

1 19. A method of detecting the presence of antibodies to pathogenic *E.*
2 *coli* in a sample, comprising:

- 3 (a) contacting said sample with a polypeptide according to one of
4 claims 10, 11 or 12 under conditions such that immunocomplexes form, and
5 (b) detecting the presence of said antibody bound to said antigen.

1 20. A kit for detecting the presence of antibodies to pathogenic *E. coli*
2 in a sample comprising at least one container means having disposed therein a
3 polypeptide according to one of claims 10, 11 or 12.

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1 21. Computer readable medium having recorded thereon one or more
2 nucleotide sequences depicted in SEQ ID NOs: 1 through 142, or nucleotide
3 sequences at least 99.9% identical thereto.

1 22. Computer readable medium having recorded thereon a nucleotide
2 sequence of at least one uropathogenic *E. coli* J96 pathogenicity island open
3 reading frame depicted in Tables 1 through 4, or a complement thereof.

1 23. The computer readable medium of claim 21, wherein said medium
2 is selected from the group consisting of a floppy disc, a hard disc, random access
3 memory (RAM), read only memory (ROM), and CD-ROM.

1 24. The computer readable medium of claim 22, wherein said medium
2 is selected from the group consisting of a floppy disc, a hard disc, random access
3 memory (RAM), read only memory (ROM), and CD-ROM.

1 25. A computer-based system for identifying fragments of
2 uropathogenic *E. coli* J96 pathogenicity islands PAI IV and PAI V that are
3 homologous to target nucleotide sequences, comprising:

4 a) a data storage means comprising a nucleotide sequence of
5 SEQ ID NOs: 1 through 142, or a nucleotide sequence at least 99.9% identical
6 thereto;

7 b) a search means for comparing a target sequence to said
8 nucleotide sequence of said data storage means of step (a) to identify a
9 homologous sequence, and

10 c) a retrieval means for obtaining said homologous sequence
11 of step (b).

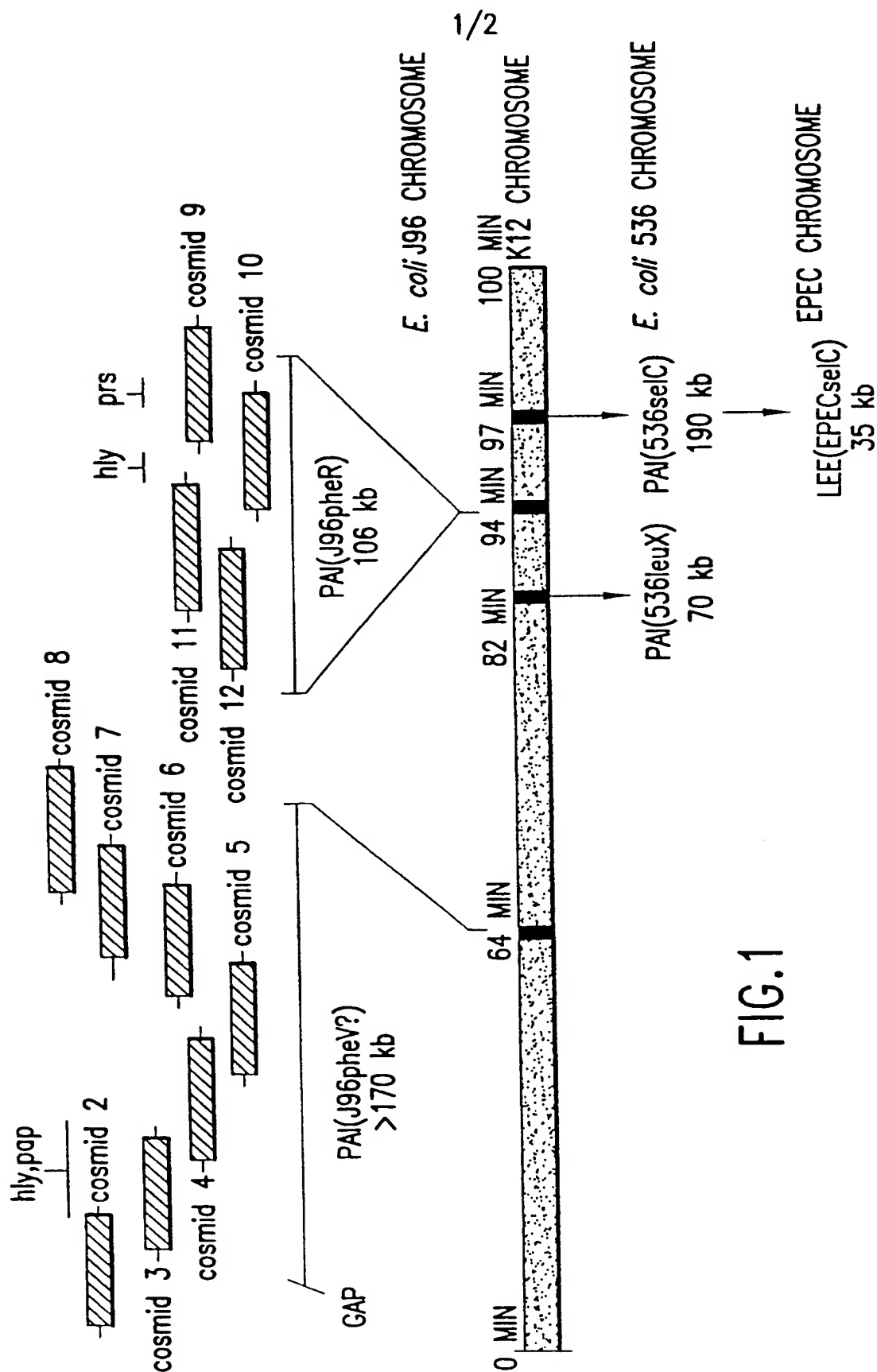


FIG.1

2/2

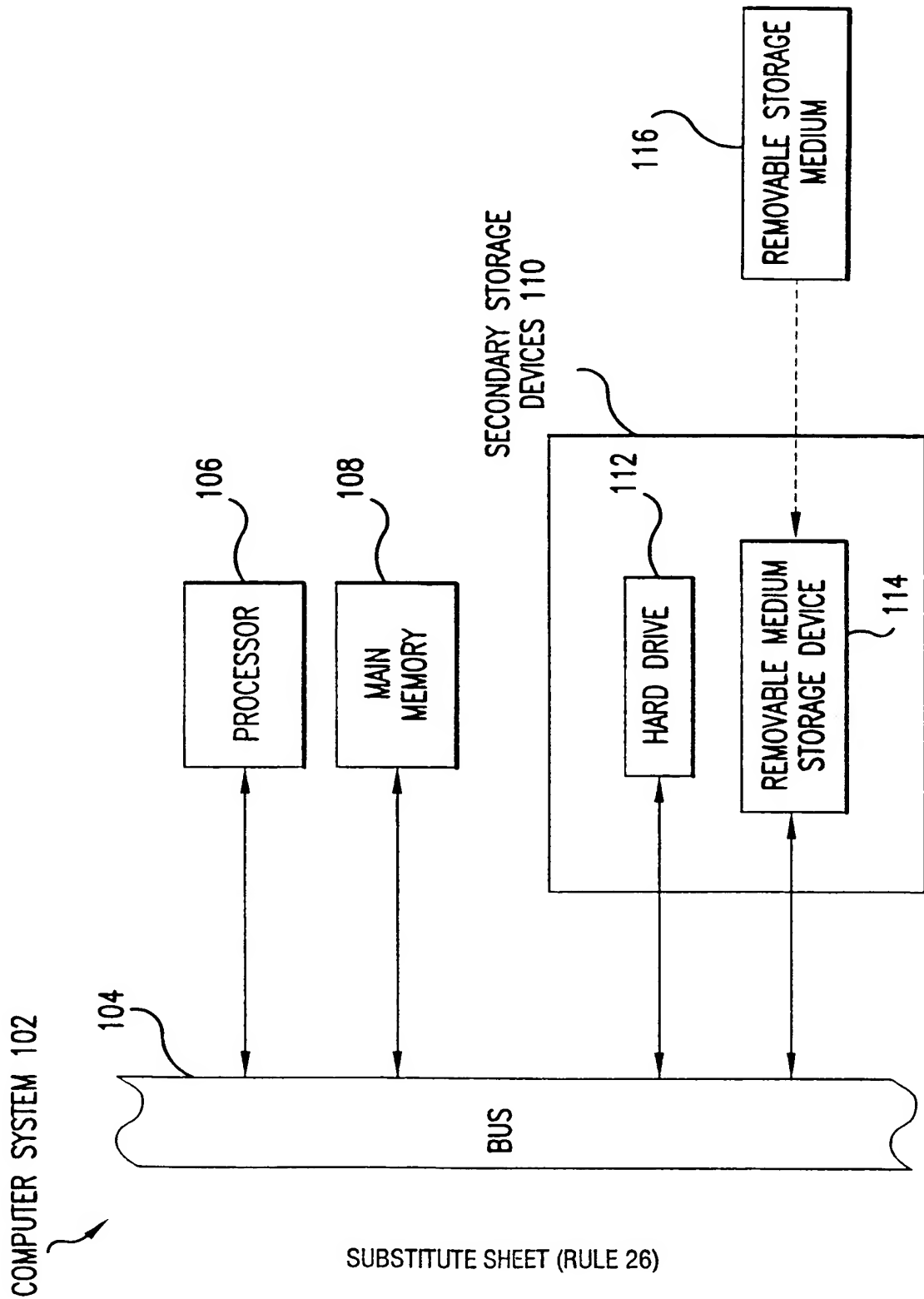


FIG.2

SUBSTITUTE SHEET (RULE 26)

Applicant's or agent's file reference number 1488.074PC02	International application No. PCT/US97/21347
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 8.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☒

Name of depositary institution
American Type Culture Collection (ATCC)

Address of depositary institution (including postal code and country)
12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit September 23, 1996	Accession Number 97726
---------------------------------------	---------------------------

C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet ☐

DNA plasmid PAI-1

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)

E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")

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reference number 1488.074PC02

International application No.
PCT/US97/21347

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Address of depositary institution (including postal code and country)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit
September 23, 1996

Accession Number
97727

C. ADDITIONAL INDICATIONS (leave blank if not applicable)

This information is continued on an additional sheet ☐

DNA plasmid PAI-2

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

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International application No.
PCT/US97/21347

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
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Address of depositary institution (including postal code and country)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit
September 23, 1996

Accession Number
98176

C. ADDITIONAL INDICATIONS (leave blank if not applicable)

This information is continued on an additional sheet ☐

Escherichia coli, 596

The applicants hereby request that, until either a Canadian patent has been issued on the basis of the application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the furnishing of a sample of deposited biological material referred to in the application only be effected to an independent expert nominated by the Commissioner of Patents.

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E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification⁶ :
C12N 15/31, 5/16, C07K 14/245, 16/12,
A61K 39/108, G01N 33/68, G06F 17/30

A2

(11) International Publication Number:

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60/061,953	14 October 1997 (14.10.97)	US

(71) Applicants (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).

(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).

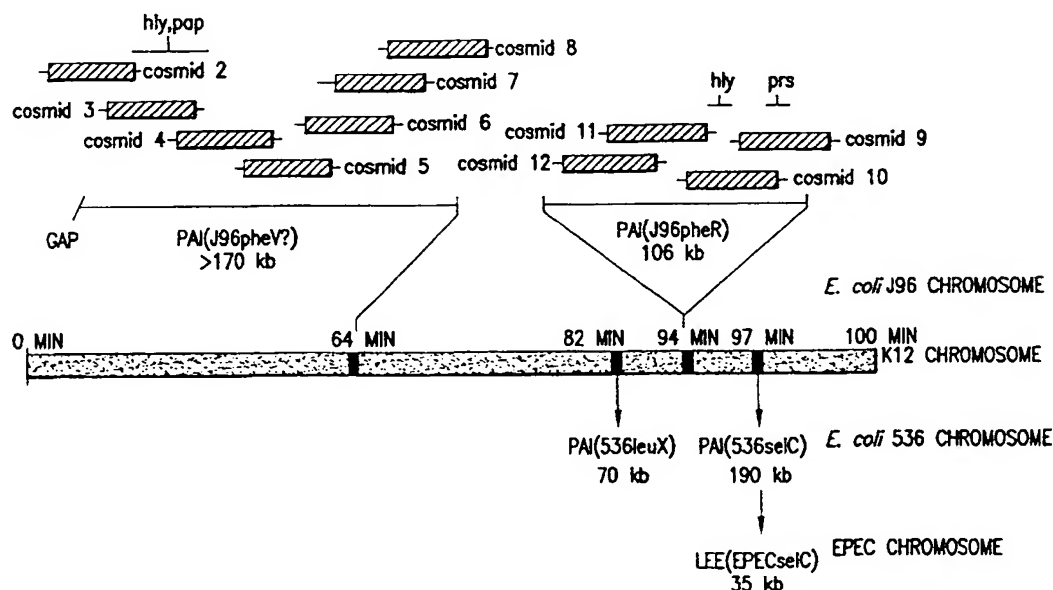
(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

With an indication in relation to a deposited microorganism furnished under Rule 13bis separately from the description.

Date of receipt by the International Bureau:
20 March 1998 (20.03.1998)

(54) Title: NUCLEOTIDE SEQUENCE OF *ESCHERICHIA COLI* PATHOGENICITY ISLANDS

(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

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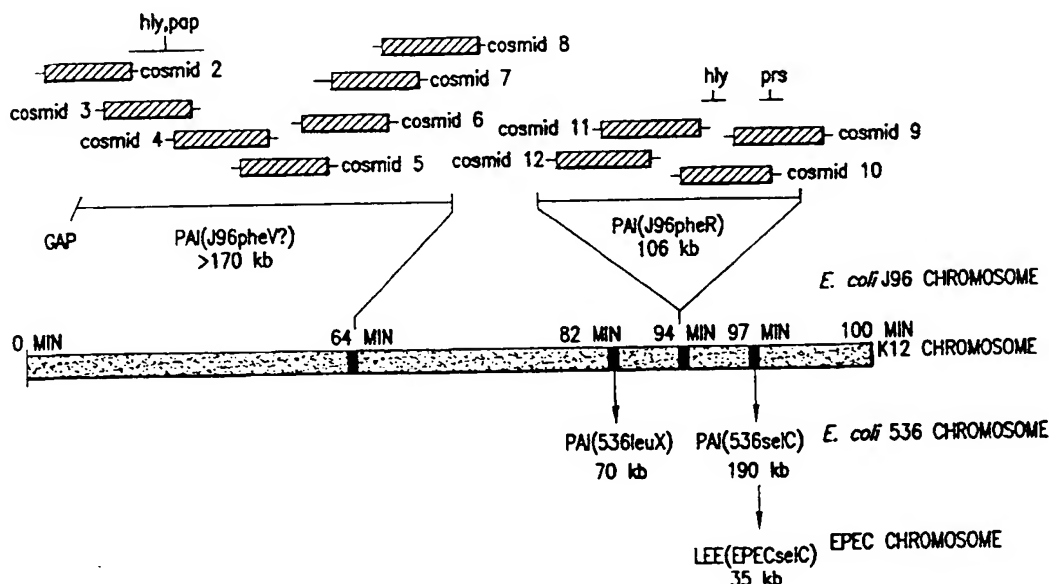


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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/11, 15/63, C07K 16/12, G01N 33/569, G06F 17/30, G11B 7/00		A3	(11) International Publication Number: WO 98/22575
		(43) International Publication Date:	28 May 1998 (28.05.98)
(21) International Application Number: PCT/US97/21347		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 21 November 1997 (21.11.97)		Published With international search report. With an indication in relation to a deposited microorganism furnished under Rule 13 ^{bis} separately from the description. Date of receipt by the International Bureau: 20 March 1998 (20.03.98)	
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(71) Applicants (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). UNIVERSITY OF WISCONSIN [US/US]; 1300 University Avenue, Madison, WI 53706 (US).			
(72) Inventors; and (75) Inventors/Applicants (for US only): DILLON, Patrick, J. [US/US]; 7508 Boxberry Terrace, Gaithersburg, MD 20879 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). WELCH, Rodney, A. [US/US]; 410 Ridge Street, Madison, WI 53705 (US).			
(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).			

(54) Title: NUCLEOTIDE SEQUENCE OF *ESCHERICHIA COLI* PATHOGENICITY ISLANDS

(57) Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/21347

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/11 C12N15/63 C07K16/12 G01N33/569 G06F17/30
G11B7/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SWENSON D.L.: "Two pathogenicity islands in Escherichia coli J96: cosmid cloning and sample sequencing" INFECTION AND IMMUNITY, vol. 64, no. 9, September 1996, pages 3736-3743, XP002069149 WASHINGTON US cited in the application see the whole document ---	1-12, 14-17
X	Database EMBL, Heidelberg, DE AC: u59875 12-NOV-1996 Yersinia pestis pesticin plasmid putative insertion sequence IS100 XP002069557 & MCDONOUGH K.A. ET AL.: J.BACTERIOL., vol. 179, 1997, pages 2081-2085, ---	1-12
	-/--	

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

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O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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Date of the actual completion of the international search

29 June 1998

Date of mailing of the international search report

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Authorized officer

Panzica, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 97/21347

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EMBL, Heidelberg, DE AC z32853 05-MAY-1994 Yersinia pestis insertion sequence IS100 XP002069152 see abstract & PODLACHIKOVA O. ET AL.: FEMS MICROBIOL. LETT., vol. 121, 1994, pages 269-274, ---	1-12
A	BURLAND V. ET AL.: "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes" NUCLEIC ACID RESEARCH, vol. 23, 1995, pages 2105-2119, XP000612159 OXFORD, GB -----	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/21347

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 97/21347

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-20 (partially)

Invention 1.

An isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence consisting of the sequence of the ORF ID 2 (Contig Id.No.65 Start: nt1902 Stop: nt1042) and uses thereof.

2. Claims: 1-20 (partially)

Inventions 2 to 175:

same as invention 1, but according to each single ORF ID as set forth in Tables 1 through 4, starting from the second of the list (2: Contig ID 65, ORF ID 3, start: nt2096 stop: nt1821; 3: Contig ID 63, ORF ID 11, start: nt7856 stop: nt9238; ... 175: Contig ID 24, ORF ID 1, start: nt492, stop: nt4)

3. Claims: 21-24

Invention 176.

A computer readable medium having recorded thereon nucleotide sequences depicted in SEQ.ID.NOs.1 through 142 or sequences at least 99.9% identical thereto, or a complementary thereof.
Said computer readable medium selected from floppy disc, hard disc, RAM, ROM, CD-ROM.

4. Claim : 25

Invention 177.

A computer-based system for identifying fragments of uropathogenic E.coli J96 pathogenicity islands PAI IV and PAI V that are homologous to target nucleotide sequences, comprising:

a) A data storage means comprising nucleotide sequences out of SEQ.ID.NOs:1 through 142 or a nucleotide sequence at least 99.9% identical thereto,

b) A search means for comparing a target sequence to said nucleotide sequence of said data storage means of step a) to identify a homologous sequence,

c) A retrieval means for obtaining said homologous sequence of step b).

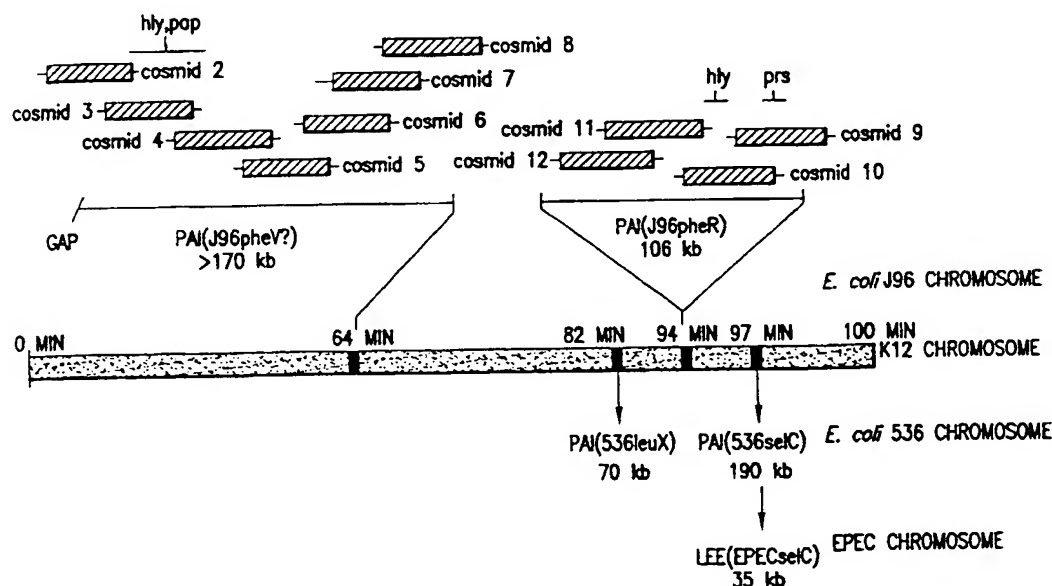


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(74) Agents: STEFFE, Eric, K. et al.; Sterne, Kessler, Goldstein & Fox P.L.L.C., Suite 600, 1100 New York Avenue, N.W., Washington, DC 20005-3934 (US).			

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Nucleotide Sequence of *Escherichia coli* Pathogenicity Islands

Background of the Invention

Field of the Invention

5 The present invention relates to novel genes located in two chromosomal regions within *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs).

Related Background Art

10 *Escherichia coli* (*E. coli*) is a normal inhabitant of the intestine of humans and various animals. Pathogenic *E. coli* strains are able to cause infections of the intestine (intestinal *E. coli* strains) and of other organs such as the urinary tract (uropathogenic *E. coli*) or the brain (extraintestinal *E. coli*). Intestinal pathogenic *E. coli* are a well established and leading cause of severe infantile diarrhea in the developing world. Additionally, cases of newborn meningitis and sepsis have
15 been attributed to *E. coli* pathogens.

 In contrast to non-pathogenic isolates, pathogenic *E. coli* produce pathogenicity factors which contribute to the ability of strains to cause infectious diseases (Mühldorfer, I. and Hacker, J., *Microb. Pathogen.* 16:171-181 1994). Adhesions facilitate binding of pathogenic bacteria to host tissues. Pathogenic
20 *E. coli* strains also express toxins including haemolysins, which are involved in the destruction of host cells, and surface structures such as O-antigens, capsules or membrane proteins, which protect the bacteria from the action of phagocytes or the complement system (Ritter, *et al.*, *Mol. Microbiol.* 17:109-212 1995).

 The genes coding for pathogenicity factors of intestinal *E. coli* are located
25 on large plasmids, phage genomes or on the chromosome. In contrast to intestinal *E. coli*, pathogenicity determinants of uropathogenic and other extraintestinal *E. coli* are, in most cases, located on the chromosome. *Id.*

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Large chromosomal regions in pathogenic bacteria that encode adjacently located virulence genes have been termed *pathogenicity islands* ("PAIs"). PAIs are indicative of large fragments of DNA which comprise a group of virulence genes behaving as a distinct molecular and functional unit much like an island within the bacterial chromosome. For example, intact PAIs appear to transfer between organisms and confer complex virulence properties to the recipient bacteria.

Chromosomal PAIs in bacterial cells have been described in increasing detail over recent years. For example, J. Hacker and co-workers described two large, unstable regions in the chromosome of uropathogenic *Escherichia coli* strain 536 as PAI-I and PAI-II (Hacker J., *et al.*, *Microbiol. Pathog.* 8:213-25 1990). Hacker found that PAI-I and PAI-II containing virulence regions can be lost by spontaneous deletion due to recombination events. Both of these PAIs were found to encode multiple virulence genes, and their loss resulted in reduced hemolytic activity, serum resistance, mannose-resistant hemagglutination, uroepithelial cell binding, and mouse virulence of the *E. coli*. (Knapp, S *et al.*, *J. Bacteriol.* 168:22-30 1986). Therefore, pathogenicity islands are characterized by their ability to confer complex virulence phenotypes to bacterial cells.

In addition to *E. coli*, specific deletion of large virulence regions has been observed in other bacteria such as *Yersinia pestis*. For example, Fetherston and co-workers found that a 102-kb region of the *Y. pestis* chromosome lost by spontaneous deletion resulted in the loss of many *Y. pestis* virulence phenotypes. (Fetherston, J.D. and Perry, R.D., *Mol. Microbiol.* 13:697-708 1994, Fetherston, *et al.*, *Mol. Microbiol.* 6:2693-704 1992). In this instance, the deletion appeared to be due to recombination within 2.2-kb repetitive elements at both ends of the 102-kb region.

It is possible that deletion of PAIs may benefit the organism by modulating bacterial virulence or genome size during infection. PAIs may also represent foreign DNA segments that were acquired during bacterial evolution that conferred important pathogenic properties to the bacteria. Observed flanking

-3-

repeats, as observed in *Y. pestis* for example, may suggest a common mechanism by which these virulence genes were integrated into the bacterial chromosomes.

Integration of the virulence genes into bacterial chromosomes was further elucidated by the discovery and characterization of a locus of enterocyte effacement (the LEE locus) in enteropathogenic *E. coli* (McDaniel, *et al.*, *Proc. Natl Acad. Sci. (USA)* 92:1664-8 1995). The LEE locus comprises 35-kb and encodes many genes required for these bacteria to "invade" and degrade the apical structure of enterocytes causing diarrhea. Although the LEE and PAI-I loci encode different virulence genes, these elements are located at the exact same site in the *E. coli* genome and contain the same DNA sequence within their right-hand ends, thus suggesting a common mechanism for their insertion.

Besides being found in enteropathogenic *E. coli*, the LEE element is also present in rabbit diarrheal *E. coli*, *Hafnia alvei*, and *Citrobacter freundii* biotype 4280, all of which induce attaching and effacing lesions on the apical face of enterocytes. The LEE locus appears to be inserted in the bacterial chromosome as a discrete molecular and functional virulence unit in the same fashion as PAI-I, PAI-II, and *Yersinia* PAI.

Along these same lines, a 40-kb *Salmonella typhimurium* PAI was characterized on the bacterial chromosome which encodes genes required for *Salmonella* entry into nonphagocytic epithelial cells of the intestine (Mills, D.M., *et al.*, *Mol. Microbiol.* 15:749-59 1995). Like the LEE element, this PAI confers to *Salmonella* the ability to invade intestinal cells, and hence may likewise be characterized as an "invasion" PAI.

The pathogenicity islands described above all possess the common feature of conferring complex virulence properties to the recipient bacteria. However, they may be separated into two types by their respective contributions to virulence. PAI-I, PAI-II, and the *Y. pestis* PAI confer multiple virulence phenotypes, while the LEE and the *S. typhimurium* "invasion" PAI encode many genes specifying a single, complex virulence process.

It is advantageous to characterize closely-related bacteria that contain or do not contain the PAI by the isolation of a discrete molecular and functional unit

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on the bacterial chromosome. Since the presence versus the absence of essential virulence genes can often distinguish closely-related virulent versus avirulent bacterial strains or species, experiments have been conducted to identify virulence loci and potential PAIs by isolating DNA sequences that are unique to virulent bacteria (Bloch, C.A., *et al.*, *J Bacteriol.* 176:7121-5 1994, Groisman, E.A., *EMBO J.* 12:3779-87 1993).

At least two PAIs are present in *E. coli* J96. These PAIs, PAI IV and PAI V are linked to tRNA loci but at sites different from those occupied by other known *E. coli* PAIs. Swenson *et al.*, *Infect. and Immun.* 64:3736-3743 (1996).

The era of true comparative genomics has been ushered in by high through-put genomic sequencing and analysis. The first two complete bacterial genome sequences, those of *Haemophilus influenzae* and *Mycoplasma genitalium* were recently described (Fleischmann, R.D., *et al.*, *Science* 269:496 (1995); Fraser, C.M., *et al.*, *Science* 270:397 (1995)). Large scale DNA sequencing efforts also have produced an extensive collection of sequence data from eukaryotes, including *Homo sapiens* (Adams, M.D., *et al.*, *Nature* 377:3 (1995)) and *Saccharomyces cerevisiae* (Levy, J., *Yeast* 10:1689 (1994)).

The need continues to exist for the application of high through-put sequencing and analysis to study genomes and subgenomes of infectious organisms. Further, a need exists for genetic markers that can be employed to distinguish closely-related virulent and avirulent strains of a given bacteria.

Summary of the Invention

The present invention is based on the high through-put, random sequencing of cosmid clones covering two pathogenic islands (PAIs) of uropathogenic *Escherichia coli* strain J96 (O4:K6; *E. coli* J96). PAIs are large fragments of DNA which comprise pathogenicity determinants. PAI IV is located approximately at 64 min (near *pheV*) on the *E. coli* chromosome and is greater than 170 kilobases in size. PAI V is located at approximately 94 min (at *pheR*) on the *E. coli* chromosome and is approximately 106 kb in size. These PAIs

-5-

differ in location from the PAIs described by Hacker and colleagues for uropathogenic strain 536 (PAI I, 82 minutes {*selC*} and PAI II, 97 minutes {*leuX*}).

5 The location of the PAIs relative to one another and the cosmid clones covering the J96 PAIs is shown in Figure 1. The present invention relates to the nucleotide sequences of 142 fragments of DNA (contigs) covering the PAI IV and PAI V regions of the *E. coli* J96 chromosome. The nucleotide sequences shown in SEQ ID NOs: 1 through 142 were obtained by shotgun sequencing eleven *E. coli* J96 subclones, which were deposited in two pools on September 23, 1996 at
10 the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession numbers 97726 (includes 7 cosmid clones covering PAI (IV) and 97727 (includes 4 cosmid clones covering PAI V). The deposited sets or "pools" of clones are more fully described in Example 1. In addition, *E. coli* strain J96 was also deposited at the American Type Culture
15 Collection on September 23, 1996, and given accession number 98176.

Three hundred fifty-one open reading frames have been thus far identified in the 142 contigs described by SEQ ID NOs: 1 through 142. Thus, the present invention is directed to isolated nucleic acid molecules comprising open reading frames (ORFs) encoding *E. coli* J96 PAI proteins, and fragments of said nucleic
20 acid molecules.

The present invention also relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of *E. coli* J96 PAI proteins. Further embodiments include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the
25 nucleotide sequence of an *E. coli* J96 PAI ORF described herein, and fragments of said nucleic acid molecules.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention and fragments thereof, host cells containing the recombinant vectors, as well as methods for
30

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making such vectors and host cells for *E. coli* J96 PAI protein production by recombinant techniques.

5 The invention further provides isolated polypeptides encoded by the *E. coli* J96 PAI ORFs or fragments of said ORFs. It will be recognized that some amino acid sequences of the polypeptides described herein can be varied without significant effect on the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

10 In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope-bearing portion is an immunogenic or antigenic epitope useful for raising antibodies.

15 The invention further provides a vaccine comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*, such as strain J96.

20 The invention also provides a method of eliciting a protective immune response in an animal comprising administering to the animal the above-described vaccine.

25 The invention further provides a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for one or more of:

(a) polynucleic acids encoding an open reading frame listed in Tables 1-4 or a fragment of said polynucleic acid;

(b) full length or mature polypeptides encoded for by an open reading frame listed in Tables 1-4; or

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(c) antibodies specific to polypeptides encoded for by an open reading frame listed in Tables 1-4.

The invention further provides a nucleic acid probe for the detection of the presence of one or more *E. coli* PAI nucleic acids (nucleic acids encoding one or more ORFs as listed in Tables 1-4) in a sample from an individual comprising one or more nucleic acid molecules sufficient to specifically detect under stringent hybridization conditions the presence of the above-described molecule in the sample.

The invention also provides a method of detecting *E. coli* PAI nucleic acids in a sample comprising:

- a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and
- b) detecting the presence of the probe bound to an *E. coli* PAI nucleic acid.

The invention further provides a kit for detecting the presence of one or more *E. coli* PAI nucleic acids in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

The invention also provides a diagnostic kit for detecting the presence of pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antibodies.

The invention also provides a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* in a sample comprising at least one container means having disposed therein one or more of the above-described antigens.

Brief Description of the Figures

Figure 1 is a schematic diagram of cosmid clones derived from *E. coli* J96 pathogenicity island and map positions of known *E. coli* PAIs (not drawn to scale). The gray bar represents the *E. coli* K-12 chromosome with minute demarcations of PAI junction points located above the bar. *E. coli* J96 overlapping cosmid clones are represented by hatched bars (overlap not drawn to

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scale) with positions of *hly*, *pap*, and *prs* operons indicated above bar. The PAIs and estimated sizes are shown above and below the K-12 chromosome map.

Figure 2 is a block diagram of a computer system 102 that can be used to implement the computer-based systems of present invention.

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Detailed Description of the Invention

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The present invention is based on high through-put, random sequencing of a uropathogenic strain of *Escherichia coli*. The DNA sequences of contiguous DNA fragments covering the pathogenicity islands, PAI IV (also referred to as PAI_{J96(pheV)}) and PAI V (also referred to as PAI_{J96(pheU)}) from the chromosome of the *E. coli* uropathogenic strain, J96 (04:K6) were determined. The sequences were used for DNA and protein sequence similarity searches of the database.

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The primary nucleotide sequences generated by shotgun sequencing cosmid clones of the PAI IV and PAI V regions of the *E. coli* chromosome are provided in SEQ ID NOs:1 through 142. These sequences represent contiguous fragments of the PAI DNA. As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system. The present invention provides the nucleotide sequences of SEQ ID NOs:1 through 142, or representative fragments thereof, in a form that can be readily used, analyzed, and interpreted by a skilled artisan. Within these 142 sequences, there have been thus far identified 351 open reading frames (ORFs) that are described in greater detail below.

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As used herein, a "representative fragment" refers to *E. coli* J96 PAI protein-encoding regions (also referred to herein as open reading frames or ORFs), expression modulating fragments, and fragments that can be used to diagnose the presence of *E. coli* in a sample. A non-limiting identification of such representative fragments is provided in Tables 1 through 6, preferably in Tables 1 through 4. As described in detail below, representative fragments of the present invention further include nucleic acid molecules having a nucleotide sequence at least 95% identical, preferably at least 96%, 97%, 98%, or 99%

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identical, to an ORF identified in Tables 1 through 6, or more preferably Tables 1 through 4.

As indicated above, the nucleotide sequence information provided in SEQ ID NOs:1 through 142 was obtained by sequencing cosmid clones covering the PAIs located on the chromosome of *E. coli* J96 using a megabase shotgun sequencing method. The sequences provided in SEQ ID NOs:1 through 142 are highly accurate, although not necessarily a 100% perfect, representation of the nucleotide sequences of contiguous stretches of DNA (contigs) which include the ORFs located on the two pathogenicity islands of *E. coli* J96. As discussed in detail below, using the information provided in SEQ ID NOs:1 through 142 and in Tables 1 through 6 together with routine cloning and sequencing methods, one of ordinary skill in the art would be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *E. coli* J96 PAI proteins. In rare instances, this may reveal a nucleotide sequence error present in the nucleotide sequences disclosed in SEQ ID NOs: 1 through 142. Thus, once the present invention is made available (i.e., once the information in SEQ ID NOs: 1 through 142 and in Tables 1 through 6 is made available), resolving a rare sequencing error would be well within the skill of the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler™ can be used as an aid during visual inspection of nucleotide sequences.

Even if all of the rare sequencing errors were corrected, it is predicted that the resulting nucleotide sequences would still be at least about 99.9% identical to the reference nucleotide sequences in SEQ ID NOs: 1 through 142. Thus, the present invention further provides nucleotide sequences that are at least 99.9% identical to the nucleotide sequence of SEQ ID NOs: 1 through 142 in a form which can be readily used, analyzed and interpreted by the skilled artisan. Methods for determining whether a nucleotide sequence is at least 99.9% identical to a reference nucleotide sequence of the present invention are described below.

Nucleic Acid Molecules

The present invention is directed to isolated nucleic acid fragments of the PAIs of *E. coli* J96. Such fragments include, but are not limited to, nucleic acid molecules encoding polypeptides, nucleic acid molecules that modulate the expression of an operably linked ORF (hereinafter expression modulating fragments (EMFs)), and nucleic acid molecules that can be used to diagnose the presence of *E. coli* in a sample (hereinafter diagnostic fragments (DFs)).

By "isolated nucleic acid molecule(s)" is intended a nucleic acid molecule, DNA or RNA, that has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells, purified (partially or substantially) DNA molecules in solution, and nucleic acid molecules produced synthetically. Isolated RNA molecules include *in vitro* RNA transcripts of the DNA molecules of the present invention.

In one embodiment, *E. coli* J96 PAI DNA can be mechanically sheared to produce fragments about 15-20 kb in length, which can be used to generate an *E. coli* J96 PAI DNA library by insertion into lambda clones as described in Example 1 below. Primers flanking an ORF described in Tables 1 through 6 can then be generated using the nucleotide sequence information provided in SEQ ID NOs: 1 through 142. The polymerase chain reaction (PCR) is then used to amplify and isolate the ORF from the lambda DNA library. PCR cloning is well known in the art. Thus, given SEQ ID NOs: 1 through 142, and Tables 1 through 6, it would be routine to isolate any ORF or other representative fragment of the *E. coli* J96 PAI subgenomes. Isolated nucleic acid molecules of the present invention include, but are not limited to, single stranded and double stranded DNA, and single stranded RNA, and complements thereof.

Tables 1 through 6 herein describe ORFs in the *E. coli* J96 PAI cosmid clone library.

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Tables 1 and 3 list, for PAI IV and PAI V, respectively, a number of ORFs that putatively encode a recited protein based on homology matching with protein sequences from an organism listed in the Table. Tables 1 and 3 indicate the location of ORFs (i.e., the position) by reference to its position within the one of the 142 *E. coli* J96 contigs described in SEQ ID NOs: 1 through 142. Column 1 of Tables 1 and 3 provides the Sequence ID Number (SEQ ID NO) of the contig in which a particular open reading frame is located. Column 2 numerically identifies a particular ORF on a particular contig (SEQ ID NO) since many contigs comprise a plurality of ORFs. Columns 3 and 4 indicate an ORF's position in the nucleotide sequence (contig) provided in SEQ ID NOs: 1 through 142 by referring to start and stop positions in the contig sequence.

One of ordinary skill in the art will appreciate that the ORFs may be oriented in opposite directions in the *E. coli* chromosome. This is reflected in columns 3 and 4. For these ORFs, the sense strand is complementary to the actual sequence given. The corresponding sense-strand of the ORF must be read as the 5'-3' complement of the antisense strand actually shown in the Sequence Listing, wherein the location is specified 3'-5'.

Column 5 provides a database accession number to a homologous protein identified by a similarity search of public sequence databases (*see, infra*). Column 6 describes the matching protein sequence and the source organism is identified in brackets. Column 7 of Tables 1 and 3 indicates the percent similarity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 of Tables 1 and 3 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. The concepts of percent identity and percent similarity of two polypeptide sequences are well understood in the art and are described in more detail below. Identified genes can frequently be assigned a putative cellular role category adapted from Riley (*see, Riley, M., Microbiol. Rev. 57:862 (1993)*). Column 9 of Tables 1 and 3 provides the nucleotide length of the open reading frame.

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Tables 2 and 4, below, provide ORFs of *E. coli* J96 PAI IV and PAI V, respectively, that did not elicit a homology match with a known sequence from either *E. coli* or another organism. As above, the first column in Tables 2 and 4 provides the contig in which the ORF is located and the second column numerically identifies a particular ORF in a particular contig. Columns 3 and 4 identify an ORF's position in one of SEQ ID NOs: 1 through 142 by reference to start and stop nucleotides.

Tables 5 and 6, below, provide the *E. coli* J96 PAI IV ORFs and PAI V ORFs, respectively, identified by the present inventors that provided a significant match to a previously published *E. coli* protein. Columns 1-6 correspond to columns 1-6 appearing in Tables 1 and 3. Column 7 indicates the percent identity of the protein sequence encoded by an ORF to the corresponding protein sequence from the organism appearing in parentheses in the sixth column. Column 8 indicates the length of the high-scoring segment pair (HSP). Column 9 provides the nucleotide length of the open reading frame.

As used herein, "open reading frame" or "ORF" refers to the nucleotide sequences as described in Tables 1 through 6. In Tables 1 through 6, each ORF is designated by a nucleotide sequence start position and stop position according to numbering of contig nucleotides in the Sequence Listing provided (Contig ID = SEQ ID NO).

In a first embodiment, the invention comprises a nucleotide sequence described in Tables 1 through 4 which begins with the nucleotide following the last nucleotide of an upstream stop codon (first nucleotide of the "ORF"), an initiation codon, in-frame putative polypeptide-encoding sequence, and nucleotides of an in-frame stop codon.

In a second embodiment, the invention comprises a nucleotide sequence of Tables 1 through 4 which contains an initiation codon (*e.g.* a methionine or valine codon) on their 5' end and a stop codon on their 3' end. The sequences of this embodiment are present within the nucleotide sequence described in Tables 1 through 4 by start and stop position as numbered in the Sequence Listing. To

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determine the 5' start position of this embodiment, one simply reads 5' to 3' from the designated 5' end position until an initiation codon is found.

In a third embodiment, the invention comprises a nucleotide sequence of the second embodiment, except that the 3' stop codon is not present.

5 In a fourth embodiment, the invention comprises a nucleotide sequence encoding a putative protein which is a sequence of Tables 1 through 4 excluding sequence encoding amino acids subject to removal by post-translational processing and sequences 3' of the last codon coding for an amino acid present in the putative polypeptide (e.g., sequences not containing the stop codon and
10 encoding the mature form of the polypeptide).

Certain embodiments of the invention may therefore either include or exclude initiation codons for methionine or valine and either include or exclude the stop codon.

Further details concerning the algorithms and criteria used for homology
15 searches are provided in the Examples below. A skilled artisan can readily identify ORFs in the *Escherichia coli* J96 cosmid library other than those listed in Tables 1 through 6, such as ORFs that are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

20 Isolated nucleic acid molecules of the present invention include DNA molecules having a nucleotide sequence substantially different than the nucleotide sequence of an ORF described in Tables 1 through 4, but which, due to the degeneracy of the genetic code, still encode a *E. coli* J96 PAI protein. The genetic code is well known in the art. Thus, it would be routine to generate such
25 degenerate variants.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of an *E. coli* protein encoded by an ORF described in Table 1 through 4. Non-naturally occurring variants may be produced using art-known mutagenesis
30 techniques and include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more

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nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *E. coli* protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to the nucleotide sequence of an ORF described in Tables 1 through 6, preferably 1 through 4. By a polynucleotide having a nucleotide sequence at least, for example, 95% identical to the reference *E. coli* ORF nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the ORF sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference ORF nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleotide sequence of an *E. coli* J96 PAI ORF can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, *Advances in Applied Mathematics* 2: 482-489 (1981),

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to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

Preferred are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence of an *E. coli* J96 PAI ORF that encode a functional polypeptide. By a "functional polypeptide" is intended a polypeptide exhibiting activity similar, but not necessarily identical, to an activity of the protein encoded by the *E. coli* J96 PAI ORF. For example, the *E. coli* ORF [Contig ID 84, ORF ID 3 (84/3)] encodes a hemolysin. Thus, a "functional polypeptide" encoded by a nucleic acid molecule having a nucleotide sequence, for example, 95% identical to the nucleotide sequence of 84/3, will also possess hemolytic activity. As the skilled artisan will appreciate, assays for determining whether a particular polypeptide is "functional" will depend on which ORF is used as the reference sequence. Depending on the reference ORF, the assay chosen for measuring polypeptide activity will be readily apparent in light of the role categories provided in Tables 1, 3, 5 and 6.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of a reference ORF will encode a functional polypeptide. In fact, since degenerate variants all encode the same amino acid sequence, this will be clear to the skilled artisan even without performing a comparison assay for protein activity. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a functional polypeptide. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not

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likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie, J.U. *et al.*, *supra*, and the references cited therein.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated nucleic acid molecule having the nucleotide sequence of an *E. coli* J96 PAI ORF is intended fragments at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length that are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-500 nt in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of an *E. coli* J96 PAI ORF. By a fragment at least 20 nt in length, for example, is intended fragments that include 20 or more contiguous bases from the nucleotide sequence of an *E. coli* J96 PAI ORF. Since *E. coli* ORFs are listed in Tables 1 through 6 and the sequences of the ORFs have been provided within the contig sequences of SEQ ID NOs: 1 through 142, generating

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such DNA fragments would be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes from the PAI DNA that is incorporated into the deposited pools of cosmid clones. Alternatively, such fragments could be generated synthetically.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of an *E. coli* J96 PAI protein. Methods for determining such epitope-bearing portions are described in detail below.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide that hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, an ORF described in Tables 1 through 6, preferably an ORF described in Tables 1, 2, 3 or 4. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5 x SSC (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 x SSC at about 65°C.

By a polynucleotide that hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., a *E. coli* ORF), for instance, a portion 50-500 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of an *E. coli* J96 PAI ORF.

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By "expression modulating fragment" (EMF), is intended a series of nucleotides that modulate the expression of an operably linked, putative polypeptide-encoding region (encoding region). A sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments that induce the expression of an operably linked encoding region in response to a specific regulatory factor or physiological event. EMF sequences can be identified within the *E. coli* genome by their proximity to the encoding regions within ORFs described in Tables 1 through 6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken 5' from any one of the encoding regions of ORFs of Tables 1 through 6 will modulate the expression of an operably linked 3' encoding region in a fashion similar to that found within the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to the fragments of the *E. coli* J96 PAI subgenome that are between two encoding regions herein described. Alternatively, EMFs can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site 5' to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence that is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed

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host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

By a "diagnostic fragment" (DF), is intended a series of nucleotides that selectively hybridize to *E. coli* sequences. DFs can be readily identified by identifying unique sequences within the *E. coli* J96 PAI subgenome, or by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format for amplification or hybridization selectivity.

Each of the ORFs of the *E. coli* J96 PAI subgenome disclosed in Tables 1 through 4, and EMFs found 5' to the encoding regions of the ORFs, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of uropathogenic *E. coli* in a sample. This is especially the case with the fragments or ORFs of Table 2 and 4 which will be highly selective for uropathogenic *E. coli* J96, and perhaps other uropathogenic or extraintestinal strains that include one or more PAIs.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the

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sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

Vectors and Host Cells

The present invention further provides recombinant constructs comprising one or more fragments of the *E. coli* J96 PAIs. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which, for example, an *E. coli* J96 PAI ORF is inserted. The vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the encoding region of an ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments (preferably an ORF) of the *E. coli* J96 PAIs described herein. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a

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lower eukaryotic host cell, such as a yeast cell, or the host cell can be a procaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)). Host cells containing, for example, an *E. coli* J96 PAI ORF can be used conventionally to produce the encoded protein.

Polypeptides and Fragments

The invention further provides isolated polypeptides having the amino acid sequence encoded by an *E. coli* PAI ORF described in Tables 1 through 6, preferably Tables 1 through 4, or a peptide or polypeptide comprising a portion of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

It will be recognized in the art that some amino acid sequences of *E. coli* polypeptides can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the invention further includes variations of polypeptides encoded for by ORFs listed in Tables 1 through 6 which show substantial pathogenic activity or which include regions of particular *E. coli* PAI proteins such as the protein portions discussed below. Such mutants include deletions, insertions,

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inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

5 Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

10 As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (i.e., are not likely to have a significant deleterious effect on a function) can be found in Bowie, J.U., *et al.*, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990).

15 Thus, the fragment, derivative or analog of a polypeptide encoded by an ORF described in one of Tables 1 through 6, may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic
20 code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as an IgG Fc
25 fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

30 Of particular interest are substitutions of charged amino acids with another charged amino acid and with neutral or negatively charged amino acids. The latter results in proteins with reduced positive charge to improve the

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characteristics of said proteins. The prevention of aggregation is highly desirable. Aggregation of proteins not only results in a loss of activity but can also be problematic when preparing pharmaceutical formulations, because they can be immunogenic. (Pinckard *et al.*, *Clin Exp. Immunol.* 2:331-340 (1967); Robbins
 5 *et al.*, *Diabetes* 36:838-845 (1987); Cleland *et al.* *Crit. Rev. Therapeutic Drug Carrier Systems* 10:307-377 (1993)).

The replacement of amino acids can also change the selectivity of binding to cell surface receptors. Ostade *et al.*, *Nature* 361:266-268 (1993) describes
 10 certain mutations resulting in selective binding of TNF- α to only one of the two known types of TNF receptors. Thus, proteins encoded for by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6, and that bind to a cell surface receptor, may include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation.

As indicated, changes are preferably of a minor nature, such as
 15 conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 7).

TABLE 7. Conservative Amino Acid Substitutions

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

Amino acids in the proteins encoded by ORFs of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science* 244:1081-1085 (1989)). The latter procedure introduces single
5 alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding or *in vitro*, or *in vitro* proliferative activity. Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.*
10 224:899-904 (1992) and de Vos *et al.* *Science* 255:306-312 (1992)).

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the polypeptides can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

15 The polypeptides of the present invention include the polypeptide encoded by the ORFs listed in Tables 1-6, preferably Tables 1-4, as well as polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above, and also include portions of such polypeptides with at least 30 amino acids
20 and more preferably at least 50 amino acids.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive,
25 Madison, WI 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman (*Advances in Applied Mathematics* 2:482-489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example,
30 95% "identical" to a reference amino acid sequence of a polypeptide is intended

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that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of said polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence encoded by the ORFs listed in Tables 1, 2, 3, 4, 5, or 6 can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The polypeptide of the present invention could be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art.

As described in detail below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting pathogenic protein expression as described below or as

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agonists and antagonists capable of enhancing or inhibiting protein function of important proteins encoded by the ORFs of the present invention. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" protein binding proteins which are also candidate agonist and antagonist according to the present invention. The yeast two hybrid system is described in Fields and Song, *Nature* 340:245-246 (1989).

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen *et al.*, *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R.A. (1983) Antibodies that react with predetermined sites on proteins. *Science* 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. Sutcliffe *et al.*,

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supra, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe *et al.*, *supra*, at 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, for instance, Wilson *et al.*, *Cell* 37:767-778 (1984) at 777. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods well known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are

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considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks. Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA* 82:5131-5135. This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten *et al.* (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten *et al.*, *supra*, at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe *et al.*, *supra*; Wilson *et al.*, *supra*; Chow, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle, F. J. *et al.*, *J. Gen. Virol.* 66:2347-2354 (1985).

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Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker
5 such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier
10 protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for
15 instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance,
20 Geysen *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely
25 by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20
30 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction

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with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to
10 Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) on Peralkylated Oligopeptide Mixtures discloses linear C₁-C₇-alkyl peralkylated
15 oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

20 The entire disclosure of each document cited in this section on "Polypeptides and Peptides" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, *E. coli* PAI polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG),
25 resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, e.g., for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins (EP A 394,827; Traunecker *et al.*, *Nature* 331:84-86 (1988)). Fusion proteins that have a disulfide-linked dimeric structure due to
30 the IgG part can also be more efficient in binding and neutralizing other

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molecules than the monomeric *E. coli* J96 PAI proteins or protein fragments alone (Fountoulakis *et al.*, *J. Biochem* 270:3958-3964 (1995)).

Vaccines

In another embodiment, the present invention relates to a vaccine, preferably in unit dosage form, comprising one or more *E. coli* J96 PAI antigens together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the one or more antigens are present in an amount effective to elicit a protective immune response in an animal to pathogenic *E. coli*. Antigens of *E. coli* J96 PAI IV and V may be obtained from polypeptides encoded for by the ORFs listed in Tables 1-6, particularly Tables 1-4, using methods well known in the art.

In a preferred embodiment, the antigens are *E. coli* J96 PAI IV or PAI V proteins that are present on the surface of pathogenic *E. coli*. In another preferred embodiment, the pathogenic *E. coli* J96 PAI IV or PAI V protein-antigen is conjugated to an *E. coli* capsular polysaccharide (CP), particularly to capsular polypeptides that are more prevalent in pathogenic strains, to produce a double vaccine. CPs, in general, may be prepared or synthesized as described in Schneerson *et al. J. Exp. Med.* 152:361-376 (1980); Marburg *et al. J. Am. Chem. Soc.* 108:5282 (1986); Jennings *et al., J. Immunol.* 127:1011-1018 (1981); and Beuvery *et al., Infect. Immunol.* 40:39-45 (1983). In a further preferred embodiment, the present invention relates to a method of preparing a polysaccharide conjugate comprising: obtaining the above-described *E. coli* J96 PAI antigen; obtaining a CP or fragment from pathogenic *E. coli*; and conjugating the antigen to the CP or CP fragment.

In a preferred embodiment, the animal to be protected is selected from the group consisting of humans, horses, deer, cattle, pigs, sheep, dogs, and chickens. In a more preferred embodiment, the animal is a human or a dog.

In a further embodiment, the present invention relates to a prophylactic method whereby the incidence of pathogenic *E. coli*-induced symptoms are

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decreased in an animal, comprising administering to the animal the above-described vaccine, wherein the vaccine is administered in an amount effective to elicit protective antibodies in an animal to pathogenic *E. coli*. This vaccination method is contemplated to be useful in protecting against severe diarrhea (pathogenic intestinal *E. coli* strains), urinary tract infections (uropathogenic *E. coli*) and infections of the brain (extraintestinal *E. coli*). The vaccine of the invention is used in an effective amount depending on the route of administration. Although intra-nasal, subcutaneous or intramuscular routes of administration are preferred, the vaccine of the present invention can also be administered by an oral, intraperitoneal or intravenous route. One skilled in the art will appreciate that the amounts to be administered for any particular treatment protocol can be readily determined without undue experimentation. Suitable amounts are within the range of 2 micrograms of the protein per kg body weight to 100 micrograms per kg body weight.

The vaccine can be delivered through a vector such as BCG. The vaccine can also be delivered as naked DNA coding for target antigens.

The vaccine of the present invention may be employed in such dosage forms as capsules, liquid solutions, suspensions or elixirs for oral administration, or sterile liquid forms such as solutions or suspensions. Any inert carrier is preferably used, such as saline, phosphate-buffered saline, or any such carrier in which the vaccine has suitable solubility properties. The vaccines may be in the form of single dose preparations or in multi-dose flasks which can be used for mass vaccination programs. Reference is made to Remington's *Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, Osol (ed.) (1980); and *New Trends and Developments in Vaccines*, Voller *et al.* (eds.), University Park Press, Baltimore, MD (1978), for methods of preparing and using vaccines.

The vaccines of the present invention may further comprise adjuvants which enhance production of antibodies and immune cells. Such adjuvants include, but are not limited to, various oil formulations such as Freund's complete adjuvant (CFA), the dipeptide known as MDP, saponins (ex. *Quillajasaponin* fraction QA-21, U.S. Patent No. 5,047,540), aluminum hydroxide, or lymphatic

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cytokines. Freund's adjuvant is an emulsion of mineral oil and water which is mixed with the immunogenic substance. Although Freund's adjuvant is powerful, it is usually not administered to humans. Instead, the adjuvant alum (aluminum hydroxide) may be used for administration to a human. Vaccine may be absorbed onto the aluminum hydroxide from which it is slowly released after injection. The vaccine may also be encapsulated within liposomes according to Fullerton, U.S. Patent No. 4,235,877.

Protein Function

Each ORF described in Tables 1 and 3 possesses a biological role similar to the role associated with the identified homologous protein. This allows the skilled artisan to determine a function for each identified coding sequence. For example, a partial list of the *E. coli* protein functions provided in Tables 1 and 3 includes many of the functions associated with virulence of pathogenic bacterial strains. These include, but are not limited to adhesins, excretion pathway proteins, O-antigen/carbohydrate modification, cytotoxins and regulators. A more detailed description of several of these functions is provided in Example 1 below.

Diagnostic Assays

In another preferred embodiment, the present invention relates to a method of detecting pathogenic *E. coli* nucleic acid in a sample comprising:

- a) contacting the sample with the above-described nucleic acid probe, under conditions such that hybridization occurs, and
- b) detecting the presence of the probe bound to pathogenic *E. coli* nucleic acid.

In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* nucleic acid in a sample comprising at least one container means having disposed therein the above-described nucleic acid probe.

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In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antibodies.

5 In another preferred embodiment, the present invention relates to a diagnostic kit for detecting the presence of antibodies to pathogenic *E. coli* antigens in a sample comprising at least one container means having disposed therein the above-described antigens.

10 The present invention provides methods to identify the expression of an ORF of the present invention, or homolog thereof, in a test sample, using one of the antibodies of the present invention. Such methods involve incubating a test sample with one or more of the antibodies of the present invention and assaying for binding of the antibodies to components within the test sample.

15 In a further embodiment, the present invention relates to a method for identifying pathogenic *E. coli* in an animal comprising analyzing tissue or body fluid from the animal for a nucleic acid, protein, polypeptide-antigen or antibody specific to one of the ORFs described in Tables 1-4 herein from *E. coli* J96 PAI IV or V. Analysis of nucleic acid specific to pathogenic *E. coli* can be by PCR techniques or hybridization techniques (cf. *Molecular Cloning: A Laboratory*
20 *Manual, second edition*, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, 1989; Eremeeva *et al.*, *J. Clin. Microbiol.* 32:803-810 (1994) which describes differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA).

25 Proteins or antibodies specific to pathogenic *E. coli* may be identified as described in *Molecular Cloning: A Laboratory Manual, second edition*, Sambrook *et al.*, eds., Cold Spring Harbor Laboratory (1989). More specifically, antibodies may be raised to *E. coli* J96 PAI proteins as generally described in *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988). *E. coli* J96 PAI-specific antibodies can also be obtained from
30 infected animals (Mather, T. *et al.*, *JAMA* 205:186-188 (1994)).

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In another embodiment, the present invention relates to an antibody having binding affinity specifically to an *E. coli* J96 PAI antigen as described above. The *E. coli* J96 PAI antigens of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, a peptide can be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well as fragments of these antibodies. The invention further includes single chain antibodies. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques, for example, such fragments include but are not limited to: the F(ab')₂ fragment; the Fab' fragments, Fab fragments, and Fv fragments.

Of special interest to the present invention are antibodies to pathogenic *E. coli* antigens which are produced in humans, or are "humanized" (i.e. non-immunogenic in a human) by recombinant or other technology. Humanized antibodies may be produced, for example by replacing an immunogenic portion of an antibody with a corresponding, but non-immunogenic portion (i.e. chimeric antibodies) (Robinson, R.R. *et al.*, International Patent Publication PCT/US86/02269; Akira, K. *et al.*, European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison, S.L. *et al.*, European Patent Application 173,494; Neuberger, M.S. *et al.*, PCT Application WO 86/01533; Cabilly, S. *et al.*, European Patent Application 125,023; Better, M. *et al.*, *Science* 240:1041-1043 (1988); Liu, A.Y. *et al.*, *Proc. Natl. Acad. Sci. USA* 84:3439-3443 (1987); Liu, A.Y. *et al.*, *J. Immunol.* 139:3521-3526 (1987); Sun, L.K. *et al.*, *Proc. Natl. Acad. Sci. USA* 84:214-218 (1987); Nishimura, Y. *et al.*, *Canc. Res.* 47:999-1005 (1987); Wood, C.R. *et al.*, *Nature* 314:446-449 (1985); Shaw *et al.*, *J. Natl. Cancer Inst.* 80:1553-1559 (1988). General reviews of "humanized" chimeric antibodies are provided by Morrison, S.L. (*Science*, 229:1202-1207 (1985)) and by Oi, V.T. *et al.*, *BioTechniques* 4:214 (1986)). Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones, P.T. *et al.*, *Nature* 321:552-525 (1986); Verhoeyan *et al.*,

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Science 239:1534 (1988); Beidler, C.B. *et al.*, *J. Immunol.* 141:4053-4060 (1988)).

In another embodiment, the present invention relates to a hybridoma which produces the above-described monoclonal antibody. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "*Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*," Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods* 35:1-21 (1980)).

In another embodiment, the present invention relates to a method of detecting a pathogenic *E. coli* antigen in a sample, comprising: a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and b) detecting the presence of said antibody bound to the antigen. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard, *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands

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(1985); and *Antibodies: A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory (1988).

5 The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is capable with the system
10 utilized.

In another embodiment, the present invention relates to a method of detecting the presence of antibodies to pathogenic *E. coli* in a sample, comprising: a) contacting the sample with an above-described antigen, under conditions such that immunocomplexes form, and b) detecting the presence of
15 said antigen bound to the antibody. In detail, the methods comprise incubating a test sample with one or more of the antigens of the present invention and assaying whether the antigen binds to the test sample.

In another embodiment of the present invention, a kit is provided which contains all the necessary reagents to carry out the previously described methods
20 of detection. The kit may comprise: i) a first container means containing an above-described antibody, and ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting
25 the presence of bound antibodies. Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits.

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One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

Screening Assay for Binding Agents

5 Using the isolated proteins described herein, the present invention further provides methods of obtaining and identifying agents that bind to a protein encoded by an *E. coli* J96 PAI ORF or to a fragment thereof.

The method involves:

- 10 (a) contacting an agent with an isolated protein encoded by a *E. coli* J96 PAI ORF, or an isolated fragment thereof; and
- (b) determining whether the agent binds to said protein or said fragment.

15 The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques. For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by an ORF of the present invention.

20 Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific

25 peptide sequence in order to generate rationally designed antipeptide ligands, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides, In *Synthetic Peptides, A User's Guide*, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry* 28:9230-8 (1989).

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In addition to the foregoing, one class of agents of the present invention, can be used to control gene expression through binding to one of the ORF encoding regions or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed and selected. Targeting the encoding region or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF encoding region or multiple encoding regions that rely on the same EMF for expression control.

One class of DNA binding agents are those that contain nucleotide base residues that hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives having base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251: 1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Computer Related Embodiments

The nucleotide sequence provided in SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to the sequences provided in SEQ ID NOs: 1 through 142, can be "provided" in

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a variety of media to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, that contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NOs: 1 through 142, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NOs: 1 through 142. Such a manufacture provides the *E. coli* J96 PAI subgenomes or a subset thereof (e.g., one or more *E. coli* J96 PAI open reading frame (ORF)) in a form that allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *E. coli* J96 PAI subgenome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, one or more nucleotide sequences of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on

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computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of dataprocessor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NOs: 1 through 142, representative fragments thereof, or nucleotide sequences at least 99.9% identical to SEQ ID NOs: 1 through 142, in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the *E. coli* J96 PAI subgenome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the *E. coli* J96 PAI subgenome and are useful in producing commercially important proteins such as enzymes used in modifying surface O-antigens of bacteria. A comprehensive list of ORFs encoding commercially important *E. coli* J96 PAI proteins is provided in Tables 1 through 6.

The present invention provides a DNA sequence - gene database of pathogenicity islands (PAIs) for *E. coli* involved in infectious diseases. This database is useful for identifying and characterizing the basic functions of new virulence genes for *E. coli* involved in uropathogenic and extraintestinal diseases. The database provides a number of novel open reading frames that can be selected for further study as described herein.

Selectable insertion mutations in plasmid subclones encoding PAI genes with potentially significant phenotypes for *E. coli* uropathogenesis and sepsis can

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be isolated. The mutations are then crossed back into wild type, uropathogenic *E. coli* by homologous recombination to create wild-type strains specifically altered in the targeted gene. The significance of the genes to *E. coli* pathogenesis is assessed by *in vitro* assays and *in vivo* murine models of sepsis/peritonitis and ascending urinary tract infection.

New virulence genes and PAI sites in uropathogenic *E. coli* may be identified by the transposon signature-tagged mutagenesis system and negative selection of *E. coli* mutants avirulent in murine models of ascending urinary tract infection or peritonitis.

Epidemiological investigations of new virulence genes and PAIs may be used to test for their occurrence in the genomes of other pathogenic and opportunistic members of the Enterobacteriaceae.

One can choose from the ORFs included in SEQ ID NOs: 1 through 142, using Tables 1 through 6 as a useful guidepost for selecting, as candidates for targeted mutagenesis, a limited number of candidate genes within the PAIs based on their homology to virulence, export or regulation genes in other pathogens. For the large number of apparent genes within the PAIs that do not share sequence similarity to any entries in the database, the transposon signature-tagged mutagenesis method developed by David Holden's laboratory can be employed as an independent means of virulence gene identification.

Allelic knock-outs are constructed using different *pir*-dependent suicide vectors (Swihart, K.A. and R.A. Welch, *Infect. Immun.* 58:1853-1869 (1990)). In addition, two different animal model systems can be employed for assessment of pathogenic determinants. The initial identification of *E. coli* hemolysin as a virulence factor came from the construction of isogenic *E. coli* strains that were tested in a rat model of intra-abdominal sepsis (Welch, R.A. *et al.*, *Nature (London)* 294:665-667 (1981)). The ascending UTI (Urinary Tract Infection) mouse model was also successfully performed with allelic knock-outs of the *hpmA* hemolysin of *Proteus mirabilis* (Swihart, K.A. and R.A. Welch, *Infect. Immun.* 58:1853-1869 (1990)).

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The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *E. coli* J96 PAI subgenome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *E. coli* genome that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

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As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the *E. coli* J96 PAI subgenome, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequence and the homologous *E. coli* J96 PAI sequence identified using a search means as described above, and an output means for outputting the identified homologous *E. coli* J96 PAI sequence. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *E. coli* J96 PAI subgenome possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

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E. coli J96 PAI subgenomes. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) can be used to identify open reading frames within the *E. coli* J96 PAI subgenome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

One application of this embodiment is provided in Figure 2. Figure 2 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114 once inserted in the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108 during execution.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Experimental

Example 1: High Through-put Sequencing of Cosmid Clones Covering PAI IV and PAI V in E. coli J96

The complete DNA sequence of the pathogenicity islands, PAI IV and PAI V (respectively >170 kb and ~110 kb), from uropathogenic *E. coli* strain, J96 (O4:K6) was determined using a strategy, cloning and sequencing method, data collection and assembly software essentially identical to those used by the TIGR group for determining the sequence of the *Haemophilus influenzae* genome (Fleischmann, R.D., *et al.*, *Science* 269:496 (1995)). The sequences were then used for DNA and protein sequence similarity searches of the databases as described in Fleischmann, *Id.*

The analysis of the genetic information found within the PAIs of *E. coli* J96 was facilitated by the use of overlapping cosmid clones possessing these unique segments of DNA. These cosmid clones were previously constructed and mapped (as further described below) as an overlapping set in the laboratory of Dr. Doug Berg (Washington University). A gap exists between the left portion of cosmid 2 and the end of the PAI IV that would represent the *pheV* junction to the *E. coli* K-12 genome.

Uropathogenic strain *E. coli* J96 (O4:K6) was used as a source of chromosomal DNA for construction of a cosmid library. *E. coli* K-12 DH5 α and DH12 (Gibco/BRL, Gaithersburg, Md.) were used as hosts for maintaining cosmid and plasmid clones. The cosmid library of *E. coli* J96 DNA was constructed essentially as described by Bukanow & Berg (*Mol. Microbiol* 11:509-523 (1994)). DNA was digested with *Sau3A*I under conditions that generated fragments with an average size of 40 to 50 kb and electrophoresed through 1% agarose gels. Fragments of 35 to 50 kb were isolated and cloned into Lorist 6 vector that had been linearized with *Bam*III and treated with bacterial alkaline phosphatase to block self-ligation. (Lorist 6 is a 5.2-kb moderate-copy-number cosmid vector with T7 and SP6 promoters close to the cloning site.) Cloned

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DNA was packaged in lambda phage particles *in vitro* by using a commercial kit (Amersham, Arlington Heights, IL) and cosmid-containing phage particles were used to transduce *E. coli* DH5 α . Transductant colonies were transferred to 150 μ L of Luria-Bertani broth supplemented with kanamycin in 96-well microtiter plates and grown overnight at 37°C with shaking. Two sets of clones, one for each PAI were ultimately assembled, as previously described (Swenson *et al.*, *Infection and Immunity* 64:3736-3743 (1996)), fully incorporated by reference herein).

The two sets of clones contain eleven sub-clones that were employed in the sequencing method described below. One set of four overlapping cosmid clones covers the *prs*-containing PAI V, ATCC Deposit No. 97727, deposited September 23, 1996. A second set of seven subclones covers much of the *pap*-containing PAI V, ATCC Deposit No. 97726, deposited September 23, 1996. See Figure 1.

A high through-put, random sequencing method (Fleischmann *et al.*, *Science* 269:496 (1995); Fraser *et al.*, *Science* 270:397 (1995)) was used to obtain the sequences for 142 (contigs) fragments of *E. coli* J96 PAIs. All clones were sequenced from both ends to aid in the eventual ordering of contigs during the sequence assembly process. Briefly, random libraries of ~ 2 kb clones covering the two J96 PAIs were constructed, ~ 2,800 clones were subjected to automated sequencing (~ 450 nt/clone) and preliminary assemblies of the sequences accomplished which result in 142 contigs for each of the two PAIs that total 95 and 135 kb respectively. The estimated sizes of the PAI IV and PAI V based on the overlapping cosmid clones are 1.7×10^5 and 1.1×10^5 bp respectively. The 142 sequences were assembled by means of the TIGR Assembler (Fleischmann *et al.*; Fraser *et al.*; Sutton *et al.*, *Genome Sci. Tech.* 1:9 (1995)). Sequence and physical gaps were closed using a combination of strategies (Fleischmann *et al.*; Fraser *et al.*). Presently the average depth of sequencing for each base assembled in the contigs is 6-fold. The tentative identity of many genes based on sequence homology is covered in Tables 1, 3, 5 and 6.

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Open reading frames (ORFs) and predicted protein-coding regions were identified as described (Fleischmann *et al.*; Fraser *et al.*) with some modification. In particular, the statistical prediction of uropathogenic *E. coli* J96 pathogenicity island genes was performed with GeneMark (Borodovsky, M. & McIninch, *J. Comput. Chem.* 17:123 (1993)). Regular GeneMark uses nonhomogeneous Markov models derived from a training set of coding sequences and ordinary Markov models derived from a training set of noncoding sequences. The ORFs in Tables 1-6 were identified by GeneMark using a second-order Markov model trained from known *E. coli* coding regions and known *E. coli* non-coding regions.

Among the important genes that are implicated in the virulence of *E. coli* J96 PAIs are adhesins, excretion pathway proteins, proteins that participate in alterations of the O-antigen in the PAIs, cytotoxins, and two-component (membrane sensor/DNA binding) proteins.

I. Adhesins. It is believed that the principal adhesin determinants involved in uropathogenicity that are present within PAIs of uropathogenic *E. coli* are the pili encoded by the *pap*-related operons (Hultgren *et al.*, *Infect. Immun.* 50:370-377 (1993), Stromberg *et al.*, *EMBO J* 9:2001-2010 (1990), High *et al.*, *Infect. Immun.* 56:513-517 (1988)) and the distantly related afimbrial adhesins (Labigne-Roussel *et al.*, *Infect. Immun.* 46:251-259 (1988)). The presence of two of these (*pap*, and *prs*) has been confirmed. In addition potential genes for five other adhesins including *sla* (described above), AIDA-I (diffuse adherence-DEAC), *hra* (heat resistant hemagglutinin-ETEC), *fha* (filamentous hemagglutinin- *Bordetella pertussis*) and the arg-gingipain proteinase of *Porphyromonas gingivalis* have been found.

II. Type II exoprotein secretion pathway. Highly significant statistics support the presence of multiple genes involved in the type II exoprotein pathway. Curiously, perhaps two different determinants appear to be present in PAI IV where one set of genes has the highest sequence similarity to *eps*-like genes (*Vibrio cholerae* Ctx export) and the other has greatest similarity to *exe* genes (*Aeromonas hydrophila* aerolysin and protease export). At present, the assembly of contigs involving these potential genes is incomplete. Thus, it is

uncertain if two separate and complete determinants are present. However, it is clear that these genes are newly discovered and novel to pathogenic *E. coli* because the derived sequences do not have either the *bfp* or *hop* genes as the highest matches. The gene products that are the target of the type II export pathway are not evident at this time.

Within PAI IV there are sequences which suggest genes very similar to *secD* and *secF*. These two linked genes encode homologous products that are localized to the inner membrane and are hypothesized to play a late role in the translocation of leader-peptide containing proteins across the inner membrane of gram-negative bacteria. In addition, in each PAI, sequences are found that are reminiscent of the heat-shock *htrA/degA* gene that encodes a periplasmic protease. They may perform endochaperone-like function as Pugsley *et al.* have hypothesized for different exoprotein pathways.

III. O-antigen/capsule/carbohydrate modification (*Nod* genes). J96 has the O4. The O-antigen portion of lipopolysaccharide is encoded by *rfb* genes that are located at 45 min. on the *E. coli* chromosome. We have found in both PAIs a cumulative total of five possible *rfb*-like genes which could participate alterations of the O-antigen in the PAIs. Overall these data suggest that PAIs provide the genetic potential for greater change of the cell surface for uropathogenic *E. coli* strains than what was previously known.

The apparent capsule type for strain J96 is a non-sialic acid K6-type. Sequence similarity "hits" were made in PAI IV region to two region-1 capsule genes, *kpsS* and *kpsE* involved in the stabilization of polysaccharide synthesis and polysaccharide export across the inner membrane. This is not altogether surprising based on the genetic mapping of the *kps* locus to *serA* at 63 minutes on the genome of the K1 capsular type of *E. coli*. This suggests that these *kps*-like genes either are participating in the K6-biosynthesis or perhaps are involved in complex carbohydrate export for other purposes.

An intriguing discovery are the hits made on genes involved in bacteria-plant interactions by *Rhizobium*, *Bradyrhizobium* and *Agrobacterium*. Four potential genes identified thus far share significant sequence similarity to genes

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encoding products that modify lipo-oligosaccharides that influence nodule morphogenesis on legume roots. These are: ORF140, carbamyl phosphate synthetase; nodulation protein 1265; phosphate-regulatory protein; and an ORF at a plant-inducible locus in *Agrobacterium*. To date there are no descriptions in the literature of such gene products being utilized by human or animal bacterial pathogens for the purposes of modification or secretion of extracellular carbohydrate. However, the sequence similarity to the capsular region-2 genes and to lipooligosaccharide biosynthetic genes in *Rhizobium* spp has been recently noted by Petit (1995).

IV. Cytotoxins. Besides the previously known hemolysin and CNF toxins in the PAIs, in each PAI sequences similar to the *shlBA* operon (cosmid 5 and 12) were found for a cytolytic toxin from *Serratia marcescens* and *Proteus mirabilis*. Ironically, the *P. mirabilis* hemolysin (HpmA) member of this family of toxins was discovered by Uphoff and Welch (1990), but not thought to exist in other members of the Enterobacteriaceae (Swihart (1990)). A *shlB*-like transporter does also appear to be involved in the export of the filamentous hemagglutinin of *Bordetella pertussis* which was described above and a cell surface adhesin of *Haemophilus influenzae*. It has been demonstrated that cosmid #5 of *E. coli* J96 encodes an extracellular protein that is ~180 kDa and cross-reactive to polyclonal antisera to the *P. mirabilis* HpmA hemolysin. Thus, there is evidence suggesting there is new member of this family of proteins in extraintestinal *E. coli* isolates. In addition, there is also a hit on the FhaC hemolysin-like gene within the PAI V although its statistical significance for the sequence thus far available is only 0.0043.

V. Regulators. A common regulatory motif in bacteria are the two-component (membrane sensor/DNA binding) proteins. In numerous instances in pathogenic bacteria, external signals in the environment cause membrane-bound protein kinases to phosphorylate a cytoplasmic protein which in turn acts as either a negative or positive effector of transcription of large sets of operons. On cosmid 11 representing PAI V were found, in two different *PstI* clones, sequences

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for two-component regulators (similar probabilities for OmpR/ AIGB and separately RcsC, probabilities at the 10^{-22} level).

In addition, the phosphoglycerate transport system (*pgtA*, *pgtC*, and *pgtP*) including the *pgtB* regulator is present in PAI IV. This transport system which was originally described in *S. typhimurium* is not appreciated as a component of any pathogenic *E. coli* genome. The operon had been previously mapped at 49 minutes, near or within one of the *S. typhimurium* chromosome specific-loops not present in the K-12 genome. It should be noted that the *E. coli* K-12 *glpT* gene product is similar to *pgtP* gene product (37% identity), but the *E. coli* J96 genes are clearly homologs to the *pgt* genes and their linkage within the middle of PAI IV element (cosmid #4) is suspicious.

VI. Mobile genetic elements. There are numerous sequences that share similarity to genes found on insertion elements, plasmids and phages. The temperate bacteriophage P4 inserts within tRNA loci in the *E. coli* chromosome. The hypothesis was made that PAIs are the result of bacteriophage P4-virulence gene recombination events (Blum *et al.*, *Infect. Immun.* 62:606-614 (1994). Data supporting this hypothesis was found during our sequencing with the identification of P4-like sequences in each of the PAIs (cosmids 7 and 9). This is a very important preliminary result which supports the hypothesis that PAIs can be identified by common sequence or genetic elements. However, there are indications that multiple mobile genetic elements involved in the evolution of the J96 PAIs. Conjugal plasmid-related sequences may also be present at two different locations (F factor and RI plasmid). Sequences for multiple transposable elements are present that are likely to have originated from different bacterial genera (Tn1000, IS630, IS911, IS100, IS21, IS 1203, IS5376 (*B. stearotheophilus*) and RHS). Of particular interest is IS100, which was originally identified in *Yersinia pestis* (Fetherston *et al.*, *Mol. Microbiol.* 6:2693-2704 (1992)). The presence of IS100 is significant because it has been associated with the termini of a large chromosomal element encoding pigmentation and some aspect of virulence in *Y. pestis*. This element undergoes spontaneous deletions similar to the PAIs from *E. coli* 536 (Fetherston *et al.*, *Mol. Microbiol.*

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6:2693-2704 (1992)) and appears to participate in plasmid-chromosome rearrangements. This element was not previously known to be in genera outside of *Yersinia*.

5 The discovery of the apparent *att* site for bacteriophage P2 in the PAIs is interesting. P2 acts as a helper phage for the P4 satellite phage. The P2 *att* site is at 44 min in the K-12 genome. The significance of this hit is unknown at present, but may be explained as either a cloning artifact (some K-12 fragments in the *Pst* I library of cosmid 5) or evidence of some curious chromosomal-P4/P2 phage history. It may indicate that the J96 PAIs are composites of multiple
10 smaller PAIs.

Example 2: Preparation of PCR Primers and Amplification of DNA

Various fragments of the sequenced *E. coli* J96 PAIs, such as those disclosed in Tables 1 through 6 can be used, in accordance with the present invention, to prepare PCR primers. The PCR primers are preferably at least 15
15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers are useful during PCR cloning of the ORFs described herein.

Example 3: Gene expression from DNA Sequences Corresponding to ORFs

20 A fragment of an *E. coli* J96 PAI (preferably, a protein-encoding sequence provided in Tables 1 through 6) is introduced into an expression vector using conventional technology (techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art). Commercially available vectors
25 and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper

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protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Pat. No. 5,082,767, which is hereby incorporated by reference.

5 The following is provided as one exemplary method to generate polypeptide(s) from a cloned ORF of an *E. coli* J96 PAI whose sequence is provided in SEQ ID NOs: 1 through 142. A poly A sequence can be added to the construct by, for example, splicing out the poly A sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use
10 in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *E. coli* J96 PAI DNA is obtained by PCR from the bacterial vector using
15 oligonucleotide primers complementary to the *E. coli* J96 PAI DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *E. coli* J96 PAI DNA 3' primer, taking care to ensure that the *E. coli* J96 PAI DNA is positioned such that its followed with the poly A sequence. The purified fragment obtained from the
20 resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions
25 outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface.

30 Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *E. coli* J96 PAI DNA

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sequence are injected into mice to generate antibody to the polypeptide encoded by the *E. coli* J96 PAI DNA.

If antibody production is not possible, the *E. coli* J96 PAI DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as a chimeric with, for example, β -globin. Antibody to β -globin is used to purify the chimeric. Corresponding protease cleavage sites engineered between the β -globin gene and the *E. coli* J96 PAI DNA are then used to separate the two polypeptide fragments from one another after translation. One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene). This vector encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides may additionally be produced from either construct using *in vitro* translation systems such as In vitro Express™ Translation Kit (Stratagene).

Example 4

E. coli Expression of an E. coli J96 PAI ORF and protein purification

An *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified using PCR oligonucleotide primers designed from the nucleotide sequences flanking the selected ORF and/or from portions of the ORF's NH₂- or COOH-terminus. Additional nucleotides containing restriction sites to facilitate cloning are added to the 5' and 3' sequences, respectively.

The restriction sites are selected to be convenient to restriction sites in the bacterial expression vector pQE60. The bacterial expression vector pQE60 is used for bacterial expression in this example. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible

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promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin sold by QIAGEN, Inc., *supra*, and suitable single restriction enzyme cleavage sites. These elements are arranged such that a DNA fragment encoding a polypeptide may be inserted in such a way as to produce that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of an *E. coli* J96 PAI is amplified from the deposited cDNA clone using PCR oligonucleotide primers which anneal to the amino terminal sequences of the desired portion of the *E. coli* protein and to sequences in the deposited construct 3' to the cDNA coding sequence. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

The amplified *E. coli* J96 PAI DNA fragments and the vector pQE60 are digested with one or more appropriate restriction enzymes, such as Sall and XbaI, and the digested DNAs are then ligated together. Insertion of the *E. coli* J96 PAI DNA into the restricted pQE60 vector places the *E. coli* J96 PAI protein coding region, including its associated stop codon, downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described in Sambrook *et al.*, *Molecular Cloning: a Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989). *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing an *E. coli* J96 PAI protein, is available commercially from QIAGEN, Inc., *supra*. Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from

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resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH8. The cell debris is removed by centrifugation, and the supernatant containing the *E. coli* J96 PAI protein is dialyzed against 50 mM Na-acetate buffer pH6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. coli* J96 PAI protein. The purified protein is stored at 4°C or frozen at -80°C.

Example 5

Cloning and Expression of an E. coli J96 PAI protein in a Baculovirus

Expression System

A *E. coli* J96 PAI ORF described in Tables 1 through 6 is selected and amplified as above. The plasmid is digested with appropriate restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1%

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agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.). This vector DNA is designated herein "V1".

Fragment F1 and the dephosphorylated plasmid V1 are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria are identified that contain the plasmid with the *E. coli* J96 PAI gene by digesting DNA from individual colonies using appropriate restriction enzymes and then analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing. This plasmid is designated herein pBac *E. coli* J96.

Five µg of the plasmid pBac *E. coli* J96 is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA.), using the lipofection method described by Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). 1 µg of BaculoGold™ virus DNA and 5 µg of the plasmid pBac *E. coli* J96 are mixed in a sterile well of a microliter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27°C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation is continued at 27°C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc.) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies

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Inc., page 9-10). After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 °C. The recombinant virus is called V-*E. coli* J96.

To verify the expression of the *E. coli* gene Sf9 cells are grown in Grace's medium supplemented with 10% heat inactivated FBS. The cells are infected with the recombinant baculovirus V-*E. coli* J96 at a multiplicity of infection ("MOI") of about 2. Six hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc.). If radiolabeled proteins are desired, 42 hours later, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then they are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled). Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the mature protein and thus the cleavage point and length of the secretory signal peptide.

Example 6

Cloning and Expression in Mammalian Cells

Most of the vectors used for the transient expression of an *E. coli* J96 PAI gene in mammalian cells should carry the SV40 origin of replication. This allows the replication of the vector to high copy numbers in cells (e.g., COS cells) which express the T antigen required for the initiation of viral DNA synthesis. Any other mammalian cell line can also be utilized for this purpose.

A typical mammalian expression vector contains the promoter element, which mediates the initiation of transcription of mRNA, the protein coding

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sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription can be achieved with the early and late promoters from SV40, the long terminal repeats (LTRS) from Retroviruses, e.g., RSV, 1HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter). Suitable expression vectors for use in practicing the present invention include, for example, vectors such as PSVL and PMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146) and pBC12MI (ATCC 67109). Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV 1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the gene can be expressed in stable cell lines that contain the gene integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful to develop cell lines that carry several hundred or even several thousand copies of the gene of interest. Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy *et al.*, *Biochem J.* 227:277-279 (1991); Bebbington *et al.*, *Bio/Technology* 10:169-175 (1992)). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

The expression vectors pC1 and pC4 contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen *et al.*, *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart *et al.*, *Cell* 41:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme

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cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors contain in addition the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene.

Example 6(a): Cloning and Expression in COS Cells

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The expression plasmid, p *E. coli* J96HA, is made by cloning a cDNA encoding *E. coli* J96 PAI protein into the expression vector pcDNAI/Amp or pcDNAIII (which can be obtained from Invitrogen, Inc.).

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The expression vector pcDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a cDNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson *et al.*, *Cell* 37:767 (1984). The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pcDNAIII contains, in addition, the selectable neomycin marker.

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A DNA fragment encoding the *E. coli* J96 PAI protein is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The *E. coli* cDNA of the deposited clone is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. coli* J96 PAI protein in *E. coli*.

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The PCR amplified DNA fragment and the vector, pcDNAI/Amp, are digested with appropriate restriction enzymes for the chosen primer sequences

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and then ligated. The ligation mixture is transformed into *E. coli* strain SURE (available from Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the *E. coli* J96 PAI protein-encoding fragment.

For expression of recombinant *E. coli* J96 PAI protein, COS cells are transfected with an expression vector, as described above, using DEAE-DEXTRAN, as described, for instance, in Sambrook *et al.*, *Molecular Cloning: a Laboratory Manual*, Cold Spring Laboratory Press, Cold Spring Harbor, New York (1989). Cells are incubated under conditions for expression of *E. coli* J96 PAI protein by the vector.

Expression of the *E. coli* J96 PAI - HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow *et al.*, *Antibodies: A Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988). To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson *et al.* cited above. Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 6(b): Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of an *E. coli* J96 PAI protein. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Acc. No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early

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promoter. Chinese hamster ovary- or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies, Inc.) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented (see, 5 e.g., Alt, F. W. *et al.*, 1978, *J. Biol. Chem.* 253:1357-1370, Hamlin, J. L. and Ma, C. 1990, *Biochim. et Biophys. Acta*, 1097:107-143, Page, M. J. and Sydenham, M.A. 1991, *Biotechnology* 9:64-68). Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, 10 as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated 15 into one or more chromosome(s) of the host cell.

Plasmid pC4 contains for expressing the gene of interest the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus (Cullen, *et al.*, *Molecular and Cellular Biology*, March 1985:438-447) plus a fragment isolated from the enhancer of the immediate early gene of human 20 cytomegalovirus (CMV) (Boshart *et al.*, *Cell* 41:521-530 (1985)). Downstream of the promoter is BamHI restriction enzyme site that allows the integration of the gene. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β -actin promoter, 25 the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. coli* protein in a regulated way in mammalian cells (Gossen, M., & Bujard, H. 1992, *Proc. Natl. Acad. Sci. USA* 89: 5547-5551). For the polyadenylation of the mRNA 30 other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the

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chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

5 The plasmid pC4 is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

The DNA sequence encoding the complete *E. coli* J96 PAI protein including its leader sequence is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the gene.

10 The amplified fragment is digested with appropriate endonucleases for the chosen primers and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction
15 enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. 5 µg of the expression plasmid pC4 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner *et al.*, *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an
20 enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methothrexate plus 1 mg/ml G418. After about 10-14 days single clones are
25 trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until
30 clones are obtained which grow at a concentration of 100 - 200 µM. Expression

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of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 7

Production of an Antibody to an E. coli J96 Pathogenicity Island Protein

5 Substantially pure *E. coli* J96 PAI protein or polypeptide is isolated from the transfected or transformed cells described above using an art-known method. The protein can also be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody
10 to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler and Milstein, *Nature* 256:495 (1975) or modifications
15 of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective
20 media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth.*
25 *Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis,

L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of
5 a single protein can be prepared by immunizing suitable animals with the
expressed protein described above, which can be unmodified or modified to
enhance immunogenicity. Effective polyclonal antibody production is affected
by many factors related both to the antigen and the host species. For example,
small molecules tend to be less immunogenic than other molecules and may
10 require the use of carriers and adjuvant. Also, host animals vary in response to
site of inoculations and dose, with both inadequate or excessive doses of antigen
resulting in low titer antisera. Small doses (ng level) of antigen administered at
multiple intradermal sites appears to be most reliable. An effective immunization
protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol.*
15 *Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum
harvested when antibody titer thereof, as determined semi-quantitatively, for
example, by double immunodiffusion in agar against known concentrations of the
antigen, begins to fall (See Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of*
20 *Experimental Immunology*, Wier, D., ed, Blackwell (1973)). Plateau
concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum
(about 12 μ M). Affinity of the antisera for the antigen is determined by preparing
competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in:
Manual of Clinical Immunology, 2nd ed., Rose and Friedman, (eds.), Amer. Soc.
25 For Microbio., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in
quantitative immunoassays which determine concentrations of antigen-bearing
substances in biological samples; they are also used semi-quantitatively or
qualitatively to identify the presence of antigen in a biological sample.

Table 1 (PAI IV)
Putative coding regions of novel *E. coli* PAI IV proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
65	2	1902	1042	gi 1655838	ORF8: putative transposase [Yersinia pestis]	100	100	861
65	3	2096	1821	gi 467612	ORF1 [Yersinia pestis]	100	100	276
63	11	7856	9238	gi 154262	transporter protein pgp [Salmonella typhimurium]	98	93	1383
65	4	2889	1915	gi 1655837	ORF4: putative transposase [Yersinia pestis]	97	96	975
138	1	2	172	gi 1208992	unknown [Escherichia coli]	97	78	171
64	6	4075	4338	gi 1143207	Description: IS630 insertion element; ORF5 protein; Method: conceptual translation supplied by author [Shigella sonnei]	92	92	264
67	1	1	273	gi 809648	ExeF gene product [Aeromonas hydrophila]	92	71	273
73	4	3029	2511	gi 799234	glucose-1-phosphate thymidyltransferase [Escherichia coli]	92	86	519
73	5	3139	2996	gi 454900	rfbC gene product [Shigella flexneri]	92	92	144
64	5	3741	4088	gi 47542	ORF (343 AA) [Shigella sonnei]	91	85	348
73	3	2613	2242	gi 46985	glucose-1-phosphate thymidyltransferase [Salmonella enterica]	91	82	372
90	1	1	366	gi 38826	ExeE gene product [Aeromonas hydrophila]	91	77	366
91	2	604	248	gi 609625	putative [Vibrio cholerae]	91	67	357
63	9	6301	5234	gi 858753	regulatory protein pgIB [Salmonella typhimurium]	89	84	1068
73	2	2179	1811	gi 294899	dTDP-6-deoxy-L-mannose-dehydrogenase [Shigella flexneri]	89	84	369
90	2	201	689	gi 38826	ExeE gene product [Aeromonas hydrophila]	89	80	489
95	2	1519	413	gi 581654	dTDP-glucose 4,6-dehydratase [Salmonella enterica]	88	81	1107
96	1	729	457	pir S43483 S434	Orf104 homolog - Escherichia coli	88	72	273
63	6	4281	3019	gi 154255	phosphoglycerate transport system activator protein [Salmonella typhimurium]	87	79	1263
67	2	251	745	gi 609628	putative [Vibrio cholerae]	87	72	495
82	12	5254	4406	gi 1208992	unknown [Escherichia coli]	87	74	849
60	1	693	4	gi 609625	putative [Vibrio cholerae]	86	57	690
95	1	428	3	gi 508238	dTDP-6-deoxy-L-mannose-dehydrogenase [Escherichia coli]	85	74	426
64	7	4336	4731	gi 47542	ORF (343 AA) [Shigella sonnei]	84	81	396
80	8	2800	2582	gi 38832	ExeK gene product [Aeromonas hydrophila]	84	53	219
82	10	4380	3829	gi 1033137	ORF_o152 [Escherichia coli]	84	72	552

Table 1 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
63	8	5399	4830	sp P37433 PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-)	83	75	570
63	10	7572	6259	gi 154258	regulatory protein pgC [Salmonella typhimurium]	83	78	1314
65	7	3351	3100	gi 1196999	unknown protein [Transposon Tn3411]	82	80	252
100	1	337	2	gi 41004	URF 2 [Escherichia coli]	82	64	336
138	2	109	429	gi 1033128	ORF_o273 [Escherichia coli]	80	62	321
74	4	1331	831	gi 38826	ExeE gene product [Aeromonas hydrophila]	79	62	501
63	7	4873	4256	sp P37433 PGTB_	PHOSPHOGLYCERATE TRANSPORT SYSTEM SENSOR PROTEIN PGTB (EC 2.7.3.-)	78	72	618
70	13	5759	5529	gi 1773143	Ilha protein [Escherichia coli]	78	58	231
91	3	1154	534	gi 609625	putative [Vibrio cholerae]	77	65	621
75	5	3524	3255	gi 463911	heat resistant agglutinin 1 [Escherichia coli]	76	62	270
63	1	2	667	gi 1574313	H. influenzae predicted coding region H11472 [Haemophilus influenzae]	75	56	666
104	2	485	315	gi 530438	arabinose transport protein [Mycoplasma capricolum]	72	41	171
63	3	2180	1629	gi 622948	transposase [Escherichia coli]	71	60	552
63	12	9688	10005	sp P39213 Y191_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN	71	57	318
61	3	1283	876	gi 581535	ORF140 gene product [Rhizobium sp.]	70	54	408
84	3	2361	3437	gi 1772623	HecA [Erwinia chrysanthemi]	70	60	1077
91	1	300	4	gi 295430	epsE [Vibrio cholerae]	70	49	297
74	1	541	2	gi 609627	putative [Vibrio cholerae]	69	54	540
67	4	1297	1581	gi 151469	PilD-dependent protein [Pseudomonas aeruginosa]	68	50	285
84	1	578	1741	gi 1772622	HecB [Erwinia chrysanthemi]	68	54	1164
84	2	1698	2363	gi 1772622	HecB [Erwinia chrysanthemi]	67	48	666
63	2	1734	1393	gi 1323798	transposase [Plasmid pRL1063a]	65	46	342
71	1	1134	4	gi 397405	kpsE gene product [Escherichia coli]	65	36	1131
64	2	2828	1839	gi 310632	hydrophobic membrane protein [Streptococcus gordonii]	64	38	990
74	2	861	355	gi 148436	secretory component [Erwinia chrysanthemi]	64	54	507
66	1	556	2	gi 1235662	RbC [Mycobacterium xanthus]	62	39	555
70	6	3017	2814	gi 1657478	similar to E. coli ORF_o208 [Escherichia coli]	62	41	204

Table 1 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
85	1	278	66	pir A45253 A452	activator 1 37K chain - human	62	56	213
126	1	3	323	gi 1778362	hypothetical protein [Escherichia coli]	62	45	321
73	1	773	3	pir S32879 S328	lipA protein - Neisseria meningitidis	61	46	771
96	2	796	644	gn PID e276217	T03F6.f [Caenorhabditis elegans]	61	46	153
67	3	743	1312	gi 609629	putative [Vibrio cholerae]	60	43	570
70	10	4666	4292	gi 1657478	similar to <i>E. coli</i> ORF_o208 [Escherichia coli]	60	45	375
81	1	1	1179	gi 1591717	spore coat polysaccharide biosynthesis protein E [Methanococcus jannaschii]	60	44	1179
80	5	2563	1790	gi 609632	putative [Vibrio cholerae]	59	41	774
137	1	73	528	gi 1736670	Adhesin AIDA-I precursor. [Escherichia coli]	59	45	456
61	1	773	3	gi 1196968	unknown protein [Insertion sequence IS66]	58	41	771
63	5	2831	2178	gi 622948	transposase [Escherichia coli]	58	41	654
64	3	3568	2690	gi 1335913	unknown [Erysipelothrix rhusiopathiae]	57	36	879
64	1	1819	917	gi 153826	adhesin B [Streptococcus sanguis]	55	30	903
64	9	7008	6685	gi 152259	lcrB gene product [Rhizobium sp.]	55	42	324
70	14	6481	6753	pir G42465 G424	hypothetical protein 88 - phage phi-R73	53	30	273
85	5	9317	1530	gi 144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	7788
64	8	5063	4806	gn PID e264304	F53C11.6 [Caenorhabditis elegans]	51	27	258
80	9	3411	2761	gi 149309	pull [Klebsiella pneumoniae]	50	40	651
88	1	98	388	gi 156087	[Brugia malayi myosin heavy chain gene, complete cds.], gene product [Brugia malayi]	50	32	291
96	3	1127	687	gi 1196964	unknown protein [Plasmid Ti]	50	38	441
89	1	981	4	gi 57633	neuronal myosin heavy chain [Rattus rattus]	48	22	978
113	1	657	199	gi 147899	extragenic suppressor [Escherichia coli]	48	25	459
118	1	654	145	pir S27564 S275	polysaccharide translocation-related protein - Escherichia coli	48	25	510
58	2	2101	4245	gi 1235662	RbC [Myxococcus xanthus]	47	35	2145
87	1	595	134	gi 1235662	RbC [Myxococcus xanthus]	42	28	462
85	2	1018	515	bbs 117606	glycine-rich protein. atGRP (clone atGRP-1) (Arabidopsis thaliana, C24, Peptide Partial, 210 aa) [Arabidopsis thaliana]	36	36	504
85	3	1779	973	bbs 157676	silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 633 aa] [Bombyx mori]	34	29	807

Table 2 (PAI IV)
Putative coding regions of novel *E. coli* PAI IV proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
58	1	1176	2120
61	2	54	560
63	4	1875	2639
64	4	3911	3627
65	6	3009	3239
65	12	6027	6683
66	2	1289	978
70	2	1418	861
70	3	1886	1476
70	4	2124	1900
70	5	2795	2220
70	7	3645	3259
70	8	4078	3680
70	9	4220	4513
70	11	4950	4498
70	12	4594	4866
70	15	6805	7449
70	16	9520	10806

Contig ID	ORF ID	Start (nt)	Stop (nt)
73	7	3247	3666
74	3	720	1301
75	1	1	165
79	1	719	354
80	6	2108	2575
80	7	2831	2469
80	10	3223	3387
80	11	3541	3362
82	8	3313	4260
82	11	4340	5218
82	13	6090	5614
84	4	3487	3281
85	4	1485	2285
85	6	8373	9320
104	1	358	2
112	1	677	105
142	1	3	143
142	2	1119	328

Table 3 (PAI V)
Putative coding regions of novel *E. coli* PAI V proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	3	2826	3686	gi 1655838	ORF B; putative transposase [Yersinia pestis]	100	100	861
14	2	1837	2907	gi 1655837	ORF A; putative transposase [Yersinia pestis]	99	99	1071
3	9	7927	7595	gi 1657499	putative transposase for insertion sequence IS3 [Escherichia coli]	89	85	333
20	6	3462	4304	gi 1208992	unknown [Escherichia coli]	87	73	843
6	6	3541	3263	pir S43483 S434	Orf104 homolog - Escherichia coli	81	62	279
20	3	1616	2332	gi 1033129	ORF_o233 [Escherichia coli]	80	61	717
9	1	1	681	gi 537112	ORF_o396 [Escherichia coli]	77	55	681
15	3	1899	1672	pir S43483 S434	Orf104 homolog - Escherichia coli	75	55	228
20	9	4302	4880	gi 1552816	similar to <i>E. coli</i> ORF_o152 [Escherichia coli]	74	60	579
14	13	12972	15359	gi 1772623	HecA [Erwinia chrysanthemi]	70	60	2388
5	3	1112	1570	gi 1001717	regulatory components of sensory transduction system [Synechocystis sp.]	68	45	459
3	1	2572	1373	gi 849022	Lactate oxidase [Aerococcus viridans]	66	46	1200
3	8	6869	6498	gi 581535	ORF140 gene product [Rhizobium sp.]	66	45	372
6	5	3265	2951	gi 642184	F19C6.1 [Caenorhabditis elegans]	66	44	315
14	12	11775	12974	gi 1772622	HecB [Erwinia chrysanthemi]	66	50	1200
20	1	545	1450	gi 1033127	ORF_o289 [Escherichia coli]	66	45	906
57	1	696	124	gi 1772622	HecB [Erwinia chrysanthemi]	66	47	573
3	3	3320	3700	gi 431950	similar to a <i>B. subtilis</i> gene (GB: BACHEMEHY_5) [Clostridium pasteurianum]	65	34	381
5	7	4565	4239	sp P39213 YI91_	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN.	65	38	327
22	2	1651	557	gi 290430	adhesin [Escherichia coli]	64	48	1095
5	4	1455	1841	gi 1575577	DNA-binding response regulator [Thermotoga maritima]	61	47	387
14	11	11161	11937	gi 1772622	HecB [Erwinia chrysanthemi]	60	39	777
14	1	930	1700	gi 1657478	similar to <i>E. coli</i> ORF_o208 [Escherichia coli]	58	47	771
5	6	3834	3391	gi 155032	ORF B [Plasmid pEa34]	56	36	444
3	5	6500	5982	gi 1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	54	25	519
14	7	8429	8809	gi 1196729	unknown protein [Bacteriophage P4]	54	41	381

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Table 3 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
14	14	15191	21793	gi 144048	filamentous hemagglutinin [Bordetella pertussis]	52	37	6603
14	16	21427	22671	bbs 117613	glycine-rich protein. atGRP (clone atGRP-4) [Arabidopsis thaliana, C24, Peptide Partial, 112 aa] [Arabidopsis thaliana]	52	39	1245
5	2	1004	381	gi 48518	HydC [Wolinella succinogenes]	51	34	624
5	5	1941	3311	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	51	21	1371
14	4	3968	5431	gi 1033120	ORF_o469 [Escherichia coli]	51	29	1464
32	1	481	227	gi 1673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from <i>E. coli</i> [Mycoplasma pneumoniae]	50	41	255
20	17	7039	7284	gi 1123054	coded for by <i>C. elegans</i> cDNA CEESN53F; similar to protein kinases including CDC15 in yeast [Caenorhabditis elegans]	48	28	246

Table 4 (PAI V)
Putative coding regions of novel *E. coli* PAI V proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	809	1165
3	2	3275	2640
3	6	6006	6425
3	7	6423	6833
4	1	3	455
5	1	501	4
6	1	2168	1749
6	2	2527	2114
6	3	2648	2331
6	4	3099	2626
14	5	7112	7699
14	6	7800	8507
14	8	9040	9624
14	10	10586	10846
14	15	21721	20921
15	1	575	826
15	2	850	1365
20	2	904	605
20	4	2330	3157
20	5	3139	3396
20	7	3812	3492
20	8	4373	3828
20	18	7282	7950
22	1	356	3
24	1	492	4

Table 5 (PAI IV)
Putative coding regions of novel *E. coli* PAI IV containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
59	1	968	54	emb X61239 ECPA	<i>E. coli</i> papABCDEFHIJK genes for F13 P-pili proteins	99	790	915
59	2	1551	805	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	99	518	747
59	3	1742	1494	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	99	182	249
61	4	1975	1220	emb X61239 ECPA	<i>E. coli</i> papABCDEFHIJK genes for F13 P-pili proteins	100	69	756
63	13	10097	10480	gb AE000133	<i>Escherichia coli</i> from bases 263572 to 274477 (section 23 of 400) of the complete genome	91	216	384
65	1	886	671	gb U06468	<i>Escherichia coli</i> 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	93	164	216
65	5	3218	2868	gb U06468	<i>Escherichia coli</i> 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	85	285	351
65	8	4064	3216	gb U06468	<i>Escherichia coli</i> 0111:H- insertion sequence IS1203 12.7 kDa protein and putative transposase genes, complete cds	86	145	849
65	9	4939	4337	emb Y00976 ECHN	<i>E. coli</i> hns gene for DNA-binding protein H-NS (5'-region)	96	53	603
65	10	4919	5266	emb Y00976 ECHN	<i>E. coli</i> hns gene for DNA-binding protein H-NS (5'-region)	98	310	348
65	11	5206	5781	gb AE000133	<i>Escherichia coli</i> from bases 263572 to 274477 (section 23 of 400) of the complete genome	89	431	576
68	1	1575	1315	emb X61239 ECPA	<i>E. coli</i> papABCDEFHIJK genes for F13 P-pili proteins	100	186	261
	2	2468	1848	emb X51704 ECPA	<i>Escherichia coli</i> papI gene for PapI protein	99	621	621
68	3	2232	2594	emb X61239 ECPA	<i>E. coli</i> papABCDEFHIJK genes for F13 P-pili proteins	99	363	363
68	4	3212	2466	emb X61239 ECPA	<i>E. coli</i> papABCDEFHIJK genes for F13 P-pili proteins	100	747	747
69	1	300	4	gb M14040	<i>E. coli</i> apt gene encoding adenine phosphoribosyl-transferase (APRT), completed cds	98	225	297
69	2	383	117	gb M14040	<i>E. coli</i> apt gene encoding adenine phosphoribosyl-transferase (APRT), complete cds	95	162	267
70	1	832	149	gb U09857	<i>Escherichia coli</i> 4787 o15:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	89	225	684
70	17	10799	11767	gb AE000291	<i>Escherichia coli</i> , asnV, erfK, cobT, cobS, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	95	553	969
70	18	11809	11045	gb AE000291	<i>Escherichia coli</i> , asnV, erfK, cobT, cobS, cobU, y152_6, y122_3, y121_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	94	595	765
70	19	12022	15222	dbj D90838 D908	<i>E. coli</i> genomic DNA, Kohara clone #348 (44 5-44 9 min.)	89	2667	3201

Table 5 (PAIV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
70	20	15316	16836	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	1488	1521
70	21	16722	17711	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	82	990
70	22	17426	16776	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	63	651
72	1	12	1061	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1024	1050
72	2	947	1285	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	96	261	339
73	6	4437	3205	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	392	1233
73	8	6177	4555	gb U28377	<i>Escherichia coli</i> K-12 genome; approximately 65 to 68 minutes	90	1133	1623
73	9	6835	6128	gb AE000380	<i>Escherichia coli</i> , glcB, glcG, glcD genes from bases 3112500 to 3126189 (section 270 of 400) of the complete genome	93	703	708
75	2	1553	1059	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	90	385	495
75	3	2579	1566	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	464	1014
75	4	3297	2743	gb U07174	<i>Escherichia coli</i> 09:H10:K99 heat resistant agglutinin 1 gene, complete cds	81	283	555
76	1	698	3	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	693	696
78	1	382	59	gb AE000360	<i>Escherichia coli</i> from bases 2885166 to 2897277 (section 250 of 400) of the complete genome	99	315	324
79	2	2620	1529	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	1084	1092
79	3	2925	2587	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	97	322	339
79	4	3576	2923	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	654	654
80	1	376	83	gb U05251	<i>Escherichia coli</i> polysialic acid gene cluster region 3, promoter region	93	210	294
80	2	638	210	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	347	429
80	3	1246	710	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	96	388	537

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
80	4	1796	1182	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	397	615
82	1	1	567	emb X74567 ECKP	<i>E. coli</i> K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	87	551	567
82	2	549	1157	emb X74567 ECKP	<i>E. coli</i> K5 antigen gene cluster region 1 kpsE, kpsD, kpsU, kpsC and kpsS genes	88	554	609
82	3	1500	1180	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	90	62	321
82	4	2163	1519	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	143	645
82	5	2594	2139	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	97	456	456
82	6	3000	2605	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	98	396	396
82	7	3463	3047	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	283	417
82	9	3831	3337	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	495
83	1	3	311	gb AE000151	<i>Escherichia coli</i> , ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	99	207	309
83	2	176	433	gb AE000151	<i>Escherichia coli</i> , ybaE, cof, mdlA, mdlB, glnK, amtB, tesB, ffs genes from bases 464774 to 475868 (section 41 of 400) of the complete genome	100	223	258
86	1	529	2	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	93	398	528
93	1	440	3	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	95	351	438
94	1	368	72	emb X14180 ECGL	<i>Escherichia coli</i> glutamine permease glnHPQ operon	100	229	297
99	1	161	586	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	98	426	426
99	2	643	476	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	168	168
99	3	532	1092	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	95	537	561
99	4	1094	1396	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	94	274	303

Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
102	1	527	3	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	100	427	525
102	2	762	373	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	99	333	390
105	1	377	3	gb AE000480	<i>Escherichia coli</i> from bases 4277211 to 4288813 (section 370 of 400) of the complete genome	100	343	375
107	1	2	397	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	390	396
107	2	406	966	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	549	561
110	1	148	2	emb X56175 ECSE	<i>Escherichia coli</i> secD and secE genes for membrane proteins involved in protein export	99	143	147
110	2	312	40	gb M63939	<i>E. coli</i> tRNA-guanine-transglycosylase (tgt) gene, complete cds	100	125	273
115	1	501	325	gb AE000459	<i>Escherichia coli</i> from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	98	177	177
117	1	3	302	gb AE000506	<i>Escherichia coli</i> from bases 4584059 to 4594314 (section 396 of 400) of the complete genome	100	263	300
121	1	2	250	gb M16202	<i>E. coli</i> papH gene encoding a pilin-like protein	98	148	249
123	1	361	2	gb AE000379	<i>Escherichia coli</i> from bases 3102169 to 3112339 (section 269 of 400) of the complete genome	99	113	360
127	1	2	229	gb AE000233	<i>Escherichia coli</i> , racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	100	200	228
127	2	227	382	gb AE000233	<i>Escherichia coli</i> , racC, ydaD, sieB, trkG genes from bases 1415432 to 1425731 (section 123 of 400) of the complete genome	97	113	156
130	1	337	2	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	335	336
131	1	510	79	gb M30198	<i>E. coli</i> recQ gene complete cds, and pldA gene, 3' end	98	304	432
131	2	743	270	gb M30198	<i>E. coli</i> recQ gene complete cds, and pldA gene, 3' end	99	314	474
133	1	1	258	gb AE000115	<i>Escherichia coli</i> , yabF, kefC, folA, apaH, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	98	237	258
133	2	192	350	gb AE000115	<i>Escherichia coli</i> , yabF, kefC, folA, apaH, ksgA, pdxA, surA, imp genes from bases 47163 to 57264 (section 5 of 400) of the complete genome	99	115	159
135	1	103	327	emb X02143 ECPL	<i>Escherichia coli</i> K-12 pldA gene for DR-phospholipase A	97	178	225
135	2	152	409	emb X02143 ECPL	<i>Escherichia coli</i> K-12 pldA gene for DR-phospholipase A	98	157	258

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Table 5 (PAI IV) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
136	1	122	532	gb AE000459	Escherichia coli from bases 4013123 to 4024654 (section 349 of 400) of the complete genome	97	237	411
140	1	576	244	gb AE000291	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	89	329	333
141	1	445	2	gb AE000291	Escherichia coli, asnV, erfK, cobT, cobS, cobU, yi52_6, yi22_3, yi21_3 genes from bases 2060089 to 2072765 (section 181 of 400) of the complete genome	77	432	444

Table 6 (PAI V)
Putative coding regions of novel *E. coli* PAI V containing known *E. coli* sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3	4	6150	4855	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	91	129	1296
3	10	8214	7723	emb X02311 ECIS	<i>E. coli</i> insertion sequence IS3	76	274	492
3	11	7867	8319	emb Z11606 ECIS	<i>E. coli</i> DNA for insertion sequence IS3	80	378	453
3	12	8462	8157	emb Z11606 ECIS	<i>E. coli</i> DNA for insertion sequence IS3	90	267	306
3	13	8487	8663	gb L19084	<i>Escherichia coli</i> RhsD genetic element; core protein (rhsD) gene, complete cds; complete ORF-D2; complete ORF-D3	96	112	177
4	2	1441	815	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	91	577	627
4	3	923	1372	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	448	450
4	4	2343	1324	gb AE000498	<i>Escherichia coli</i> from bases 4493507 to 4503769 (section 388 of 400) of the complete genome	92	244	1020
7	1	3	743	emb X61239 ECPA	<i>E. coli</i> papABCDEFHJK genes for F13 P-pili proteins	100	741	741
7	2	977	615	emb X61239 ECPA	<i>E. coli</i> papABCDEFHJK genes for F13 P-pili proteins	99	363	363
7	3	741	1214	emb X51704 ECPA	<i>Escherichia coli</i> papI gene for PapI protein	98	459	474
8	1	438	4	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	435	435
10	1	1932	2426	emb X61238 ECPR	<i>E. coli</i> prsEFG genes for F13 pili tip proteins	97	462	495
11	1	903	1550	gb M10133	<i>E. coli</i> (J96) hlyC, hlyA, hlyB and hlyD genes coding for chromosomal hemolysins C, A, B and D	99	452	648
12	1	2559	1531	gb U82598	<i>Escherichia coli</i> genomic sequence of minutes 9 to 12	100	1029	1029
12	2	1594	1860	emb X13668 ECIS	<i>E. coli</i> insertion element 5 (IS5) DNA	100	267	267
12	3	1858	2235	gb U95365	<i>Escherichia coli</i> transposon IS5, transposase (is5B) gene, complete cds	99	354	378
13	1	93	1424	emb X61239 ECPA	<i>E. coli</i> papABCDEFHJK genes for F13 P-pili proteins	99	885	1332
14	9	9832	10515	gb U09857	<i>Escherichia coli</i> 4787 o115:v165:f165 fimbrial regulatory f1652I, f1652B and f1652 A genes, complete cds	92	225	684
16	1	1	375	gb U07174	<i>Escherichia coli</i> 09:H10:K99 heat resistant agglutinin I gene, complete cds	94	320	375
16	2	263	616	gb U07174	<i>Escherichia coli</i> 09:H10:K99 heat resistant agglutinin I gene, complete cds	98	283	354
17	1	282	4	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	98	240	279
17	2	410	174	emb Y00529 ECPA	<i>E. coli</i> papC gene involved in formation of pap pili	100	168	237

Table 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
19	1	1	369	gb AE000418	<i>Escherichia coli</i> from bases 3550279 to 3561054 (section 308 of 400) of the complete genome	99	347	369
20	10	5401	4829	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	468	573
20	11	4874	5371	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	96	453	498
20	12	5245	5679	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	89	235	435
20	13	5732	6139	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	93	329	408
20	14	6316	5822	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	95	239	495
20	15	6048	6590	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	406	543
20	16	6569	7075	gb AE000292	<i>Escherichia coli</i> , yeeA, sbmC, yeeC, sbcB, yeeD, yeeE genes from bases 2072708 to 2083664 (section 182 of 400) of the complete genome	87	136	507
20	19	8686	9915	gb M67452	<i>Escherichia coli</i> lysine decarboxylase (cadB, and cadC, complete cds, and cadA, 5' end) genes	98	1205	1230
20	20	10604	11938	gb U14003	<i>Escherichia coli</i> K-12 chromosomal region from 92.8 to 00.1 minutes	98	1308	1335
20	21	11940	12368	gb M76411	<i>E. coli</i> cadA gene, 5' cds and cadB and cadC genes, complete cds	100	363	429
21	1	369	4	emb X03391 ECPA	<i>E. coli</i> major pilu subunit genes papI, papB, papA and papH 5'-region	98	201	366
23	1	1	879	gb U14003	<i>Escherichia coli</i> K-12 chromosomal region from 92.8 to 00.1 minutes	98	879	879
23	2	900	16	gb U14003	<i>Escherichia coli</i> K-12 chromosomal region from 92.8 to 00.1 minutes	98	885	885
23	3	953	1186	emb X77707 ECCY	<i>E. coli</i> ORF112, DIPZ and ORF191 genes	99	225	234
23	4	1223	2677	emb X77707 ECCY	<i>E. coli</i> ORF112, DIPZ and ORF191 genes	97	1454	1455
25	1	536	171	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	164	366
25	2	1128	562	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	99	459	567
27	1	708	436	emb X61239 ECPA	<i>E. coli</i> papABCDEFGHIJK genes for F13 P-pili proteins	100	252	273
28	1	309	4	emb X77707 ECCY	<i>E. coli</i> ORF112, DIPZ and ORF191 genes	98	278	306
28	2	431	213	emb X77707 ECCY	<i>E. coli</i> ORF112, DIPZ and ORF191 genes	96	150	219

Table 6 (PAI V) (CONTINUED)

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
30	1	399	4	gb M26893	<i>E. coli</i> amidophosphoribosyltransferase (purF) gene, complete cds	98	295	396
31	1	706	170	emb X56780 ECRR	<i>E. coli</i> terminator sequence of RNA G operon gene	99	513	537
37	1	2	400	gb M63703	<i>E. coli</i> pyruvate kinase type II (pykA) gene, complete cds	98	399	399
38	1	463	2	emb X13463 ECGU	<i>Escherichia coli</i> gutM gene and gutR gene for activator and repressor proteins	99	363	462
42	1	413	3	gb M64367	<i>Escherichia coli</i> DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	97	316	411
42	2	115	591	gb M64367	<i>Escherichia coli</i> DNA recombinase (recG) gene, complete cds, spoU gene, 3' end, and gltS gene, 3' end	98	266	477
46	1	2	277	emb X77707 ECCY	<i>E. coli</i> ORF112, DIPZ and ORF191 genes	98	187	276
48	1	1	171	gb AE000491	<i>Escherichia coli</i> from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	162	171
48	2	105	464	gb AE000491	<i>Escherichia coli</i> from bases 4413548 to 4424699 (section 381 of 400) of the complete genome	98	144	360
49	1	2	172	gb U00800	<i>Escherichia coli</i> cloning vector Pk184, complete sequence, kanamycin phosphotransferase (kan) and (lacZalpha) genes, complete cds	98	167	171
50	1	414	4	gb AE000341	<i>Escherichia coli</i> , glyA, hmpA, ginB, yfhA, yfhG genes from bases 2677406 to 2687636 (section 231 of 400) of the complete genome	99	411	411
52	1	2	307	emb X60200 ECTN	<i>E. coli</i> transposon Tn1000 (gamma delta) tnpR and tnpA genes for resolvase and transposase	100	284	306
53	1	280	41	gb M36536	<i>E. coli</i> htrA gene, complete cds	100	131	240
53	2	558	214	gb M36536	<i>E. coli</i> htrA gene, complete cds	99	315	345
54	1	9	263	gb AE000381	<i>Escherichia coli</i> from bases 3125914 to 3136425 (section 271 of 400) of the complete genome	94	111	255
55	1	1	675	gb AE000179	<i>Escherichia coli</i> , modA, modB, modC, ybhA, ybhE, ybhD genes from bases 794199 to 805132 (section 69 of 400) of the complete genome	98	332	675

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While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

5 All patents, patent applications and publications recited herein are hereby incorporated by reference.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

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APPLICANTS/INVENTORS: Dillon, Patrick J.
Choi, Gil H.
Welch, Rodney A.

(ii) TITLE OF INVENTION: Nucleotide Sequence of *Escherichia coli*
Pathogenicity Islands

(iii) NUMBER OF SEQUENCES: 142

(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
(B) FILING DATE: 22-NOV-1996 AND 14-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.074PC02/EKS/CBM

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CNTANATTAG GCCTGCTNAA TGTATTTATA TCTAAAAAAA TTCGCATCCA AAAGGAATCC	60
AATCTGTACT GTTTTTTCTT GTGCTGACAT CTTCTTTTCC CTGGCTGGTA TGGCAAGTGA	120
CGGAGACAAG AGAAACGTTT TAAGCTCAGT TATCTCCGCC ATCACTTTCC ACGAATGACA	180
AGTAATTTTG CCTATTTTAA AACCATGCAA AAGGCAGGGT AAAAGGAGAA AATTTCGATCG	240
AATCGATCGA CAAAATCGAT CATACATGAT GAAGATTTCT TATCGAATCC ATAAAAATAG	300
TGACAGCTAA CCGGCGTTGC AGGAACAGTC AGAAATGGGC GTTTGGGAAA GAGCCATAGC	360
ATACGTCGTC GCTGACATAG AGGAACTGTG CTTTGTTGAT AAGATCCTTT ATACGGCAAC	420
CAATCCACTG GACAAAAGAT GAACTACGTA ATCACCAGGT TCTCACTGAC GAAATACAGA	480
AGTTAATGAC ACAACTGTGC CATGCACCTT GTACAACAGC GGTGGAAAGC TCTCAGAACA	540
ATGGAATTGC AGAAAGGTGT TAAAACGATG AAAGCCTTCA TACCCAAATC GAATGTAAGA	600
ACGGCAGTAA AGACTGAATT GCGTAACCTT GCAGTAGCTC GAGTATTACA CTGCATAGTG	660
TGCAGGGTTA TCTCCCATCG AGAAAATATC GGCGCCAGCG AATAACGTCA CCTTAGATGT	720
AGCAGTTGCC AAATAGTGAC TCAAGGGCGG GCTTACCGCA TACACTGACA CTTAGCGGAT	780
CGACAGAATA TTATTAGCAG ATCATCACTG AACGCTACGT AATTATCGTA ATAAAGGCTT	840
TTTCTGGCTA CCAGGAAGAC CTGACATGGC TCTGCTCTGG AACCAGGCCG CAGGAAGCAT	900
CAATCTGGAG TTTATCAGCT ACTGGAATTC CGGTGTATTG GCAGCCCCTG ATAATCACCT	960
GACCCACGAA GAGCGCTCTG CTTTGCAGAA ACTCTGGGGC GGTTCGGAGA CAGGAGATGT	1020
AACGATTATA GGACGTTCTG ATGAAGTCCA TGATTTTACC TCCGCCTTAA TTAAGTGT	1080
TCTTTCTGAA GAAGAAATTG TCTGGTGGCA ATCAGGTGGC ATTTTCCCGG ATCCTTGGCC	1140
CGCTAATATA TCCCGGCTGA ACTGACGATT AACGCGAT	1178

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCCTATTCA TTTTGCCATG ACGGGCGAAC TCCAGATAAA GGTTTTGAAA GTAATGAGAA	60
ATTATTAATT CATCCATGTT ACTGGCTTGG TTTGAATCTA AATCGTAATG CACTTGCTCC	120
AGAGGAAGCA GAGGAGATAA ATGACGAATA TGATATTAAT ATTATTTTCA ATAATTCAGC	180

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CATTAGAAAT AAAACAATAG GTCAAATAAC TACTCATCTA GATCAGATAC CGATAGGAAA	240
TGAAGGTGCC ACTGAATTTG AACAATGGTG TTTAGACGCA CTAAGAATAG TATTTGCATC	300
CCACCTAACA GACATCAAGT CCCATCCAAA TGGTAACGCA GTTCAGAGAC GAGATATTAT	360
AGGCACCAAT GGTGGCAAAT CTGAWTTTTG GRAACGAGTA TTGGAGGACT ATAA	414

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGGATCTG GTACANTCCA CCCAGCGGCA TTATCCNGAA GGCAATATTT TTAAGGATTA	60
TTCTGCCACA AAATCAGTAC TGGAACCAGG CTCAAAAAAG GCTTTAACGT GACCTGCTNC	120
CATCTACAGT AGATGTACAA CCTGTTAAGT TAATTGAAAA TGGTGTTAAT CCGGTTGTTT	180
CTCCAGGGGT AGCAAGGGCC TTATTCGATA CAGTGGGTAA TGTTACTGTA AAATTACCAT	240
CATTCCCTGT GGTCACATTG CAGGTCTGAG CTACAACTTT GCCTGTAAAC GTAATTGTTC	300
CGTCATAGGC CATAGCTGAA CCAACAAACA CAGCAGAAAC AAATGTAGCC AATGCTATAA	360
CTTTTATTTT CATAAAATGA ATTCTGTGTT AATTCCGGTA TTGATCATTT GTTCAGCAAT	420
CATCCCCAAC AAAACAATCA TTTTCAAAAT GTTTTACCG ATCGATAACC AGCACATGAT	480
AGATTGCACC TATCATGATT GCTAAAACGA TCGGGAAAAG CGATCAAAAA CCATATTTAT	540
TGTGTTGGTA ATGACAAAAG ATATGCTTTA CCCTGAAATG AGCGACCTAT TCATGAAAAT	600
ATGTAGGTCT GTATTTGATT ACTATCATTG CTATATTTCC ACTATCCAAT TTATATTTCA	660
TGATTAAAAAT ATACCTTTTT AACTATTAT TTATTTGTTG CAGCTTGCCT GGCTTTATCT	720
TATTCGACT ATTTTATGGT AGATACAGAA TACAATTAAT TAACTTATT TAAAGATTTT	780
ATAAATACCA TATTGGAGTT GACCGATAGA TACCTACTAA CAAGAGCAAT CACCACCACC	840
CCATGAGGTG TTTAGGAATA CAATCAATAA ACAACATCCA TGCCCGGCGA CGTACATACC	900
TGTTTGCTAT GATATCTGTT ACGCTACGCT TGCTAATTTA CTGAAACTCA GCATCTGTCTG	960
ACGGAGATTC GTCCGGGCCC TGATACAACA AGGGCAAGAA AACCACCCGA AATACAGATA	1020
TTCTTATAAA AATGGATCAT ATTTCCATGT GCAAGTTCAG CTGGCATCGT CCAGAATGCG	1080
TGTCCAAGAA ATGAAGCAA CACGGTATAC AGGCACAGAA TAATGCTCAC TGGCCGGGTG	1140
AAAAAGCCRA AAACAATCAT TAATGCTCCA ACGATTTCTGA CAAGGACCAC TATTGCTGCA	1200
GTAATCGCCG GAAATATAAG CCCAAGAGAG GCCATTTTAT CGATAGTGCC AGTGAATGAT	1260 -
AGCAGCTTGG GAACGCCGA TATCATATAA AGGCATGCCA GCATCAGACG GGCAAGGAGC	1320

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AACAATGCCG ACGTGTAAAT TCCCATATTA AAATACCTGA TTTTATCCAC TATCAATGCT	1380
CAGTCTCCTT GTTTCTGATA AAGCCCTGAG CCAAATCCTT AAGTGTACGA GCACCACTCA	1440
GTAACATTGC CGTCCTCAGC TCCGTCTTCA GGTGCTCAAT GACTACTGGCA ACGCCCCCGA	1500
CACCACCTGC TGCATGCCA TAAAGAACAG GACGTCCGAC CGCAACAGCC GTTGCCCCAA	1560
GAGAGATAGC CCTTACAACA TCAACCCCCC TGCGAATACC GCTGTCAAAA ATGACCGGAA	1620
CTTTGTGCCC GACTCTTGCA GCAACTTCCT GCAACTGGCT GATGGCAGAA GGAACACCAT	1680
CAATCTGGCG ACCACCATGA TTAGACACCT GGATGGCATC TGCTCCTGCA TCAATGGCGA	1740
CCACTGCATC CTCACCTCTG AGGATGCCCT TGACAATGAC TGGCAGCCCG GTGATTTTTT	1800
TTACAAACTC AATATCAGCC GGGGTGAGCT CAACTTTTTG GTTAAAAAAA TCACCTTTGC	1860
CACCGTAACG GGGGTCATGA TTACCGAAGC TCGCTCCTGC AGGGAAAGGC GAGCTCATGC	1920
TGAGAAAAGC ATCACTTGTC CCGGGACCAA GCGCATCCGC TGTGATAATA ATGGCTGAAT	1980
AGCCTGCCGC TTTTGCACGC TCCAGTAAAC TTCGGGTCAC ACCAGCATCC GCGTTAAAAT	2040
ACAGCTGGAA CCATTTAGGT CCTTTACTGG CTTTTGCAAT ATCCTCCAGA GAGCGGTTGG	2100
ATGCCCCTGA TGATTCATAA AGTGCCCCGG CTTTTTCTGC ACCCGCTGCA GCAATCACCT	2160
CCCCTTCCGG ATGGACGAAC ATATGCGCGC CCATAGGTGC TATCAGCAGG GGATGTTCCA	2220
GATGATGGCC CAAAAGGTCA GTCCGGATAT CAATGCTGTG GGCAGCAACT CCACTGAGTC	2280
GGTGAGGTAA CAAAGGATAA TCACTGAANT GCCTGCGGTT CTCATGATAC GTCCACTCAT	2340
CTCCAGCACC ATGAGCAATA TATGCATACG CAGCTTCCGT CATCACATCT TTTGCTGAAG	2400
TCTYCAGTCT GTCCAGACTG ATGATATGAA GAGATTTGCT GGTCGATGTA TCAGCATGTC	2460
CAGACGTTTT ACTGATGATA TGTGCCGTTG AAGATGAGAT ATTTTTGGCA AGGGCCGGCG	2520
CAGTTGACAG CCTGCGGCAG ATATTCCTAA AACGGCATTG TGAATAAAAT TACGTCGGGA	2580
AAGAGGCATA ATAAGCTCCA TATATTATAA ATAAGCCAGG TCTCCCTGGC TTATAATGAT	2640
CATGCCACGC CCTGAAGCGG GTTGGTGTTG AAGGTATAAA GGAAAATTTT CCATTACCA	2700
TTAATTTTAC TGAGGACAAA AACTTCACGG TTCAGGTCAA TAATGGTTTT CTGCTCTTTA	2760
AAGTTCGTTA CAACAGAACC CACATGGTGG TGAGTGCGGA CAACCGCGGT ATCTCCGTTG	2820
ATCCAGATAG AGTCAAACGC AAAATCGGTC TCAAACTTTT CACGCTTGAA CAGATCATCG	2880
TACTGCCCCT GCGTTTTTTC TGTATTGTCA GCCGTCAACT TATCATTCCA CTGGAATAA	2940
CTTTCATCAG CAAACAGGCC CAGGATGGTT TTTGTATCCC CGGCATTCAG TCGTTCTGA	3000
TACTTGATTA TCGTGTCATA CAGTTCTTTC TGCTCAGTAG CAATCTTACT GTCTGTGGAG	3060
TATTTGAATG TACCGCCGGA TTGTTCAAGT GAGCTTTCCT TCTGTGCTGT CGACGATGAG	3120
GCAGCCAGAG CATTAGAGCC GAAAAGAAGG GATGATGCCA TGA CTGCTGT TGCTATAAAA	3180 -
TGTTTCATAT ATTCTCCATC AGTTCTTCTG GGGATCTGTG GGCAGCATAT AGCGCTCATA	3240

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CTATGCTGCT GTTTC AATAT TAGCGGCAGA CGTCAGCCTT ACCGCACTAC TTATTGGATA	3300
AGAATATCAA AAGTGACCGT GAAGTCAATT TTATCACAAC ACAGAAGGCC ACTATTTATG	3360
CCCAGAAAAT ATGAATCGTC CTCATCATGC ACGAAAGACT CAGTAGTTGCA GCCCCGAAAA	3420
AACTGCCAGG ACACGACAGC AGATAGCCCG GGCAGCACTT GAGGAGTTCT CTGCACAAGG	3480
GTTGCTCGC GCCACATNCA GCAATATCAG CAAGCGCGCA GGAGTAGCTA AAGGCACGGT	3540
ATATAACTAC TTCCCAACAA AGGAATTATT GTTTGAAGCG GTTCTGAAGG AGTTCATTGC	3600
TACCGTCCGT ACTGAACTGG AATCTTCCCC CCGCCGCAAC GGGGNAAACC GTAAAAGCCT	3660
ATCTGTTGAG AGTGATGTTA CCTGCCGTCA GGAAAATTGA CGACGCATCA ACAGGCAGAG	3720
CCAGAATAGC CCACCTGGTT ATGACAGAAG GGAGCCGGTT CCGGTAATC GCTCAGGCTT	3780
ATTTACGGGA AATACATCAG CCACTACAGC AAGCCATGAC CCAACTGATT CAGGAAGCAG	3840
CATCAGCCGG AGAGTTAAAA GCAGAGCAAC TGCTCTGCKT CCCCTGTTTA TTGCTGGCTC	3900
CAAACCTGGT TGGCATGGTG TATAACGAAT TCTGAACCCG GCAGCACCGG TCAGTACAGG	3960
CGATCTTTTT GAAGCCGGAA TTGGTGCTTT TTTCCGATAG ACACATAACT GTCAGTATTA	4020
TGACCATGCC GTCAGGAGGA GGTATACCAG TGATACCCTG CCATGACCCG GTAACGTCTC	4080
CTGGCTGCCT TAAACCTGAA AGACCTGGCC CCACCACACT GCCGGTTACG CATCAAGATG	4140
CAGCAACCCT TGCATAAGGC TGTTTTGTGC AGAGGGCTAC CGGAAAGATA ATAACGTCAC	4200
AGCCCGTATG CATCAGATAA AACAGTGTAT TTTATCTGTC AGCAGTCACT GGAGCGGATT	4260
GTGGGGCGAG ATTCAGGTGC TGATACTGTA ACGACTCTGC GCCGCTGCTG CCGTAAAAGC	4320
GGCTGCCACC AGGCACGGTT ATCAGAGGAG GATGACCGTG TCCGCCCTG GTGGTGATGA	4380
ACTCTCCATC ACAATCAATA ATGCCGCCGG GTGGATGAAG CAGACAGGGA TGGCAAGTCC	4440
CACTATCCCG GATAAAATGG GCTCTGGGCG CTCAGAAGAC CTGTGTGTCA GGCAGGGGTG	4500
AGAACGGTGA TGTTTTTTGT TGTCTGAAAG TCCAGCTCCA GCATTGCCTG CCAGCCTCAA	4560
GACTTCCGCT TTCTGCCCTT TCCGGCATT TCTTCCGTTA CCATCATTTCT GTTAATTGAG	4620
AGGCGTAGTA GTAGTAAACG TAATACATAT CCGGGAGGAT GAAGTCATCT AATCCTGCTC	4680
CCCGAATATC ATACAGCCAT TCCTGAGTGT GACTGCACCA TTTCCAATTA TGCAGTCTGT	4740
CCTCATCACA AAAATGTTGC AAGCAGTGCG GAGTCACGTT CCGTATTCAT GCCCTCTGCC	4800
AGATATTGAG CGGGGGAGAA ATGTGTAAGC GTCAACAGAG CGCCGTATTG ACACTTATTT	4860
ATCGGTGAAA ACTACGTTCC ATGGCAGCAG TTCGTCAACA CGGTTGGAGG GCCATTCCGG	4920
CAGTACGCTC AGGATATGGC GCAGATACGC TTCTGGATCG ATACCGTTCA ACCGACAGCT	4980
CCCGATTAGT CCGTACAGCA GAGCTCCGCG CTCGCCTCCA TGATCGTTGC CGAAGAACAT	5040
GTAATTCTTT TTCCCGAGAC AGACGGCAGC AAGCGCTCTT TCTGCTGTGT TATTGTCCGC	5100 -
CTCCGCCAGA CCGTCATCAC TGTAATAACA GAGGGCGTCC CACTGATTCA GGACATAGCT	5160

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GAACGCTTSR CCCAGTCTGG ATTTTTTCGA CAACGTGCCA TTCTTCTCCA CCATCCATTC	5220
ATGCAGCGAC GTCAGTAACG CTTTGCTTCG CTGCTGCCTG GCTGCAAGAC GTTCAGACTC	5280
CGGTAAGCCC CGTATTTTCAT CMTCAATGGC GTACAGTTCA CTGATGCGCT TCAGAGCTTC	5340
TTCTGCCGTC GTA CTTTTCG TGCTGATGTA TACATCGTGG ATTTTTCGCC GGGCATGGGC	5400
CCAGCAACGCA ACTTCTGTCA GTGCACCACC TTCACGTTTCG GCACTGAACA GCCGATCGTA	5460
ACCGCTGAAT GCATCCGCCT GCAGGATACC CCGGAAGGGA CGAAGSTGTT GTACCGGATG	5520
TTTTCCCTGC CTGTCTGGTG AGTAGGCGAA CCAGACCSCC GGTGGCTCTG ATGAGCCCGC	5580
ATTCCGGTCA TCCCSGACAT ACGTCCAGAT GCGTCCTGTT TTTGCCTTTT TTCTGCCCCG	5640
TGCCAGCACT TTTACTGGTA TGTCGTCAGT GTGAACCTTG CGGGTGTTCA TCACGTAACG	5700
GTACAGGGCA TCATTCAGCG GAGTCATTAA CTGGCAGCAC GCGTCAACCC AGTTGGAGAG	5760
TAATGCACGG CTCAGTTCGG CACCCTGTCG GGCAAAGATT TCACTCTGAC GATACAGTGG	5820
CAGGTGTTTCG CAGTATTTTC CCGTTAACAC GCGGGCAAGT AATCCGGAGC CCGCGATGCC	5880
GCGCTCTATC GGGCGGGACG GCGCTGGCGC TTCAACTATA CAGTCACATT TTGTACAGGC	5940
TTTTTTTACC CGAACAGTGC GGATCACTTT CAGGGCGCTA CTCACCAGTT CCAGCTGCTC	6000
AGCACTAACT TCACCCAGAT AATCCAGCTC ACTGCCACAC TCCGGGCAAC AACTTTCTTC	6060
AGGCTCCAGG CGGTGTATTT CACGGGGAAG ATGTGCTGGT AACGGACGAC GATGACGTGA	6120
TTGTGCGAAC TGGCGGGGAA CTGCGGGTCA TCCTCACGCC CACTGTAACG ATCGCTTTCC	6180
TGTTGCGGTT GTTTCAGTTG GGCCTCAGCC TGTTCAACCT CACGCTGCAG TTTTTCAGAA	6240
CGGGTACCGA ACAGCATCCG GCGCAGTTTT TCTATCTGGG CCCTCAGATG TTCTATTTCC	6300
CGCTCCTCCT CTTGATCTT TTCTTCGGCA CGTGCCARTG CAGAGCGCAG GAAGGCCTCC	6360
GTCTCTTCAA CCAGACTCAG TTGCTGATCT TTCTGACGGA GGGCTTCAGC CTGCTCAGAG	6420
AGTAGCCTTT CCAGCTCAGT GATACGAATG AGGTATTTCC GACTCATGAC CGTTTTTATA	6480
ATCCGGCCAT GACATTTTTA CAACATTGTC AGTGCAATTA GCGGGATGT TTTGGGTGA	6540
CGCCAGTCCA GTTTATCGAG GAGCATTGCC AGCTGCGAGC GGGTAATGGA TACCTTACCG	6600
TCACGCACCG CAGNCCAGAT AAAGTGGCCT TCCTCCAGAC GTTTGGTGAA CAGGCACAGA	6660
CCATCAGCAT CAGCCACAG GATTTTAATC GTGTCACCCC GTCGGCCGCG AAAGATAAAC	6720
AGGTGACCGG AGAAGGGGTT CTCATCCAGC ACATGTTGTA CCTGTTTACC CAGACCGTTG	6780
AAGGATTTAC GCATATCAGT AACGCCGGCA ACCAGCCAGA TTCGAGTGTC TGATGGGAGC	6840
GAGATCATCG TCCTCTCCCG GTCAGTTCAC GGATCAACAC CGTGAGCAGC TCTGGTGAAG	6900
GATTTTCCAG CGTCATGTTA CCGTGGCGGA ACTCAACTTT ACAGGAACTG GCACTGACTG	6960
TGCTTTGTGA AGGAGTGGAT AAAAGCGGAG TAAGAGCCGC CATAGGCTCT TTCTGCTCAT	7020
CAGGCGTTAT CTCAACAGGT AATAATTCAA CGCCAGCGCC AGAAGAGGTT GTTACCGGAA	7080

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GACGCCGCGA TATACGCCCT TCGTTCTGTC AGAGCCTGAG CCATTTGAAC AGGAGGTTAT	7140
CATTGATATC GTGTTCCCTG GCAATACGGG CAACAGAGGC TCGTGGTTGT GAAGCCAGTT	7200
TAACCATTTG AAGTTTAAAC TCATTTGAAA ATGTTCTGCA GGTTTCTGCG GATAATATTT	7260
TCTGTTCCAT AACAGGTGTC CACTAGTTGA AAAAGTGGGC ACCTACGTTA CCAATACTGG	7320
CTTAATGGCT ACATACGGCG GTCAGTTTAC GCTTACAGAA ATGTAATGAA CACGTCTAC	7380
CATTAACTGA AGAGCATGGT GACGGATGAA GGAAAAAGCA GGAGTGTGTG GTGCCTCACA	7440
GATTTCCGAC ATCATAGCTG TCAACGACGG ATGAAAAGCG GCTCTTCCGC AACTTGGGTG	7500
GAAGAAAATG GATGAACTT TCTGGTGTGA GAACCTTAAG GAAACAACAT GTTGGGTGGA	7560
GCGGACAATC CAAATGGTGA ATTACCGTCT TATATCACTG GCGCTGACAT TCCGGGCGTC	7620
TTCTCCGCCA CAACGCCATT TGCAGTGCAT CACAGGCCAG TTGTGCTGTC ATTCGCGGTG	7680
ACATCGACCA GCCAATAACG GCGCGTGACC ACAGGTCGAT GACTACTGCG AGATACAACC	7740
AGCCCTCATC GGTACGCAAG TAMGTGATGT CACCCGCCCA MTTCTGGTTC GGAGCCTGGC	7800
GCTGAAGTTC CTGCTCCAGC AGATTCTCCA ATACGGGCAG GCCATGTGCA CGGTAGCTGA	7860
CCGGGCTGAA CTTCCGGCTG CTTTCGCCCG CAGCCCCTGA CGACGCAGGC TGGCGGCAAT	7920
GGTTTTAATA TTGAACTCCG GCATTTCTGTC AGCAAGGCGG GGAGCACCGT ATCGCTGCTT	7980
TGCCTCAATG AATGCCTTAT GGACAGCGGC ATCGCAGGTG AGCCGAAACT GTTGGCGCAG	8040
GCTCATCTGG TGACGACGCC TGAGCCAGAC ATACCAGCCG CTGCGGGCAA CCCGAAGTAC	8100
ACGACACATC GCTTTGATGC TGAACCTCTGC CCGATGATTT TCGATGAAGA CATACTTCAT	8160
TTCAGGCGCT TCGCGAAGTA TGTCGCGGCC TTTTGGAGGA TGGCCAGTTC CTCAGCCTGC	8220
TCCGCCAGTT GTCGTTTAAG GCGGACATTT TCAGCGGCCA GTTCGCTTTC GCGCTCTGAC	8280
GAACTCATTT GTTGCTGCTG TTTACTGCGC CAGGCATAAA GCTGAGATTC ATACAGGCTG	8340
AGTTCACGGG CTGCGGCGGC CACACCGATG CGTTCAGCGA GTTTCAGGGC TTCGTTACGA	8400
AATTCAGGCG TATGTTGTTT ACGGGGCTTC TTGCTGATTG AACTGGTTT TGTCATGAGT	8460
CACCTCTGGT TGAGAGTTTA CTCACTTAGT CCTGTGTCCA CTATTGGTGG GTAAGATCAC	8520
TCAGCAACGT ATCAAAAGTC TGTAATAATCA TGGGCGTTTC GCGTGATACA TTTTATCGTT	8580
ACCGCGAACT GGTGATGAA GGCAGGTGTG ATGCGCTGAT TAATCGTAGT GCCGCGCTCC	8640
TAACCTTAAG AACGTACCGA TGAGGCAACT GAACAGGCTG TTGTTGATTA CGCCGTCGCT	8700
TTCCCGGCAC ACGGTCAGCA CCGGACCAGC AAACAAGCTG CGTAAACAGG GC	8752

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TGGTCAAAGA TGCAACTGCA TTTCGTCGCG GCTTTGCGGC AAATACTTAC ATCGCAGAAA	60
TACTGTGCGG AAATCTGCAT CCATTTCAC TTGCTGTATG GCATAACTTT TCAGGCGGTC	120
CGGATACTGC CGAAGATTAT TATGCCACAT ACCACCCGTT ATGGGGGCAA TATCGGAAG	180
CATTGCTGTT TGTAAACTGG CTCTATAATC ATTCCTCTGT GCTGCATGAA CGGGCAGAAA	240
TCATTAAATG CGCCGAAATG CTGATGCAGG AAGATGATTT CGAAATATGC GAAAGTATTT	300
TAAGACAGCA GGAGAAGTTG CGTGAAAGAA TTGATGAGAC GCTTTCTGAG AAAATTGTAC	360
AGAAATGCAG AAATATGAAT GGTGAATATG TCTGGCCCTG GATATTGCCG TTTTCAGCGG	420
CAGGCATGAA ACATACTGGC ATACAGTATC AGTAGATATT GCATTAGTGT ATCCTGCACA	480
CAAGTAATAA TTTATCCACC AATAATAACA CTGTTAATGT CCCCTTCCCC TGGTTGTCAG	540
CCAGGGGTTA TCTTCTGAAT ATTTCTTTTG AAAAGGATAA CACAATAAAT TATTTTTATG	600
AATTATCCCA TGGACTCATT AACACCCCTT CATAATGTTT TATTGTCAA CACGTTATGG	660
CTGACATCAA AAAAAACCGG ATTCCTCTG CCAGCGGGTA ATCACCTCCC CGGTGTTTTT	720
GGTTGGTCTG GTTACTCCTG TCTGGTTATT AGCAAGATAA TTGCTATAAA CAGTGAAAA	780
CTCATCGTAC ATAATCTGGT GATGAACATT ACGCTTATTT TCCCTTGACC GGAAGAATCA	840
GAGGCTGCGG TTTCAGACTG TCTGCCGGTA CATTCTCTC TCCGTTAAAA ACCATAATGG	900
GTTTATTATC TTCGTCTGTC AGTAGATTGA ATGGCGGTAT ATTTTCAGTA CGAATGCCGG	960
TCAGCCACTG AAAAATACCT GCGAAATGAC GGGCACTGAT TTTTCTGCTG ACGGACTGAT	1020
GAGACGTGAT GTCACTGGCG GTAATAATCA GGGGAACGCT GTAGCCTCCC TGCACATGAC	1080
CATCATGATG AACAGGATTA GCACTGTGCG TGACCGACAG CCCATGGTCA GAAAAGTAAA	1140
GCATGACGAA ATGACGGGAA TGCCGGCGAN GGATACCATC AAGCTGACCG AGAAAGTTAT	1200
CCAGTTTACT GATGCTGGCG AGGTAACAGG CAACCTTTTCG GGGATACTGC TCCAGGTAAT	1260
GATTTCGGCCA GGAGTGAAGC CGGTCACACG GGTTTCGGATG AGACCCCATC ATGTGCAGGA	1320
ATATCACCTT CGGAGAGGAT TTATCCGCCA GCGCACGTTT TGTTTCCTGT AACAACAACA	1380
TGTCATCCGT TTTACGGGAA GCGAATGCSC TTTCTTGAGG AAAACGGTAT GCTCCGCATC	1440
AGAAGCAATA ACAGAGATGC GTGTGTCATG CTCTCCAGT TTTCCCTGAT TGGATATCCA	1500
CCATGTGCTG TATCCTGCTT TTGCTGCCAG CGCCACCACG TTGTTGCCGG AATCAGGGTT	1560
CTGCTCATAG TCATAAATCA GTGTCCSGCT CAGGGAAGGT ACGGTAAGT CTGCTGCCGA	1620
TGTATAGCCG TCAATAAATA AACCGGGAGC TGTCATTCCA GCCACGGCGT GGTTGGCCAC	1680
GGGATAACCA TATACCGACA TATAATCCCT GCGCACACTC TCACCAAGTGA CAATCACAAT	1740
CGTGTCATAT AACGGTGTTT CCCGGCCAGG ATTTTCCCAG TTGTCAGCCC CGTGCTGACT	1800

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CAGTTGTTTA TAATGCTGCA TTTCACGCAA TGTGTCASTT GTCCCCACAA CAGTTCCTTT	1860
AACCATCCGC AACGGCCAGC TGTTTACTGA GCATAATACG AACAGCAGCA GTGCCAGCCA	1920
GTTACGGTGA CCACGGCGGT GTGTTCGCCA GAAAATCACC ATGAATACCT GAATCGCGGC	1980
ACTGACCAGA AAATGATAAA CAGGAATCAT CCCGGTAAAC TCCGCTGCCT CATCAGTTGT	2040
GGTCTGCAGC AACGCGACAA TAAACTGTT GTTGATTTTA CCGTACGTCA TACCGGCAGG	2100
CGCATACAGT GCACAACAGA ACAGAAATAA CAGCGCTGTA ATGGATGTGA GGGTATTTCT	2160
GTGTGCAAGG AGCAGAAGGA GAAACAGAAG CAGCACATTT CCTGTTGCAT TCCTCTCAGT	2220
GSTATCCGCAT GCAATTGTGG TTATTGCAGA CACAACAAAA AAGAATAAAA ACAATAAAAT	2280
CCGGGGGGGG TTGCCCGGAC AAAACAGTTT TCTGATATTC ATCGGAGTAT ATCGACAACA	2340
TTATTATGAA GAGAACAGGA TAATAAAAT CAGAAATTAT TGTAACACAG ATAAAGCAN	2400
CNATGCAGTA ATAGACT	2417

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGACAAAAAC CAGTTACGGT TATCACGTAC CAGCCCCCGT ATTTCCAATT TATAATCCTG	60
GCCATCAATT ACTGGGATCT CTTCTTCTCC ATAGAAGGCA TTAAAAGGGA ATGGAGTGGT	120
AATGTCCTCT GGAAGATATT CTGGTGCCAC ACTGTTTTTG CTGAACAGAA AACTTTGAAT	180
CCGGTCATTA AATCTGGATA TACGGAACAA TGCTTTTTCA ATATCATCAT TATTGCTTAT	240
ATCACAGCCA GTCAGCATCA TAATTCCCCC AAGCGTCAGT CCCTGTTGGA GTAAACGACG	300
TCTGTCCGGC GCAAGGATTT TTTCTGCATC TTTCACCACG TAATGGGCAT CACTGTCAGA	360
CAAAAAACGT TTTTCTTCA TTAGTGACCC CGTATCATAG ATAACAATGC ACGCGGAACC	420
AATAACACCA TAACCAGGTG AATAATAATG AACAGTACCA TAATGTTTAT GCACAGAAAG	480
TGGATATAAC GCGCTGTATC ATAACCACCG RATAGTATAG TCAGAAGGGA AAAGTGAACG	540
GGTTTCCATA AAACCAGACC AGACAATAGA AGAGCAGCGC CATCTAAAAT AATCAGAATA	600
TAGGCGACTT TTTGCACCAT ATTGTATTCC TGCATATTCG TATGATGCAG CTTTCCATAC	660
AGTGCCTGCG TAAGGGATTT TTTCAGTGAG GTCCATGACA GCGGGAAAAA CTTGCTCCGG	720
AAACGTCCGC TACAAATTCC CAGAGTAAGA TAGATCGTGG CATTAAATCAG CAGAATCCAC	780
ATCAGGGCGA AGTGCCACAG TAACGCACCG CCAAGCCAGC CACCGAGAGT TAATGCTGCC	840
GGATAGTTAA AAGAAAACAA AGGAGAAGCA TTATAAATGC GCCATCCACT ACATATCATG	900

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CCTGCGACAG TAACAGCATT AATCCAGTGG CAACAGCGTA ACCACAGAGG RTGTATTTGT	960
TTTAACGGTA ATGGCTGCAT TATGTGATCT CTGTCTGTAA ACTAAGTATA TTATGGAAAG	1020
GAATGTTTCAT CACATCCTCA CAAGAGTTTA AAAAAAATGT GACAANTCAT CGTCAAATGC	1080
TGGGGTAAAA TTCAGATAAA GAATATGTGG ATAACTTTGT ATGAATAACG TAAAAAAAT	1140
ACTGCTGATG GAAGATGATT ATGATATTGC AGCTCTGTTG CGGCTTAATC TGCAGGATGA	1200
AGGGTATCAG ATAGTTCATG AAGCGGATGG CGCCAGAGCT CGTTTATTAC TAGACAAGCA	1260
GACCTGGGAT GCCGTAATAC TTGATCTTAT GCTGCCTAAT GTTAATGGGC TGGAGATTTG	1320
CCGTTATATC CGTCAGATGA CCCGTTATCT GCCTGTGATT ATCATCAGTG CCCGTACCAG	1380
CGAAACCCAC CGCGTCTGG GACTGGAAAT GGGGGCTGAT GACTATCTAC CGAAACCCTT	1440
TTCCATTCCT GAGCTGATTG NCCCGCATCA AAGCGTTGTT TCGTCGTCAG GAAGCCATGG	1500
GGCAAAATAT TCTCCTGGCA GGTGGACTGA TTTGCTGTCA CGGTCTGTGC ATCAATCCAT	1560
TTTCACGTGA AGTTCATTTG CATAATAAAC AGGTTGATCT TACCCACGC GAGTTTGATC	1620
TGCTGCTCTG GTTTGCACGT CATCCTGGCG AAGTTTTTTC CCGTCTTTCA CTGCTGGATA	1680
ATGTCTGGGG GTATCAGCAT GAAGGATATG AGCATACAGT CAACACGCAT ATCAACCGTC	1740
TTCTGTGCCAA AATTGAACAG GATGCAGCAG AGCCAAAGAT GATCCAGACC GTCTGGGGAA	1800
AAGGGTATAG GTTTTCAGTT GACAATGCAG GAATGCGATA AATGAATTGT AGCCTGACAT	1860
TAAGCCAGAG GTTAAGCCTA GTATTTACAG TCGTTTTGCT GTTTTGCGCC GTGGACATGT	1920
GGCGTTCATA TTTACAGCAG TAATCTGTAT GGCAATGCAA TGGTACAGCG TTTATCTGCA	1980
GGCTGGCGCA ACAGATTGTC ATCACGGAGT CTCTGCTGGA TAATCGTGGG CAGGTGAATC	2040
ACCGGACATT AAAGAGTCTG TTTGAGCGTC TGATGACGCT TAATCCCAGT GTGGAGCTGT	2100
ATATTGTCTC GCCGGAAGGT CGGCTGCTTG TGGAGGCCGC CCCTCCAGGT CATATCAAAC	2160
GTCGGTATAT CAATATAGCG CCCTTGAAAA AATTTCTCTC CGGTGCTGTC TGGCCCGTAT	2220
ATGGTGATGA TCCCCGAAGT GTAAATAAGA AAAAAGTTTT CAGTACCGCA CCGCTTTACC	2280
TGAGGGATGA TCTGAAAGGA TATCTGTATA TTATTTTACA GGGAGAGGAA CTTAATGCTC	2340
TTACTGATGC AGCCTGGACA AAGGCACTAT GGAATGCACT GTACTGGTCG CTGTTTCTGG	2400
TAGTGATATG TGGTCTGCTG TCGGGTATGC TGGTCTGGTA CTGGGTAACC CGTCCCATAC	2460
AGCAACTAAC TGAAAATGTC AGCGGGATAG AGCAGGACAG TATTAGTGCC ATTAACAAC	2520
TGGCAATTCA GCGCCCTGCC ACCCCCCCTA GCAACGAGGT CGAGATATTA CACAATGCCT	2580
TCATTGAACT GGCCCGTAAA ATATCCTGTC AGTGGGATCA ACTTTCAGAA AGTGATCAAC	2640
AGCGCCGTGA ATTTATTGCC AATATCTCCC ATGATTTACG GACGCCATTA ACATCACTTC	2700
TGGGATATCT GGAAACCCTG TCAATGAAGT CGGATTGCT ATCATCAGAG GACTGTCATA	2760 -
AATATCTGAC AACAGCTCTC CGGCAGGGAC ACAAGGTCAG GCATCTGTCC TGTCAGCTTT	2820

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TTGAGCTGGC	ACGTCTTGAG	CATGSTGCTA	TAAAACTCA	ACTGGAGCAA	TTTTCTGTCT	2880
GTGAACCTAT	TCAGGATGTA	GCTCAAAAAT	TTGAGCTCAG	CATAGAAACC	CGTCGATTGC	2940
AACTAAGAAT	TATGATGTCA	CATTCCCTGC	CTCTTATCAG	GGCAGATATT	TCAATGATAG	3000
AGCGTGTGAT	AACAAATTTA	CTGGATAATG	CTGTACGCCA	CACACCTCCG	GAAGGCTCGA	3060
TCAGGCTGAA	AGTCTGGCAG	GAAGATAATC	GGTTGCACGT	CGAAGTGGCT	GACAGCGGCC	3120
CTGGACTAAC	TGAAGATATG	CGAACTCATC	TTTTCCGGCG	GGCATCAGTG	TTATGTCATG	3180
AACCGTCAGA	AGAGCCCCGG	GGAGGACTGG	GATTGCTGAT	TGTACGCAGG	ATGCTGGTAC	3240
TACACGGTGG	TGATATCAGG	TTGACTGATT	CAACGACTGG	AGCCTGCTTT	CGTTTTTTTC	3300
TTCCATTATA	ACATCAGGCG	GCATATTTTG	GGGTGGTTAT	GTGTATCTGC	CTTTGTAAAA	3360
GGGATACAAG	TTCTGTAGTG	GAGCACAAAA	TCAGGACACC	GGAATAACCT	GTTTCCACTT	3420
TTCTTCATGT	AAGCAAGGCG	GTAAACCATC	GTTGTTCGTG	TGAGGTCGAT	AAACGTTGTA	3480
ATAACCATTA	ATCCACTGGT	TTATATCACG	TACCGCATGG	ATAAAATCAC	CATAACCACC	3540
TTTCGGAAGC	CATTCATTTT	TAAGGCTGCG	AAAGACTCTT	TCCATCGGCG	AATTATCCAG	3600
GCCATTCCCT	CTGCAACTCA	TACTTTGCAT	TACCCCATAA	CGCCAGAGTA	ACTTTCTGTA	3660
TTTATTGCTT	TTATACTGAA	CACCTTGATC	TGAATGAAAC	AGCAGGCGGC	CATCACGCGG	3720
TCGAGTTTCC	AGTCCGTTAC	GCAAAGCCCT	ACACACCAAC	TCAGCATCAG	CGGTTAATGA	3780
GAGGGCTGAA	CCGATAATCC	GCCGTGAATA	TAAATCAACA	ACGAGCGCGA	GCTAACACCA	3840
TTTGTCTCTG	AGGCGAATAA	AACTGATGTC	GCGCACCAGA	CGCAGTTTGG	TGCGGCGGGG	3900
TGAAATTGCC	GGTTCAGTAA	ATTTGGCAAT	GGCGGACTTT	TGTCTTCGTT	TACCCGGTTG	3960
TGATGTTTTAA	CCGGCTGTCT	ACTTGTGAGC	CCTCATTCCC	GCATCAGTCG	TCATGCCAGC	4020
CACCGGCCTG	CATCAACGCC	ACTCTGGCGC	AACATCTGAC	TGATTGCCCC	GCTACCCGGC	4080
TGCGCCACGA	CTGAGAGCAT	GGAAAGCCCT	CACCCGGCTT	CGTAATTCAA	TTCTTTGCAC	4140
ATTAACAGGA	CGCTTCACCT	GCGCGTAATA	AACGCTACGG	TTAATACCGA	ATAAATGACA	4200
AATAACCCAC	ACTGGCCACT	TTGCTTTTCT	CTGTGTGATT	AGCGCGACAG	CTTCCCGGGG	4260
ATTTGCTCTA	TCAGCACGGC	AGCCTGCTTT	AGTATTTCTT	TTTCCATCTC	AACGCGCTTT	4320
ATCTGCGCTT	TAAGCTGCTG	AATTTGCGGT	TGTTTCAAGG	TAATAGCATT	ACCAGCTGGC	4380
TCAATACCCT	GAAGTTCCTG	CTTATACAAC	CGTATCCATT	TACGCAAATG	GTCAGGGTTG	4440
AGCTCGAGTG	CCTGCGCGAC	TTCTCTGACA	TCACGCTGGT	ATTTAACCAC	CACCTGCTCG	4500
AAAGCTTCAA	GCTTGAACCT	CGGGGAAAAG	GTACGTTTAG	TCCGACGAGT	TTTGATCATG	4560
CATCACCTCA	TTTTCACGTG	TTTAACATTA	ACAGGATTTT	GAGGTGTCCT	GAATTACCGA	4620
TCCACTACAA	AGTACGACAG	GTAAGTGGA	GGTACTCCCG	TAAAGACGGC	CATCAAGCTC	4680
CCGCTCCGAC	ATACCTGCGG	GCAGAGGCCA	TGAAAAGCCA	GCTTTGCGAA	AGCGCACGAA	4740

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CATACCACAA GCTGTTGATT TTGGTACGCC CAGGCGACGC CCGACCACAA CCTGGGGTAA	4800
ATGTTCTTCA AAGTGAAGAC GTAAAGCTTC AGTGATCCAA GTCCGGTGTT TCATACGATA	4860
GTGTCCATTA AAAATGATGG ACATTATTTT TGTAAAACCG GAGGAAACAG ACCAGACGGT	4920
TTAAATGAGC CGGTTACATG TAATCCATAC TCATCCAAGG TTTAATTCTG ACACAATAAG	4980
AAAATATGGA AAGTCTCGCT CTAGAGATGG GGAGAGGGAT ATTGAAGTGT ATGATATTCC	5040
AAGAACTGCC GGAGATATCC TCGTAAATGG ATTTTCCAGT GCAAACCTGAT AACAAATTCG	5100
AAGTCATTAT CTGCAACAAG ATTGATTGAT GTAGGGGATA TGTTAGAGCA TTATAATGCT	5160
CAAGGATTTG GCGTGATGAC ATCTGCGCCA ATTGATGCGA CACTATATGA TAAACTGGAT	5220
GCTATTTGCA GTAAGTGTA AATAGAACAA ATAAATTTTT CAGTATTAGA GTCAGAACGC	5280
GCACTATATT ATGACGATAT ATTAAGATGC CGTTACTTTG GTAAATAMCA TAAAATTAAT	5340
CAATATGGTA ATATATCAGT TGTAATTGAT CGAAACAAAG CACATAAATG CCATCTTATA	5400
AAGATGGTGT TTKTTAAGCA TATAAAATAT ATTTTCTATA AGATATAGGG CAAACTAAAT	5460
TTCTTGACTT CTATGATGGA CTAAGTAGAT ATACATGCCG CCAGTTTTTA TAAAACGACG	5520
GCATATATAA TCATTTATAT ATCTTTTGAT TTTATTCGTA ACCACTCATG TTGATCTAAA	5580
CCTATTCTTG ACAGATTAGC AACAATATCA GTTGTATTT TTTGCGCGTA CGTTGTTTTT	5640
ATTTCCCGA TCCATTTCAA TACTTTTGA GTAGATATTT TTTCAACGAG TAAAGGAACG	5700
AATGAGATAT AGTCAGTATT AACTAGATTG TTCTTTTCC CTATGATGAC ACCGTTTCCA	5760
TTTTCGACTC CAAATGAAAA TGAAATAATA TTAGAAGCTT TTGCCGGCAT TTTAATTTTA	5820
TAAAACCGC CATATTCATC TTCGATTAAC AAATTGTAAT TATTATCGTC CAGTGTTCCC	5880
CTGAGGAATA AAAAATCGGC TTTTTCATGC AATCTGACGC TATCACATAA TGGTTGTATG	5940
CATAGATAGA CAAAATTATA TGCATCTAAA AGTAAAGTTC CTTGTTTTAA GGACACATTA	6000
TCTATATGAG AATGATATCT TAACTCCTG CGCGTGATTT CCAGAGAGCA TAATTGCATT	6060
AACTTTTTAT CTTCTTCACC ATCTTGGCTT AAGTATTCCT TTTTACCTAA AGATGCGTGT	6120
TCAATAGCGT GTTGAATTTT TTCTAAAGAA TCAGCAGAGA GTATATTCCT TAGATGTTCT	6180
ACTGATAAGT CTTTTTGTTT TTTTCCAGTT AATAGAAAAT TCTTACAACC ATTTTTTGCA	6240
TAGTGAAAAA TAGGCCAATG GGATAAGGAG TTTTGTCTTA GAGATTTCTG GGGA	6294

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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TATTCCTTTC	TCTCCCATGA	TAGGGCGAAA	GGCTTTATTA	CTATCCACTG	CTGGTTTATT	60
AATTGCATCA	TCGTGATTA	ATTTGCTGGA	GSTTCCAATA	GTCAACCACC	TCTCTTCAAA	120
TTCATCGGTT	GTCATACCTA	ATCCATCATC	TCTCAAGATA	AGAAGATTTT	CTTTCCTAAA	180
AAAATCAACT	TCGACATTAT	CAGCATAGGC	ATCATGAGCA	TTTTTAAATA	ACTCACTCAA	240
GGCAGTAGGT	ATACCTGCAA	TTTGTTGTCT	GCCAAGCATG	TCCAAAGCTC	GAGCCTTTGT	300
TCTTATTTTA	GCCATATATC	TATGAATCCT	TATTAGTACA	ATTTTCTATG	AGATGTAGCC	360
CAAATAGTCT	AGCGAGTTCG	CAAGGTACAG	CATTGCCGAT	TTGCTTTGCC	ATTGAATTCA	420
GCGAACCTTT	AAAAACATAG	CTTAAAGGAA	ATGTTTGTA	TCTTGATGCT	TCTCTTATGC	480
TAATTGCTCT	ATGTTGAGTG	GGGTCAGGAT	GCCCAAACG	ACCATTGGAG	TAACATTATC	540
ATTTTCGTCG	AAGTGTAGGC	GCAGGCTTAT	CCCAACTCAT	TCTTCCATAA	GTATCTGTGT	600
GGCCATCATA	ATTTTTATGG	CATTTATTAA	CTAACTCTTC	TGGCCAATTT	CTTCTATCCC	660
CTCCTTCTGG	AGTGTGCATA	AKTCTTTTTA	GGTTAAGAGG	GCTCAGTGTT	CCAGCCCTAT	720
GTAAAGGATC	TTTGGGGTCG	GTTTCTCCTG	AACATAACTT	TGTGAAGTCC	TGGATATAAT	780
CTCGTACAGT	TTTGAATGGG	ATTTTATTTT	TACCATGGGT	TATCTCTGGT	AGGGTAACTT	840
TACCTACTCG	ACTAGCTAAG	AGCACGAGTC	TTTTTCTTCT	TTGGGGAATC	CCATAGTTCT	900
CAGCATTGGC	TATAAAAGAT	ATATAGTTAT	ACTCTAACTC	TTTAAGTAGC	TTAATAAACT	960
CCTGAAATGG	GCCTTCTTTT	TCTTCATCAA	TTTTTTGCAT	TCCAGGAACA	TTTTCAAGCA	1020
TAATATATTC	AGGAAGAAGT	TCTCTAATAA	AACGATGAGT	TTCATTTAGT	AGATTTCTCC	1080
TTGAGTCGTC	ACTAGTTTTA	TTTTTATTCT	GTTGCGAAAA	TGGTTGACAT	GGTGACATG	1140
CACTCAGTAA	CAAAGGCCGT	TTAGCTTTAA	TATCAATGAT	GTCGGAGATA	TCTTGAGGTT	1200
CGATTTTCCT	AATATCATCT	TGGATGAATT	TTGCATCAGG	GAAATTAGCT	TTAAATGTTT	1260
CTGATGCTTG	TTGGTCAATA	TCTAATCCAA	GCTCGATATC	AAAGCCAGCC	TGACGTAGCC	1320
CTTCACTGGC	TCCACCACAG	CCACAAAAAA	AATCTATAAC	TATCAATTTG	ATACCTTCTT	1380
TGAACTAAAT	AAAACAACCTC	GAATAAGTTG	ATATTTTAAA	TAAAAATAAT	TGGTATGGAT	1440
ATGAACTTTG	GTCACGCTAC	CGCCCTGAGK	TCATGGCCAT	CCCCAGACCT	TTTAAAGGGA	1500
TTATGAACAA	CACCCAGCCG	ACGTTCAACG	GTGTTACCCA	TACATATCAC	AAAGTTAGTT	1560
AATTGGTTGG	TCGTAAATTG	ACCTAAAATG	GATTGAGGGC	AATGCAAAAA	TCATTGGGAA	1620
ATCCAGGCGA	CACAGATGTT	CGGAAGAGAC	TGAATGTTAA	AAATATAGAA	TGTATATTCT	1680
CAAAAAAGAG	ATATTTTCATT	ACATTTTATA	TGTGTATAGG	AAAGTGAGAT	TGGCGAATCA	1740
CCTCCCAATC	ATCCCGCCAG	CGCTCCATTC	AGCGCCACGC	CAACCCTCAC	TCCAGCCCAC	1800
GTCATCGCCC	CCAGCCAGAA	TGTCGGCAAC	ACCAGAAACA	TCAACCTCAT	CACCAGATTG	1860
ATAATCACGT	CATCCTGCGT	ATTCTGGATC	CCGGCTAAAT	TCCAGCTACT	GTGGGTATCG	1920

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CTGTTGTAGA GCACATCCAG CAGCCAGCTA TCAAGCCACC GTGCCAGTTC CCACCAAAAG	1980
GTGAGGAAAA ATAGTGCAAA CTGCACAAAC GTCAGCGTCA TCACTACTTT CACATCCCAC	2040
GCCGAACAGA GCGTTATCAG CGGAATACAG ATCACCAGCG CTATTTGCAG TGCGCCTGTA	2100
CCATCGGTAG TGCCTAACGC ACGCTGTCTA ATGCCGTACA TGCCGCTATG CTGCCGAGGA	2160
TATTTCTAGC GCCGGATGCC AACC GSGTGG CGGCATTGGC GACGGTGCCA TCAACGTTAC	2220
CGCCATAGCT TGGATAAACG CGCCCATTCT GCGATACCTG CATATTTCTG TCACTGACCC	2280
GCGAGCGCAG CACGGCCTCT TCATACACTA CCTGCGACTG GTCGATTTTT TTAAACGCCG	2340
TCCAGATATC TAGGGCAGGA AGTTGCAGTA GACGGGCTTT CAGCCCAAGC GGTGTCGTCG	2400
CCCCACCGCT GTTTACAAGT GGGATAGCCG CCCGCGCCCG TATCGGCCAG CCCGGCATCG	2460
CGCGATGCAC TGTACGGCCA AGCACTGTGT GGTGAAAGCG CATGGTCGGA AAAGGCCTGT	2520
TCAGCTAACC AAGCACATCC CACCATCACA AGAATCGCCA GAAAACCAAA CTCAGTCAGA	2580
ATAACTCTTC CTGATTCAGG CTTTGCTCCT GCATTATGGC TACCACTATT GTTTGCCTGC	2640
ACGTATCATC TGATAACGGT TAATTAAGTG ATTTAGCGCC ATTTAGCCT GTTTTTGCTG	2700
CTGTTCACTG CCATTCTGGT TACGGACTTC ACCGTAGCGA CGTAACTGCT CTTCCGCCGG	2760
GATATGCCGG TTAAAAGCCT GCATGATGCC AAACACCTCC GTTTTCAGTT CACTGACCGT	2820
CATGTATTTT CCCCCTGTT CATCCTGACG GTTCAGGCGC TCAGCCAAGT GCTGTAAGCG	2880
GATCATGCCT TCGTTCCAGC CCGTCATCGC CTCTCCGGG AGCGCACGAC TCCTTAACT	2940
CTTCTGCCAG TTATCCACCA TTTCTGAAC ACGGGGATTG CCGGGGACAA GAACCCTCAG	3000
TTGCTGCAGC AGCTGCGCAC TGCACCGCAG GTTGTATGCT GGAGGTAATT CTGCCAGTCG	3060
CGTTATCTGC TGACCGGAAA GGGTTATCCA GTGCACTCAG GGCAGATACC GGATTCAGGT	3120
TAATTTTTTC AAACAGGGAA GCATATACGC TGTCGCCGGT ATGCGTTTCA GATACCACAC	3180
TCTCTGCGAC GTTCTTTTCT TTCTGTACAG ACATCAGCAT TTTCTGTAAG CGTACAGCGA	3240
GGGCCGTATT GACGGGGATG TGTATTTCAG CTGGCAGTGC TATGCGCCAC GGAAGCAGTT	3300
CGCTGACCCG GTTGACCGGC CAGTCTGCTA TGACGGCAAG CACATGGCGA AGGTAGCTTT	3360
CTGGATCCAC GTCATTCACT TTGCACGTCC CGATCAGGCT GTACAGTAGC GCTCCCCGCT	3420
CACCACCATG GTCAGAGCCG AAGAACAGGA AGTTTTTACG ACCCAGACTG ACCGCCCCGA	3480
GGNCATNTTT CAGCGATGTT GTTGTGATT TCCACCCAGC CATCGTTTCG ATAGTACGTC	3540
ATGCCGGCCA CTGGTTAAGT GCGTACGCGA ACGCCTTCGC CACCATCAGG CTGGACAGGG	3600
GACTTTCACC CCCAAGCTGC TGAACATGCC CGGCACACAA AGAAGATCTC GGCTCAGTGG	3660
CCGGGATTAG TTATACAATT ATCTGATTGA TTTTAAATAT ATCTTTTCTT AAATCATCGT	3720
TAATATCTGA CGGTTCTAGC TGGTTTATAA GTTGCCCTTAT TTGGGTAAAG GTAATTTTCT	3780
GATCTTTTAG ATCTTCTCCT TTTATCGTTG ATAAAGCTGC AATTAGTTCA CCATCGTAAT	3840

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ATTACCCCGC TAACGGCTCT TTAGTTAGAA CTTC AACAC TCTTGGCATC AACTGATCAA	3900
TACATAAATT TTGTCGGATA GCGCGGCAAA GATCTTCCAC TGTAACTTT TCAAGAGGCA	3960
CATCTATGAT ACGTTCGAAC CAGAGTTCAA GCGGTGATTG TTGCTCAGGC TCTTTTGTC	4020
TATTGATGTT TCCAATCAAT TTACGTAAGG TAATCATATT CCATATCCTT TCAAGGCTGA	4080
TTCTATTTTA TTAATAGCAT CTGTTGCTCT GCCATACGCA GCCTGAGCTT CAGGATTGTT	4140
GACGTTTTTC AACGTATCCG CATGATTTCT TAATCCTCTG AGCGTATTTT GCATTTCTCTG	4200
CATATGATCC CAATATCCTC CATTCTCTTT AGGAACTGGC TTACCATCCA TATCCTTGAG	4260
AGTTCCAATT AATATCATGA ATCTTTTCAG ANCATTTTTT TAATAGTGGT TAATCGANTC	4320
TTCTTTAANT CGGCAACTTT TCTTGGCCTT CCTGGAATTA AAGGCTTTAA TCCTAACAAG	4380
TTTTTTTCTC AATTTTTGGC TGGCTTTAGG GAATCAATTT TTCCCGGATT GGGTGGGTGG	4440
GTGGTAACCC GGGTTTCCCT TGAAGCCCGG GAAACCCGGC CCAAGTTCT TACTTTTTTT	4500
CCCGCAATCG GGTCAAGAT	4519

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATTACAGAAT GTGGAAATTA AGTATGATTC GAAAAAGAT TCTGATGGCT GCCATCCCC	60
TGTTTGTTAT ATCCGGGGCA GACGCTGCTG TTTCGCTGGA CAGAACCCGC GCGGTGTTTG	120
ACGGGAGTGA GAAGTCAATG ACGCTTGATA TCTCCAATGA TAACAAACAA CTGCCCTATC	180
TTGCTCAGGC ATGGATAGAA AATGAAAATC AGGAAAAAAT TATTACAGGG CCGGTTATTG	240
CCACCCCTCC GGTTCAGCGC CTTGAGCCGG GTGCGAAAAG CATGGTCAGG CTGAGTACCA	300
CACCGGATAT CAGTAACTT CCTCAGGACA GGGAATCACT GTTTTATTTT AATCTCAGGG	360
AAATACCGCC GAGGAGTGAA AAGGCCAATG TACTGCAGAT AGCCTTACAG ACCAAAATAA	420
AGCTTTTTTTA TCGCCCGGCA GCAATTAAAA CCAGACCAAA TGAAGTATGG CAGGACCACT	480
TAATTCTGAA CAAAGTCAGC GGTGGGTATC GTATTGAAAA CCAACGCCC TATTATGTCA	540
CTGTTATTGG TCTGGGAGGA AGTGAAAAGC AGGCAGAGGA AGGTGAGTTT GAAACCGTGA	600
TGCTGTCTCC CCGTTCAGAG CAGACAGTAA AATCGGCAAA TTATAATACC CCTTATCTGT	660
CTTATATTAA TGACTATGGT GGTGCGCCCG TACTGTCGTT TATCTGTAAT GGTAGCCGTT	720
GCTCTGTGAA AAAAGAGAAA TAATGTACCG CAATAACGGT TAAATGCGGG TGGGATATTA	780 -
TGGTTGTGAA TAAAACAACA GCAGTACTGT ATCTTATTGC ACTGTCGCTG AGTGTTTCA	840

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TCCATACTTT CCTGCGGGCT GAAGAGCGGG GTATATACGA TGACGTCTTT ACTGCAGATG	900
AGTTGCGTCA TTACCGGATA AATGAACGGG GGGGACGCAC CGGAAGCCTG ACCGTCAGTG	960
GTGCACTGCT GTCCTCACCC TGCACGCTGG TGAGTAATGA GGTGCCGTTA ARCCTCCGGC	1020
CGGAAAATCA CTCTGCGGCA GCCGGAGCAC CTCTGATGCT GAGGCTGGCA GGATGTGGGG	1080
ACGGTGGTGC ACTTCAGCCC GGAAAACGGG GCGTTGCGAT GACAGTCTCC GGCTCACTGG	1140
TAACCGGTCC CGGAAGCGGA AGTGCTTTAC TTCCTGACCG TAASCTATCC GGCTGTGACA	1200
TCTTGTTATA CAC	1213

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACGCTCTAGT ATTCTCTGTC GTTCTGCCTG GGCCACTGCA GATAGAATAG TGACAACCAT	60
TTTACCCATC TCCCCATCGG TACTGATTCC GTCATCAATA AACCGAATGG ATACACCTTG	120
GGCGTCAAAC TCTTTTATTA ACTGGATCAT GTCAGCAGTA TCGCGCCCAA GGGGTTCAAG	180
TTTCTTCACC AAGATGACGT CACCTTCCTC CACCTTCATC CTCAGCAAGT CCAGCCCTTT	240
CCGATCGCTT GAACTGCCCC ATGCCTTGTC AGTAAAGATG CGATTTGCTT TCACGCCTGC	300
GTCTTTGAGT GCCCGAACCT GAATATCGAG AGATTGCTGG CTGGTTGATA CCCGTGCGTA	360
ACCAAAAAGT CGCATAAAAA TGTATCCYAA ATCAAATATC GGACAAGCAG TGTCTGTTAT	420
AACAAAAAAT CGATTTNAAT TAGACACCNT T	451

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACAAGGCTT ATAACTCAC TGACGGGGCT GGCATGTTCC TGCTGGTACA TCCTAATGGT	60
TCCCGTTACT GGCCTCTCCG TTATCGTATT CTGGGTAAGG AGAAGACTCT GGCATTGGT	120
GTGTATCCAG AAGTTTCTCT CTCCGAAGCT CGTACAAAAC GGGATGAGGC CCGAAAAC TG	180
ATTCGGAGG GGATTGACCC TTGCGAACAG AAAAGAGCTA AAAAAGTAGT CCCTGATTTA	240
CAGCTCTCTT TTGAACATAT TGCACGACGC TGGCATGCCA GTAATAAACA ATGGGCACAA	300

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TCACACAGCG ATAAAGTACT CAAAAGCCTC GAAACACACG TTTTCCCCTT TATCGGCAAC	360
CGGGATATCA CAACACTCAA TACCCCGGAT CTGCTTATCC CTGTTCTGTC TGCASAAGCT	420
AAACAAATTT ATGAAATCGC CAGTCGTCTG CAGCAAAGAA TATCTGCCGT AATGCGTTAT	480
GCCGTACAGT CTGGCATCAT CAGATATAAT CCTGCTCTGG ATATGCTGCG CGCATTGACT	540
ACGGTAAAAC GCCAGCATCG CCCCCTCTT GATCTTTCAC GTCTGCCTGA ACTTCTGTCTG	600
CGTATTAACA GTTATAAAGG NCAGCCTGTC ACCCGGCTTG CGTTGATGCT GAATTTACTG	660
GGTTTTTATT CGTTCCAGTG AACTCAGATA CGCCCGCTGG TTCTGAAAAT TGATATTGGA	720

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2920 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

NCNTTAATTT TATATCTCGT AAAATAAAAT GTTTTCTGTA CCGCTCTCCG GAGGGGGGAA	60
TGATTTCGTTT ATCATTATTT ATATCGTTGC TTCTGACATC GGTCGCTGTA CTGGCTGATG	120
TGCAGATTAA CATCAGGGGA AATGTTTATA TCCCCCATG CACCATTAAT AACGGGCAGA	180
ATATTGTTGT TGATTTTGGG AATATTAATC CTGAGCATGT GGACAACTCA CGTGGTGAAG	240
TCACAAAAAC CATAAGCATA TCCTGTCCGT ATAAGAGTGG CTCTCTCTGG ATAAAAGTTA	300
CGGGAAATAC TATGGGAGGA GGTCAGAATA ATGTACTGGC AACAAATATA ACTCATTTTG	360
GTATAGCGCT GTATCAGGGA AAAGGAATGT CAACACCTCT TACATTAGGT AATGGTTCAG	420
GAAATGGTTA CAGAGTTACA GCAGGTCTGG ACACAGCAGC TTCAACGTTT ACCTTTACTT	480
CAGTGCCCTT TCGTAATGGC AGCGGGATAC TGAATGGCGG GGATTTCGG ACCACGGCCA	540
GTATGAGCAT GATTTATAAC TGAGTCATAC CCAAATGAAT AACTGTAATT ACGGAAGTGA	600
TTTCTGATGA AAAAATGGCK CCCTGCTTTT TTATTTTAT CCCTGTCAGG CTGTAATGAT	660
GCTCTGGCTG CAAACCAGAG TACAATGTTT TACTCGTTTA ATGATAACAT TTATCGTCST	720
CAACTTAGTG TTAAAGTAAC CGATATTGTT CAATTCATAG TGGATATAAA CTCCGCATCA	780
AGTACGGCAA CTTTAAGCTA TGTGGCCTGC AATGGATTTA CCTGGACTCA TGRTCTTTAC	840
TGGTCTGAGT ATTTTGCATG GCTGGTTGTT CCTAAACATG TTTCTATAA TGGATATAAT	900
ATATATCTTG AACTTCAGTC CAGAGGAAGT TTTTCACTTG ATGCAGAAGA TAATGATAAT	960
TACTATCTTA CCAAGGGATT TGCATGGGAT GAAGCAAACA CATCTGGACA GACATGTTTC	1020
AATATCGGAG AAAAAAGAAG TCTGGCATGG TCATTTGGTG GTGTTACCCT GAACGCCAGA	1080
TTGCCTGTTG ACCTTCCTAA GGGGGATTAT ACGTTTCCAG TTAAGTTCTT ACGTGGCATT	1140

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CAGCGTAATA ATTATGATTA TATTGGTGGG CGCTACAAAA TCCCTTCTTC GTTAATGAAA	1200
ACATTTCCCTT TTAATGGTAC ATTGAATTTT TCAATTAAAA ATACCGGAGN ATGCCGTCCT	1260
TCTGCACAGT CTCTGGAAAT AAATCATGGT GATCTGTCGA TTAATAGCGC TAATAATCAT	1320
TATGCGGCTC AGACTCTTTC TGTGTCTTGC GATGTGCCTA CAAATATTCG TTTTTTCCTG	1380
TTAAGCAATA CAAATCCGGC ATACAGCCAT GGTCAGCAAT TTTCGGTTGG TCTGGGTCAT	1440
GGCTGGGACT CCATTATTTT GATTAATGGC GTGGACACAG GAGAGACAAC GATGAGATGG	1500
TACAGAGCAG GTACACAAAA CCTGACCATC GCAGTCGCCT CTATGGTGAA TCTTCAAAGA	1560
TACAACCAGG AGTACTATCT GGTTCAGCAA CGCTGCTCAT GATATTGCCA TAAATGGTTT	1620
ATCCGGAGCC GGATAGTGTG TTGTGGATAT CTGGCATGCC CCGGGAAGTC ACCTTTCAGA	1680
CGGGCGGAGG GCTGGTGAAT TATCCGCGAT TACTGAGCAG TATGGATAAT CCTTTTTTAC	1740
AGACTTGTCG GCAGCCAGCA TTTATGTTCT TTTATCTGAG GGAATTTATC TGTACGCTGT	1800
GCCGGGATAT CTCAGTTATA CAGAAATCAG GCAGGAATAA ATTGTAGTGG AAAGTCGATG	1860
TTTACCGGAT GACTGATGCG CGTTGTACA CAGACAGTGT GTTTCAGTAA TATGGAGAAT	1920
AATGAAATGA ATAACACAGA CACATTAGAA AAAATAATCA GACACCAAAA AAACAAAGAC	1980
CCCGCATATC CTTTCGGGAA CATTTGTTGA TGCAGCTCTG TATTCGCACA AATAAAAGAA	2040
TGCAGGATAA TATATCTGAA TTTCTGGGGG CGTATGGAAT AAATCACTCA GCATATATGG	2100
TCCTCACCAC ATTATTCGCA GCGGAGAACC ATTGTCTGTC ACCTTCAGAG ATAAGCCAGA	2160
AACTTCAGTT TACCAGAACT AATATTACCC GCATTACAGA TTTTTTAGAA AAAGCCGGAT	2220
ATGTAAAAAG GACGGATAGC AGGGAGGATC GCCGTGCTAA AAAAATCAGT CTGACATCTG	2280
AAGGTATGTT TTTTATTCAG AGGCTCACTC TTGCACAAAG CATGTATCTG AAAGAAATCT	2340
GGGATTATCT GACCCATGAT GAACAGGAAC TGTTTGAAAGT CATTAAATAA AAATTACTGG	2400
CACATTTTTT TGATGCCAGC TCATAAAGTG CGAAATATCT GAGGATGCCG GATAGCTTCA	2460
GGCAAAATAA TAATGATTCT TGCAGATGTG TTTTCCGGA TACAAAAACA AATGATAAAA	2520
ATTGCAGCGC CAGGCACCTT TCAAAGCAGG GAGACCTGTA CCGCGTCGAA AATTTAGCC	2580
AGTTAATATC ATTGTCTGAA CCAGGCACCT TGCCCGGGCA GGAGAAGGAG TTGTGGCGGT	2640
CTCAGCCCGG AACAATTTGA AAACCATAAT CTCGCTTAGG GCCGTGTCCA CATTACGTGG	2700
GTAGGATCAC TCCTGGATTT TCTCTTTTTG GACATTGACG TCTCCATTGG TTAAACACG	2760
GCAATGGAGA CTGCGGTGAA AAGAGTTAAT TCCCGGAGTG ACTGGCTGGA TGCCAATCAA	2820
TGATCGGAAG CATGCCAAAC TGTGAACGGA GATGGATGCC GCCAAATCAT GATCGATTCA	2880
GATGCCATAT TTGCAATATC GCGTTAATCG TCASTTCAGC	2920

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGTAAGGAAG TTATATATAT GAGCAACTAT ACATCTTAGA TGTATGATAA AGAAAAAGAT	60
AACAGTTCTT TAGAATATGT ATATTGAAGA GAATGCAATA GCATGGTTTA TATAAATTAC	120
GCATAAAAAT AAGCATATGT AAGCATTTTG GTTTGCTTTT TTTAACCTGC CACCGCAATG	180
AATGCTTTTT TTATGTTAAT GTGCGTTATG AAATAAAATG CAAGAAACAT ATTTAAAGGA	240
TTAATATCGT TCTCTCACAG ACTCCGTTTA CTTATTCAAG AATATAATTT AATTTATAGT	300
GAGCTTATTA TGAATATGAA CAATCCATTA GAGGKTCTTG GGCATGTATC CTGGCTCKGG	360
GGCCAGTTCC CCATTACACA GAAACYGGCC AGTTTCTTTG TTTGCAATAA ATGTATTACC	420
TGCAATACGG GGCTAACCAA TATGCTTTAT TAACCCGGGG ATAATTACCC TGTTGCATAT	480
TGTAGTTGGG GCTAATTTAA GTTTAGAAAA TGAAATTTAA TATCCTAATG ATGTTACCTC	540
ATTAGTCGCA GAAGACTGGA CTTCAGGTGA TCGTAAAKGG TYCATTGACT GGATTGCTCC	600
TTTCGGGGAT AACGGTGCCC TGTACAAATA TATGGGAAAA AAATTCCCTG ATGAACTATT	660
CCGAGCCATC AGGGTGGATY CCAAACTCA TGTGTTGTTAA GTATCAGAAT TTCACGGAGG	720
TAAAATTGAT AAACAGTTAG CGAATAAAAT TTTTAAACAA TATCACCACG AGTTAATAAC	780
TGAAGTAAAA AACAAGACAG ATTTCAATTT TTCATTAACA GGTTAAGAGG TAATTAAATG	840
CCAACAATAA CCACTGCACA AATTAAAAGC AACTACAGT CTGCAAAGCA ATCCGCTGCA	900
AATAAATTGC ACTCAGCAGG ACAAAGCACG AAAGATGCAT TAAAAAAGC AGCAGAGCAA	960
ACCCGCAATG GGGGAAAACA GACTCATTTT TACTTATCCC TAAAGATTAT AAAGGACAGG	1020
GTTCAAGCCT TAATGACCTT GTCAGGACGG CAGATGAACT GGAATTGAA GTCCAGTATG	1080
ATGAAAAGAA TGGCACGGCG ATTACTAAAC AGGTATTCGG CACAGCAGAG AAATCATTG	1140
GCCTCACCGA ACGGGGAGTG ACTATCTTTG CACCACAATT AGACAAATTA CTGCAAAAGT	1200
ATCAAAAAGC GGGTAATAAA TTAGGCGGCA GTGCTGAAAA TATAGGTGAT AACTTAGGAA	1260
AGGCAGGCAG TGTACTGTCA ACGTTTCAAA ATTTTCTGGG TACTGCACTT TCCTCAATGA	1320
AAATAGACGA ACTGATAAAG AAACAAAAAT CTGGTAGCAA TGTCAGTTCT TCTGAACTGG	1380
CAAAAGCGAG TATTGAGCTA ATCAACCAAC TCGTGGACAC AGCTGCCAGC ATTAATAATA	1440
ATGTTAACTC ATTTTCTCAA CAACTCAATA AGCTGGGAAG TGTATTATCC AATACAAAGC	1500
ACCTGAACGG TGTTGGTAAT AAGTTACAGA ATTTACCTAA CCTTGGATAA TATCGGTGCA	1560
GGGTTAGATA CTGTATCGGG KATTTTATCT GCGRTTCAG CAAGCTTCAT TCTGAGSCAT	1620

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GCAGATGCAG ATACCGGRAC TAAAGCTGCC AGCAGGTGTT GGATTNACCA ACGGAANT

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(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGGATTACT TTGGAATCTG ACAACAAAGT TACTATGAAA AAGAACTAAC AAAGTTATAT	60
AATGACGCTA AAAATGCTTT GAAAGATGTG CAATCTAAAG CAAATAGGTT AATTTCTGAT	120
AATAAGANAA AACATAAGAG TGAACAAAA AACATTTCTT ATGAATTCCA ATCAACTAAT	180
CTCAATGGCA AAGATACTGC GTATATATTG GATGTARAAA GAAATCTAGA AAGTAAAATT	240
GAGAATACTT CAAACGAATG AGTGTAATGA AATAAGAAAA CTAACCGACC AGATTGCAAT	300
AATTAGTGAT AGTACCACTT CTGAAAATTT ATCATCGGCT CAAGTAACTG AAGCAATCGA	360
AACTGAACTT GAACATTTAC GAGACCAACA AGCAAATAAC GCAGAGTTAA TACTACTTGG	420
CATGGCTCTT TCTGTAGTAC ATCATGNATT TAATGGTAAT ATTAGGGCAA TTAGAAGTGC	480
GCTAAGGGAA TTAAAAGCAT GGGCTGACAG AAATCCTAAG CTTGATATTA TATACCAAAA	540
AATCAGAACT AGTTTTGATC ACTTAGATGG TTATTTAAAA ACCTTTACAC CATTGACAAG	600
ACGTTTAAAGT CGCTCTMAAA CCAATATAAC TGGAAGTACC ATTTTAGAAT TTATCAGAGA	660
TGTATTCGAT GATCGTCTTG AGAAAGAAGG AATTGAATTA TTCACTACCT CAAAGTTTGT	720
TAATCAAGAA ATTGTAACCT ACACATCAAC CATTTACCCT GTCTTTATAA ATCTAATTGA	780
TAACGCAATA TACTGGCTTG GGAAAACAAC TGGAGAAAAA AGACTTATAC TTGATGCKAC	840
TGAAACAGGA TTTGTTATTG GTGATACTGG TCCCGGTGTT TCAACTAGAG ATCGAGATAT	900
AATATTTGAT ATGGGATTTA CACGAAAAAC AGGAGGGCGT GGAATGGGAT TATTCATTTT	960
CAAAGAGTGT TTATCTCGAG ATGGATTTAC TATAAGATTG GATGATTACA CTCCTGAACA	1020
GGGTGCTTTC TTTATTATTG AGCCATCAGA AGAAACAAGT GAATAGCGGA TATAAATAAA	1080
TGACAAGCTC TACTGATTTN CATAAACTTT CTGAAGACTG CGTTCGCCGT TTTTACATT	1140
CTGTAGTTGC TGTAGATGAC AATATGTCTT TTGGAGCTGG TAGTGATACT TTCCCTACAG	1200
ACGAAGATAT TAATGCTTTA GTTGATCCCG ACGATGATCC TACACCAATA ATAACAGCAT	1260
CAGCATCCCC AAGGATAGAA TCAACTAAAT CAAAAGCAAA GGTAACAAAAC CATCCTTTTG	1320
ATTACCAAGC TCTAGCAGAA GCTTTCGCCA AAGATGGTAT TGCTTGTTGC GGATTATTAG	1380
CTAAGGAAGG TGCGAATAAG CGGGGAAATT CTTCTCGGCT GACTCAGTCA TTTCAATTTCT	1440
TCATGTTTGA GCCGATTTTT TCTCCCGTAA ATGCCTTGAA TCAGCCTATT TAGACCGTTT	1500

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CTTCGCCATT TAAGSCGTTA TCCCAGTTT TTAGTGAGAT CTCTCCCACT GACSTATCAT      1560
TTGGTCCGCC CGAACAGGT TGCCAGCGT GAATAACATC GCCAGTTGGT TATCGTTTTT      1620
CAGCAACCCC TTGTATCTGG CTTTCAGGAA GCCGAAGTGT CGCTTGATGA TGCAGAAATGG      1680
GTGCTCCACC CTGGCCCGGA TGCTGGCTTT CATGSTATTCG ATGTTGATGG CCGTTTTTGT      1740
CTTGCGTGGA TGCTGTTTCA AGGTTCTTAC CTTGCCGGGG CGCTCGGCGA TCAGCCAGTC      1800
CACATCCACC TCGGCCAGCT CCTCGCGCTG TGGCGCCCGT TGGTAGCCGG CATCGGCTGA      1860
GACAAATTGC TCCTCTCCAT GCAGCAGATT ACCCAGCTGA TTGAGGTCAT GCTCGTTGGC      1920
CGCGGTGGTG ACCAGGCTGT GGGTCAGGCC ACTCTTGGCA TCGACACCAA TGTGGGCCTT      1980
CATGCCAAAG TGCCACTGAT TGCCTTTCTT GGTCTGATGC ATCTCCGGAT CGCGTTGCTG      2040
CTCTTTGTTC TTGGTCGAGC TGGGTGCCTC AATGATGGTG GCATCGACCA AGGTGCCTTG      2100
AGTCATCATG ACGCCTGCTT CGGCCAGCCA GCGATTGATG GTCTTGAACA ATTGGCGGGC      2160
CAGTTGATGC TGCTCCAGCA GGTGSCGGAA ATTATGATG GTGGTGCGGT CCGGCAAGGC      2220
GCTATCCAGG GATAACCGGG CAAACAGACG CATGGAGGCG ATTTCTGACA GAGCATCTTC      2280
CATCGCGCCA TCGCTCAGGT TGTACCAATG CTGCATGCAG TGAATGCGTA GCATGGTTTC      2340
CAGCGGATAA GGTCGCCGGC CATTACCAGC CTTGGGGTAA AACGGCTCGA TGACTTCCAC      2400
CATGTTTTGC CATGGCAGAA TCTGCTCCAT GCGGGACAAG AAAATCTCTT TTCTGGTCTG      2460
ACGGCGCTTA CTGCTGAATT CACTGTCGGC GAAGGTAAGT TGATGACTCA TGATGAACCC      2520
TGTTCTATGG CTCCAGATGA CAAACATGAT CTCATATCAG GGACTTGTTT GCACCTTCCC      2580
TAAGAGTTTT AATGTTTGAA GAAAGAGATA TAATTACAGC ATCATCCAC AAAGCAGATA      2640
TTACAATACC TTGACTGGGN TATTGCCAAG CGGATA      2676

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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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AAATTTGTCC TCCGNTCTT TTCCCGTGGA TACGGGCATT GAGACCCGAA AGGSCCTGTA      60
TTTGCGACCG GAGAGGCATC CTGGGGGCTC AGTAAACCAG TGGTCGCTGT ATGGCGGGGC      120
TGTGCTTGCC GGTGATTATA ATGNCAGTGG SAGCCGGTGC CGGCTGGGAC CTGGGTGTGC      180
CGGGGACCCT TTCCGCTGAT ATCAAGCACT CAGTAGCCCG TATTGAGGGA GAGAGAACGT      240
TTCAGGGAAA ATCCTGGCGT CTGAGCTACT CCAAACGGTT TGATAATGCG GATGCCGACA      300
TTACGTTCCG CGGGTATCGT TTCTCAGAGC GAAACTATAT GACCATGGAG CAGTACCTGA      360

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ACGCCCCGCTA CCGTAATGAT TACAGCAGTC GGGAAAAAGA GATGTATACC GTTACGCTGA	420
ATAAAAACGT GGCGGACTGG AACACCTCTT TTAACCTGCA GTACAGCCGT CAGACATACT	480
GGGACATACG GAAAACGGAC TATTATACGG TGAGCGTCAA CCGCTACTTT AATGTTTTCG	540
GACTGCAGGG TGTGGCGGTT GGATTGTGAG CCTCAAGGTC TAAATATCTG GGGCGTGATA	600
ACRRTTCTGC TTACCTGCGT ATATCCGTGC CGCTGSGGAC GGGGACAGCG AGCTACAGTG	660
GCAGTATGAG TAATGACCGT TATGTGAATA TGGCCGGCTA CACTGACACG TTCAATGACG	720
GTCTGGACAG CTACAGCCTG AACGCCGGCC TTAACAGTGG CCGTGGACTG ACATCGCAAC	780
GTCAGATTAA TGCCTATTAC AGTCATCGTA GTCCGCTGGC AAATTTGTCC GCGAATATTG	840
CATCCCTGCA GAAAGGATAT ACGTCTTTCG GCGTCAGTGC TTCCGGTGGG GCAACAATTA	900
CCGGAAAAGG TGCGGCGTTA CATGCAGGGG GAATGTCCGG TGGAACACGT CTTCTTGTTG	960
ACACGGATGG TGTGGGAGGT GTACCGGTTG ATGGCGGGCA GGTGGTGACA AATCGCTGGG	1020
GAACGGGCGT GGTGACTGAC ATCAGCAGTT ATTACCGGAA TACAACCTCT GTTGACCTGA	1080
AGCGCTTACC GGATGATGTG GAAGCAACCC GTTCTGTTGT GGAATCGGCG CTGACAGAAG	1140
GTGCCATTGG TTACCGGAAA TTCAGCGTGC TTAAAGGGAA ACGTCTGTTT GCAATACTGC	1200
GTCTTGCTGA TGGCTCTCAG CCCCCGTTTG GTGCCAGTGT AACCAGTGAA AAAGGCCGGG	1260
AACTGGGCAT GGTGGCCGAC GAAGGCCTTG CCTGGCTGAG TGGCGTGACG CCGGGGGAAA	1320
CCCTGTCGGT AAACCTGGGAT GGAAAAATAC AGTGTCAGGT AAATGTACCG GAGACAGCAA	1380
TATCTGACCA GCAGTTATTG CTTCCCTGTA CGCCTCAGAA ATAAATGAAA GTCCGGAATA	1440
TTAACGGCTG ATTGAATTGC GGTTTATGCC ATTTTCCCGG ACCAA	1485

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTACCAATTT CATCGTCCGG TACATCCTCC AGAACATCTC GCAATAAACT CTCGTCTGCC	60
TCATTCCATG CCACACCAGC ATTTGGGAAA CGAGGATCGA TCTCTCTTTC CTTCTTCTCC	120
TTCTTACTTT GCTCTTTTCG GGATGATACA GATACGACAG AACGTTCTTT TACCGCTGTA	180
ATTGCCATAA CTGCATTGAG CAGAGATCTG CGCTCCACAT CGTTCAGCAT TTTTCCTTCA	240
CAGATCAAAT CATTGAGGAT GTCAATGACT AGATTGAGAC TTTCTTCTGT TAGCTTCATA	300
TTTCAGACCT TGAAGTATGT AGATAATCAG CACAATTACT AATGTGATAA ATATCAGAAG	360
ATAATTTACA GGTAAACCGG AAAATACATC TGAAGAATAA AGGCCTCAGC TTAACGTTTC	420

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AGCCAGTTTG TGAGCTGATT GAGGTACGGC GATGACATTA ACGGGAATTA CTCCCCTATA	480
GCTCTGAGCT TATTTTTCAC CCTGGCAACA TATGSTGGCT ACTGCGCATG GTTTTGGAGT	540
AGATATCTTA CTACTCGTAG AATTGTGCTT ACTGCTCAGG CCAGCGCACA GGCATTCCGT	600
GCAATCAATA GAACACTGGT TTTTGTAGTCT TCCGTTACCC ATCAGGATGT TAGTGCAGAT	660
TCCGGTGTAT TCGATCAGTT GTTCGGCGAA TCAGCGATCG ATCACGATGC GATTTTCGTAT	720
GTTAGGGATG CTGGTATGAT TACTCGCTGA AAAATAATGT GAAAAGGCAG TTTTCTTTA	780
GACATTTAGC TCATTCATGC TGTGTTTTTA CGTTTTGCTG TCGTGTGCAG GATTATCTTT	840
TCGTTACGGG ACGATTCATT CCGTTTTAAT CAGGAGCTAT TGGCGTTGCT CATTGGTGGG	900
ATGCCGTAAA GTTTTACCGC GCGGATTAAT GATGTGAAGT CAATCCAAAT CAACGGAGAT	960
CTCTCATCAT GAATCAACCA ATACACAATG ATTACTGGTT ATCCCGTTTT GAAAGTATTC	1020
TCAACAGTGC CCTGGTGCAA CACCGTGCCG TCTCGTTAAT CTGGGTGGAT TTACGTTTCC	1080
CTGAGCATAT GCCTGTCACC ATCATGGATC CCGATCCGGA TTCAGCGGTG ATTTCTCGTT	1140
TTTTCGAATC CCTGAAAGCC AAAATTCAGG CTTACCAGCG GAAAAACGA CGTACCAACA	1200
AGCGTGTGCG TGCAACCACC CTGCATTATT TCTGGTGTGCG GGAGTTTGGC AAGGAAAAAG	1260
GCAGGAAACA TTATCACGTG ATATTACTGC TCAACAAAGA TACCTGGTGC TCGCCAGGGG	1320
ATTTACCCGT TCCTTCTTCG CTGGCGACGC TGATCCAAC TGCATGGTGT AGCGCTCTGC	1380
ATCTTGAGCC CTGGCAGGGT AATGGACTGG TTCATTTTTC CAGGCGGACG CYTTTCCGTA	1440
AACCGGTATC ATCTGATGCT CGCCCTTCTT CCGATGATAC GCCTTTGTGCG GGTGGATGTT	1500
CTGAAACCAG GAAGGCTTCA GACAAAAAGC CGGGTGAAGC CGCTGTTCTC TGGATCAAGC	1560
GTGGTGTATG GGAAGCGATG CAGAAAGCCA TGGAGAGAGC CCGTTATCTC GTGAAGTATG	1620
AGACGAAGCA GCATGACGGT TCTGGTCAAC GTAATTATGG TTGCAGCCGT GGAGCGGGGC	1680
GTCTACTGGA TGGCAGGTGA ACCCTGTAAA ACGGCATCCG GTGCCAGAGT ATATGTCACA	1740
GTAAGGGCGT GGTTGATGCC CTTAGCTCGT TTTCTGAAAA AGTCGTCCTG AAGTCATGTG	1800
TCACGAACGG TGCAATAGTG ATCCACACCC AACGCCTGAA ATCAGATCCA GGGGGTAATC	1860
TGCTCTCCTG ATTCAGGAGA GYTTATGGTC ACTTTTGAGA CAGTTATGGA AATTAAAATC	1920
CTGCACAAGC AGGGAATGAG TAGCCGGGCG ATTGCCAGAG AACTGGGGAT CTCCCGCAAT	1980
ACGGTTAAAC GTTATTTGCA GGCAAAATCT GAGCCGCCAA AATATACGCC GCGACCTGCT	2040
GTTGCTTCAC TCCTGGATGA ATACCGGGAT TATATTCGTC AACGCATCGC CGATGCTCAT	2100
CCTTACAAAA TCCCGGCAAC GGTAATCGCT CGAGAGATCA GAGACCAGGG ATATCGTGGC	2160
GGAATGACCA TTCTCAGGGC ATTCATTCGT TCTCTCTCGG TTCCTCAGGA GCAGGAGCCT	2220
GCCGTTCCGT TCGAAACTGA ACCCGGACGA CAGATGCAGG TTGACTGGGG CACTATGCGT	2280
AATGGTCGCT CACCGCTTCA CGTGTTCTGTT GCTGTTCTCG GATACAGCCG AATGCTGTAC	2340

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ATCGAATTCA CTGACAATAT GCGTTATGAC ACGCTGGAGA CCTGCCATCG TAATGCGTTC	2400
CGCTTCTTTG GTGGTGTGCC GCGCGAAGTG TTGTATGACA ATATGAAAAC TGTGGTTCTG	2460
CAACGTGACG CATATCAGAC CGGTGAGCAC CGGTTCCATC CTTGTTGTG GCAGTTCGGC	2520
AAGGAGATGG GCTTCTCTCC CCGACTGTGT CGCCCTTCA GGGCACAGAC TAAAGGTAAG	2580
GTGGAACGGA TGGTGCAGTA CACCCGTAAC AGTTTTTACA TCCCACTAAT GACTCGCCTG	2640
CGACCGATGG GGATCACTGT CGATGTTGAA ACAGCCAGCC GCCACGGTCT GCGCTGGCTG	2700
CACGATGTGG CTAACCAACG AAAGCATGAA ACAATCCAGG CCGTCCCTG CGATCGCTGG	2760
CTCGAAGAGC AGCAGTCCAT GCTGGCACTG CCTCCGGAGA AAAAAGAGTA TGACGTGCAT	2820
CCTGGTGAAA ATCTGGTGAA CTTGACAAA CACCCCTGC ATCATCCACT CTCCATTTAC	2880
GACTCATTCT GCAGAGGAGT GCGGTGATGA TGGAACTGCA ACATCAACGA CTGATGGCGC	2940
TCGCCGGGCA GTTGCAACTG GAAAGCCTTA TAAGCGCAGC GCCTGCGCTG TCACAACAGG	3000
CAGTAGACCA GGAATGGAGT TATATGGACT TCCTGGAGCA TCTGCTTCAT GAAGAAAAAC	3060
TGGCACGTCA TCAACGTAAC CAGGCGATGT ATACCGAAT GGCAGCCTTC CCGGCGGTGA	3120
AAACGTTTCA AGAGTATGAC TTCACATTCG CCACCGGAGC ACCGCAGAAG CAACTCCAGT	3180
CGTTACGCTC ACTCAGCTTC ATAGAACGTA ATGAAAATAT CGTATTACTG GGACCATCAG	3240
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GCCGTTATAA AACGACGCTT CAGCGTGGAG TAATGGCCCC CCGCCTGCTC ATCATTGATG	3420
AAATAGGCTA TCTGCCGTTT AGTCAGGAAG AAGCAAACT GTTCTTCCAG GTCATTGCTA	3480
AACGTTACGA AAAGAGCGCA ATGATCCTGA CATCCAATCT GCCGTTCCGG CAGTGGGATC	3540
AAACGTTTGG CCGGTGATGCA GCCCTGACCT CAGCGATGCT GGACCGTATC TTACACCACT	3600
CACATGTCTG TCAAATCAAA GGAGAAAGCT ATCGACTCAG ACAGAAACGA AAGGCCGGGG	3660
TTATAGCAGA AGCTAATCCT GAGTAAACG GTGGATCAAT ATTGGGCCGT TGGTGGAGAT	3720
ATAAGTGGAT CACTTTTCAT CCGTCGTTGA CATCATGCAA TGTTTCCTGG TTTTCATGCA	3780
TCCATCATTT GTCGCTGCGA TGCCAGACTT CTGGATGCAC ACATGTTGTT TTACTTTTGT	3840
CAGCATCATA AATGCGCCGG GACTGGTGAA TGGAGATAAG CCATTTTATT ATCGACGTCA	3900
GCGAACATAC TCACCATGCC GGTATSTTCC TGAAGTGAAC AATAAGTTTT GCGCTGATTA	3960
CAGTATGTGA AGGAGGTCCG TTACAATGAA TTCCGCTTAT ATGCAATCCT TGCAGACATC	4020
CCACCACTTC CCAGCTGATT TAACCTACAG ATTATTTCTT AGTGAGCTTG CATATCTCAT	4080
TGACGACTTA TATGAAAGTA CCCAACTTCC GCTGGAGCTC ATTTTAAATA CTGTACTGGC	4140
AACGCTCTCA CTCTCCTGTC AGTCACTGGT TGACGTTGTT CATCCTCACA CCAACATGCC	4200
GGAACCCCTG TCACTTTATC TGTTGGCAAT CGCAGAGCCA GCGCGGGGAA AAACAACGAT	4260

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AAACAGACTG GTGATGAACC CCTGTTACGA ATTTGCCGAT CGACTCATTG AACAAATACGA	4320
AGAGAGAAAC AAAGATTATA AGACTGAACT ACAGATCTGG AATACCCGGC AGAAAGCGCT	4380
TGCTGCCAAT TTAAGAAAGG CTGTTAACCG GGGGTATCCG GGGGAACAGG AAGAAGAGGC	4440
GCTGCGTAAT CACGAAAGAA ATAAACCGAC ACGTCCGGTT CGACCGAATT TTATCTATGA	4500
AGATGTTTCG CTTAAAGCGC TTGTGGAAGG GCTCAATGAA CATCCTGAGG CAGGGGTTAT	4560
TTCTGACGAG GCGGTCACTT TTTTCAGAAAG CTATCTGAAA AATTATCCGG GCCTGTTGAA	4620
TAAAGCATGG AGTGGACAAC CGTTTGATTT TGGACGGGCT GACGAGAAAT ACCATATCAC	4680
GCCACGTCTG ACATTTTTCGT TAATGTCCCA GCCGGATGTC TTTACGAATT ATATAAATAA	4740
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AAGTCCTTCC CGGGTACGGG ATTATACGAG AGGCGAGTTC AGAACAAAAC CAACCCCTGGA	4860
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GAGCACCGAA ASGAAAACAT TAAAACTTGC AAAGAAAGCG TTGGGGGAGT GGCAGGAAAA	4980
CCAGATTAAG ATTGAAAGAA AAGCGCTTGC AGGAGGGGAG TGGGAACACA TCAGAGATAT	5040
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TATCAGGAAA ACAGACATTG AAAGATATGG TCCCAATCGT CTGAGAAGAG CAGAAAAACT	5340
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TTGTTTGATT CTTGCCGTGA TGAGTGCTGG GGTATATGAC GATGTGCTC TCTTTCTGAA	6000
TAACAAATTA TTATTCGTCT GTTACTGATA AGGGATGCGA TTCATGTTTT AATAGAGGGT	6060
TGAAGAAAAT TAATTTGATA TTTTTTTGTA AGGGAATGGA ACTGTCCGGA ATATGTTTCAG	6120 -
AACGGCGGAT TTCTCATTTT CATTCATTAA ACATGGATAA TTTTAATTTA GGTATTATTAC	6180

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TATTATTATA CTCACTCCCT TTTTCATACA ATCTCTATTG TTATTTACTT CCTGTCTTTA	6240
CTCACTCTCT ATCTTTACGA TTATATTCAC TCTATCGTTA CACATTCCAT TAGTATTACT	6300
CTTGTTATCG TATTCATTCC ATCCCTCAAT CATATTTACT GTAACTCATA TGATGTTTCTAG	6360
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GCAATTGATT TTAATCTTAT CCATCATGAA CTGTATTTGC TTAACAATGA TTGTTTATCT	6480
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CGATTTCTTA CAACCTGATC ATCGCTGGCT TGAATTGCAG TTGCGTATGA TGCTGGAGCA	7320
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CCGCTGCACA TATCAGCCGC ATTATACATA CAACATCAAC ATTCCTGTGC GCCACAACGA	7560
TCCTGAAAGC ATCGATAATA TTCGCGGTGC CCTGCATTAT CTGGCGAAAG AAGAGCAAAA	7620
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GGGCTGCGCA TAACGGAACA TATCTTATGA ATGCTATTCC TTATTTGAC TATAGCCTGG	7980
CACCCTTCTG GCCATCTTAT CAGAACAAAG TCATCGGCGT CCTTGAGCGT GCGCTGCGTG	8040 -
AGCAGTCCGG CTCACGGATA CGGCGGATCC TGCTTCGTCT GCCGTGGGAA CATGACAACG	8100

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CCTTCAGCAG CAGAAAGATC TGGTTCGGTA TGGACTTTAT CGAAACCGTC AGTGCGCTGA	8160
TGAATGCGAA ACCCGGACGC GACCTTTGCT GGCTCCTGAC CCGTCATCCG GAAAAGCCGG	8220
AATACCACGT GGTGCTGTGC GTCAGACAGG AGTATTTCTGA CGGCCCCGAA CTGGATCGGT	8280
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ACCAGAAGCA GATCACCCGG GATGTGGTAC TGGATCGCCG GTCACCGGAC TGCGAAGCCC	8400
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ATCCGGAAGC CCGTTGCCTT GCCGGCAATC CCGGTTGGCA GTGCTGAAAG CAGCACGCCA	8520
TCCCATCCCC CGTATTACCC CATTCTTCAT AAATCTCACT GAGGACATTC TGACCATGTT	8580
GACCACAACA AGCCACGACA GCGTATTGCT GCGTGCCGAC GATCCCCTGA TCGACATGAA	8640
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CGAATTGACT ATCTGGCGGA TAAATACTCT TTTACCGAAC GGAATGAATC TCCACGCCTT	9960
CGCCGGCAGT GGCAGGATGT TCTGGAGGAG TGTCGGCTGA CAGAGGCCGG ACCAGAAGAA	10020

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TTGTTGCTTA CTCGTACACC ACAACTGATT GCCGCGCTTC GGAAGAATG	GGGCCTCAGC	10140
CAGAAAAATG TGGTGTTCAG CGATAAACGG TTTGGCTGCG TGTACAGCCT	GAAGGCCAGT	10200
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TGGTCTGGTA GTCAGCGCAT TGGCGCTGAT ATCCTGAGAC TGAGAAAGAG	CGGAATGCCG	10440
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ACACCCTGAG TGGTTTTTAC AGCTTGCCCTC CGGGGATGAG GATTAACAGG	CAAATTATGC	10860
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CAGGATAACT TACTGGCGAA CAGAAATTTG TTGCCTGGTA TGGTTTCCG	TCAGTACGCA	11280
TTCAGGATCC GTACCTTATC TCAGGTGGTA CGCTATTTTT CCCTCCTCCC	CTGCCTTTGC	11340
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GCCGTGACGG ACGGCTATAT ACGCCGGGGA TATATACCA GCCGGGCCTT	TCTGACAGAG	11700
CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT	GCAGCAAATC	11760
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GGGAAGGTTT TGAAGTGGG GATATTGAGC AGGGGATGGA GCAGATTAAT	CGTCTGCGTA	11880
CGGAGCCGGT ACAGATTGAA ATATCGCCCC GTGACCGTGA GGGATGGTCG	GTGGTGACAC	11940

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CTGACAACCTG GTTTGTCAGC GGGGGACGGA GCAGTGAAGT TTCGGTGTCA CATGATGCGA	12120
GGAATTTTGC CGCCGGTGTC AGTCTGCCGT ATGGCTATAC CCTGGTGGAT TACACGTATT	12180
CATGGAGTGA CTACCTCAGC ACCATTGATA ACCGGGGCTG GCGGTGGCGT TCCACGGGAG	12240
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CAGCACTGAC CGGAGGTCTG CAGCACCGCA TTATTCACAA TTATCTGGAT GATGTTCTGC	12360
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AGGCGCTGGA GGTGACTGAA GGCAGTATCA CCATCAATGG CGCGGGCCTG GACGGCACCC	13560
GGAGCGATGC CGTATCCATT ATTGCCCCGT CAACGGAAGT GAATGCCGCG CTTCATGCGA	13620
AGGATTTAAC TGTCATGCA GGCCTAACC GGATAACTGC AGATGGTCGC GTCAGTGCCC	13680
TGAAGGGCGA AGGTGATGTG CCGAAAGTTG CCGTTGATAC CGGCGCGCTC GGTGGAATGT	13740
ACGCCAGGCG TATTCATCTG ACCTCCACTG AAAGTGGTGT CCGGGTTAAT CTGGGTAACC	13800
TTTATGCCCC CGAGGGCGAT ATCATACTGA GCAGTSCCGG AAAACTGGTC CTGAAGAACA	13860

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GCCTTGCCGG CGGCAATACC ACCGTAACCG GAACGGATGT CTCACTTTCA GGGGATAACA	13920
AAGCCGGAGG AAATCTCAGC GTTACCGGGA CAACGGGACT GACACTGAAT CAGCCCCGTC	13980
TGGTGACGGA TAAAAATCTG GTGCTGTCTT CATCCGGGCA GATTGTACAG AACGGTGGTG	14040
AACTGACTGC CGGACAGAAC GCCATGCTCA GTGCACAGCA CCTGAACCAG ACTTCCGGGA	14100
CCGTGAATGC AGCTGAAAAT GTCACCCTTA CCACCACCAA TGATAACCACA CTGAAAGGCC	14160
GCAGCGTTGC CGGGAAAACA CTCACTGTCA GTTCCGGCAG CCTGAACAAC GGTGGGACAC	14220
TGGTTGCCGG GCGCGATGCC ACGGTGAAAA CCGGGACATT CAGTAATACC GGTACCGTCC	14280
AGGGGAATGG CCTGAAAGTT ACCGCCACTG ACCTGACCAG CACCGGCAGT ATTAAAAGTG	14340
GCAGCACACT CGATATCAGC GCCC GCAATG CCACACTGTC CGGTGATGCC GGTGCAAAAG	14400
ACAGTGCCCG CGTTACCGTC AGCGGTACAC TCGAAAACCG CGGCAGACTT GTCAGCGATG	14460
ACGTGCTGAC GCTCAGTGCC ACGCAGATAA ACAACAGCGG TACCCTCTCC GGGGCAAAGG	14520
AACTTGTTGC TTCTGCAGAC AACTGACCA CCACAGAAAA ATCGGTCACA AACAGTGACG	14580
GTAACCTCAT GCTGGACAGC GCGTCTTCCA CACTGGCGGG TGAAACCAGT GCGGGTGGCA	14640
CGGTGTCTGT AAAAGGCAAC AGTCTGAAGA CCACGACCAC TCGCAGACG CAGGGCAACA	14700
GTGTCAGCGT GGATGTGCAG AACGCACAGC TTGACGGAAC ACAGGCTGCC AGAGACATCC	14760
TTACCCTGAA CGCCAGTGAA AAGCTCACCC ACAGCGGGAA AAGCAGTGCC CCGTCGCTCA	14820
GCCTCAGTGC GCCGGAAGT ACCAGCAGCG GCGTACTTGT TGGTTCCGCC CTGAATACAC	14880
AGTCACAGAC CCTGACCAAC AGCGGTCTGT TGCAGGGGGA GGCCTCACTC ACCGTTAACA	14940
CACAGAGGCT TGATAATCAG CAGAACGGCA CGCTGTACAG TGCTGCAGAC CTGACGCTGG	15000
ATATACCGGA CATCCGCAAC AGCGGGCTTA TCACCGGTGA TAATGGTTTA ATGTTAAATG	15060
CTGTCTCCCT CAGCAATCCG GGAAAAATCA TCGCTGACAC GCTGAGCGTC AGGGCGACCA	15120
CGCTGGATGG TGACGGCCTG TTGCAGGGCG CCGGTGCACT GCGCTTGCT GCGGACACCC	15180
TCTCACAGGG TAGTCACGGA CGCTGGCTGA CGGCGGACGA CCTCTCCCTC CGGGGCAAAA	15240
CACTGAATAC CGCAGGACCA CGCAGGGACA GAATATCACC GTGCAGGCGG ACAGATGGGC	15300
GAACAGTGGT TCCGTGCTGG CAACCGGTAA CCTTACTGCT TCGGCAACCG GTCAGTTGAC	15360
CAGTACCGGC GATATCATGA GCCAGGGTGA CACCACGCTG AAAGCAGCCA CCACGGACAA	15420
CCGGGGCAGT CTGCTTTCGG CCGGCACGCT CTCCTTGAT GGAAACTCAC TGATAACAG	15480
CGGCACTGTC CAGGGTGACC ATGTCACGAT TCGCCAGAAC AGTGTCACCA ACAGTGGCAC	15540
GCTCACCGGG ATCGCCGCGC TGACGCTTGC CGCCCGTATG GTATCCCCTC AACCTGCGCT	15600
GATGAATAAC GGAGGTTTAT TGCTGACCAG CGGCGATCTG ACAATCACCG CAGGCAGTCT	15660
GGTAAACAGC GGGGCGATCC AGGCGGCTGA CAGCCTGACT GCACGTCTGA CGGGTGAGCT	15720
CGTCAGCACA GCGGGCAGCA AAGTCACCTC GAACGGTGAA ATGGCGCTCA GTGCACTGAA	15780

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TTTAAGCAAC	AGCGGACAAT	GGATTGCAAA	AAATCTGACC	CTSAAGGCGA	ACTCACTGAC	15840
CAGTGCGGGT	GACATCACCG	GTGTGGATAC	TCTCACGCTC	AGGCTGAATC	AGACGCTGAA	15900
CAATCAGGCG	AACGGAAAAC	TGCTCAGTGC	AGGTGTGCTG	AGGCTGAAGG	CAGACAGTGT	15960
CACAAACGAC	GGGCAATTAC	AGGGAAATGC	CACCACCATC	ACGGCAGGAC	AACTCACAAA	16020
CGGCGGGCAT	CTGCAGGGCG	AAACGCTGAC	GCTGGCCGCC	TCCGGTGGCG	TGAACAACCG	16080
TTCCGGTGGT	GTTCTGATGA	GCCGGAATGC	ACTGAATGTC	AGTACTGCGA	CCCTGAGTAA	16140
CCAGGGCAGC	ATACAGGGTG	GTGGCGGGGT	TTCCCTGAAC	GCCACTGACC	GTCTGCAGAA	16200
CGACGGCAAA	ATCCTCTCCG	GCAGTAACCT	CACGCTGACG	GCGCAGGTGC	TGGCGAACAC	16260
CGGCAGCGGA	CTGGTACAGG	CTGCCACCCT	GCTGCTGGAT	GTGGTGAATA	CTGTCAACGG	16320
CGGACGCGTA	CTTGCCACCG	GCAGTGCCGA	CGTTAAAGGA	ACCACGCTGA	ATAATACCGG	16380
TACGCTTCAG	GGTGCGGACC	TGCTGGTGAA	TTACCACACA	TTCAGCAACA	GCGGTACCCT	16440
GCTGGGAACC	TCCGGGCTTG	GCGTCAAGGG	CAGTTCACTG	CTGCAAAATG	GTACAGGGCG	16500
GCTGTACAGT	GCAGGCAACC	TGCTGCTTGA	CGCTCAGGAC	TTCAGTGGTC	AGGGGCAGGT	16560
GGTGGCCACC	GGTGATGTCA	CACTGAAACT	GATTGCTGCC	CTCACGAATT	ACGGTACCCT	16620
GGCCGCAGGG	AAAACCCTTT	CCGTCACGTC	GCAAAATGCC	ATCACCAACG	GCGGTGTCAT	16680
GCAGGGTGAT	GCCATGGTGC	TCGGTGCCGG	AGAGGCATTG	ACCAACAATG	GAACGCTGAC	16740
TGCCGGTAAA	GGCAACAGTG	TTTTCAGCGC	ACAGCGTCTT	TTCCTTAACG	CACCGGGTTC	16800
ACTTCAGGCC	GGTGGCGATG	TGAGTCTGAA	CAGCCGGAGT	GATATCACCA	TCAGTGGTTT	16860
TACCGGCACG	GCAGGCAGTC	TGACAATGAA	TGTGGCCGGT	ACCCTGCTGA	ACAGTGCCT	16920
GATTTATGCG	GGGAATAACC	TGAAGCTGTT	TACAGACCGT	CTGCATAACC	AGCATGGTGA	16980
TATCCTGGCC	GGCAACAGTC	TGTGGGTACA	GAAGGATGCT	TCCGGCGGTG	CAAACACAGA	17040
GATTATCAAT	ACTTCCGGGA	ATATTGAGAC	GCATCAGGGC	GATATTGTTG	TAAGAACCGG	17100
GCATCTTCTG	AACCAGCGGG	AGGGATTTTC	TGCCACAACA	ACAACCCGGA	CTAACCCCTC	17160
ATCCATTGAG	GGAATGGGAA	ATGCTCTGGT	TGATATTCCC	CTTCCCTTC	TTCCTGACGG	17220
CAGCTATGGC	TATTTACCCC	GTGAAGTTGA	AAATCAGCAC	GGTACGCCCT	GCAACGGGCA	17280
CGGGGCATGC	AATATCACAA	TGGATACGCT	TTATTATTAC	GCTCCGTTTG	CTGACAGTGC	17340
CACACAGCGC	TTTCTCAGCA	GCCAGAACAT	CACAACAGTA	ACCGGTGCTG	ATAATCCGGC	17400
AGGCCGCATT	GCGTCAGGGC	GTAATCTTTC	TGCTGAGGCT	GAACGACTGG	AAAACCGGGC	17460
GTCATTTATC	CTGGCGAATG	GGGATATCGC	ACTCTCGGGC	AGAGAGTTAA	GCAATCAGAG	17520
CTGGCAGACG	GGGACAGAGA	ATGAATATCT	GGTATACCGC	TACGACCCGA	AAACGTTTTA	17580
CGGTAGCTAT	GCAACAGGCT	CTCTGGATAA	ACTGCCCTTG	CTGTCACCGG	AATTTGAAAA	17640
CAATACCATC	AGATTTTCAC	TGGATGGCCG	GGAAAAAGAT	TACACGCCCG	GTAAGACGTA	17700

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TTATTCCGTT ATTCAGGCGG GCGGGGATGT TAAGACCCGT TTTACCAGCA GTATCAATAA	17760
CGGAACAACC ACTGCACATG CAGGTAGTGT CAGTCCGGTG GTCTCTGCAC CTGTACTGAA	17820
TACGTTAAGT CAGCAGACCG GCGGAGACAG TCTGACACAG ACAGCGCTGC AGCAGTATGA	17880
GCCGGTGGTG GTTGGCTCTC CGCAATGGCA CGATGAACTG GCAGGTGCCC TGAAAAATAT	17940
TGCCGGAGGT TCGCCACTGA CCGGTCAGAC CGGTATCAGT GATGACTGGC CACTGCCTTC	18000
CGGCAACAAT GGATACCTGG TTCCGTCCAC GGACCCGGAC AGTCCGTATC TGATTACGGT	18060
GAACCCGAAA CTGGATGGTC TCGGACAGGT GGACAGCCAT TTGTTTGCCG GACTGTATGA	18120
GCTTCTTGGA GCGAAACCGG GTCAGGCGCC ACGTGAAACG GCTCCGTCGT ATACCGATGA	18180
AAAACAGTTT CTGGGCTCAT CGTATTTTCT TGACCGCCTC GGGCTGAAAC CGGAAAAAGA	18240
TTATCGTTTC CTGGGGGATG CGGTCTTTGA TACCCGGTAT GTCAGTAACG CGGTGCTGAG	18300
CCGGACGGGT TCACGTTATC TCAACGGACT GGGTTCAGAC ACGGAACAGA TGCGGTATCT	18360
GATGGATAAC GCGGCCAGAC AACAGAAAGG ACTGGGATTA GAGTTTGGTG TGGCGCTGAC	18420
AGCTGAACAG ATTGCTCAGC TTGACGGCAG CATGCTGTGG TGGGAGTCAG TCACCATCAA	18480
CGGACAGACA GTCATGGTCC CGAAACTGTA TCTGTGCGCG GAAGATATCA CCCTGCATAA	18540
CGGCAGCGTT ATCAGCGGGA ACAACGTGCA GCTTGCGGAC GGCAATATCA CCAACAGCGG	18600
CGGCAGCATC AACGCACAGA ACGACCTTTC GCTCGACAGT ACCGGCTATA TCGACAACCT	18660
GAATGCAGGG CTGATAAGCG CGGGCGGTAG CCTGGACCTG AGCGCCATCG GGGATATCAG	18720
CAATATCAGC TCAGTCATCA GCGGTAAAC CGTACAAC TGAAAGCGTGA GTGGCAACAT	18780
CAGCAATATC ACCCGGCGTC AGCAATGGAA TGCGGGCAGT GACAGCCGAT ATGGTGGTGT	18840
GCATCTCAGC GGTACGGACA CCGGTCCGGT TGCGACCATT AAAGGCACTG ATTCACTTTC	18900
ACTGGATGCA GGGAAAAACA TTGATATTAC CGGGGCAACG GTCTCGTCCG GTGGAGACCT	18960
TGGAATGTCT GCGGGTAATG ACATCAACAT TGCCGTAAAC CTGATAAGCG GGAGCAAAAG	19020
TCAGTCCGGT TTCTGGCACA CTGATGACAA CAGTTCATCA TCCACCACCT CACAGGGCAG	19080
CAGCATCAGC GCCGGCGGTA ACCTGGCGAT GGCTGCAGGC CATAATCTGG ATGTCACAGC	19140
ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTCTGCA GGTAACGACC TGAGTCTGAA	19200
TGCAGTCAGG GAAAGCAAAA ACAGTCGCAA CGGCAGGTCA GAAAGTCATG AAAGCCACGC	19260
AGCTGTGTCC ACGGTGACGG CGGGCGATAA CCTCCTCCTT GTTGCCGGTC GTGATATTGC	19320
CAGTCAGGCT GCCGGTATGG CTGCGGAAAA TAACGTGGTC ATCCGGGGCG GACGTGATGT	19380
GAACCTGGTG GCAGAGTCTG CCGGCGCAGG CGACAGCTAT ACGTCGAAGA AAAAGAAAGA	19440
GATTAACGAG ACAGTCCGTC AGCAGGGAAC GGAAATCGCC AGCGGTGGTG ACACCACCGT	19500
CACCGCAGGA CGGGATATCA CCGCTGTTGC GTCATCCGTT ACCGCAACCG GCAATATCAG	19560
CGTGAATGCC GGTGCTGATG TTGCCCTGAC CACGGCGACA GAAAGTGAAT ATCACTATCT	19620

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GGAAACGAAG	AAAAAAGCG	GAGGTTTTCT	CAGTAAGAAA	ACCACCCACA	CCATCAGTGA	19680
GGACAGTGCC	TCCCGTGAAG	CAGGTTCCCT	GCTGTCGGGG	AACCGCGTGA	CCGTTAACGC	19740
CGGTGATAAN	CTGACGGTAG	AGGGTTCGGA	TGTGGTGGCT	GACCGGGATG	TGTCAGTGGC	19800
GGCGGGTAAC	CATGTTGATG	TTCTTGCTGC	CACCAGTACA	GATACGTCCT	GGCGCTTTAA	19860
GGAAACGAAG	AAATCCGGTC	TGATGGGTAC	CGGCGGTATT	GGTTTCACCA	TTGGCAGCAG	19920
TAAGACAACG	CACGACCGCC	GCGAGGCSGG	GACAACGCAG	AGTCAGAGTG	CCAGTACCAT	19980
CGGCTCCACT	GCCGGTAATG	TCAGTATTAC	CGCGGGCAAA	CAGGCTCATA	TCAGCGGTTC	20040
GGATGTGATT	GCGAACCGGG	ATATCAGCAT	TACCGGTGAC	AGTGTGGTGG	TTGACCCGGG	20100
GCATGATCGT	CGTACTGTGG	ACGAAAAATT	TGAGCAGAAG	AAAAGCGGGC	TGACGGTTGC	20160
CCTTTCCGGC	ACGNTGGGCA	GTGCCATCAA	TAATGCGGTC	ACCAGTGCAC	AGGAGACGAA	20220
GGAGAGCAGT	GACAGCCGTC	TGAAAGCCCT	GCAGGCCACA	AAGACAGCGC	TGTCTGGTGT	20280
GCAGGCCGGA	CAGGCTGCGG	CAATGGCCAC	CGCAACCGGT	GACCCGAATG	CGACGGGAGT	20340
CAGCCTGTCTG	CTTACCACCC	AGAAATCGAA	ATCACAACAA	CATTCTGAAA	GTGACACAGT	20400
ATCCGGCAGT	ACGCTGAATG	CCGGGAATAA	TCTGTCTGTT	GTCGCAACCG	GCAAAAACAG	20460
GGGAGATAAC	CGCGGAGATA	TTGTGATTGC	AGGAAGCCAG	CTTAAGGCCG	GTGGTAACAC	20520
AAGCCTGGAT	GCCGCGAATG	ATGTTCTGTT	GAGTGGCGCT	GCAAACACAC	AAAAACAAC	20580
GGGCAGGAAC	AGCAGCAGTG	GCGGTGGCGT	GGGTGTCAGT	ATCGGTGCCG	GTGGTAACGG	20640
TGCCGGTATC	AGCGTCTTTG	CCAGCGTTAA	TGCGGCAAAA	GGCAGCGAGA	AAGGTAACGG	20700
TACTGAGTGG	ACTGAAACCA	CAACAGACAG	CGGTAAACC	GTCACCATCA	ACAGTGGTCG	20760
GGATACGGTA	CTGAACGGTG	CTCAGGTCAA	CGGCAACAGG	ATTATCGCCG	ATGTGGGCCA	20820
CGACCTGCTG	ATAAGCAGCC	AGCAGGACAC	CAGTAAGTAC	GACAGTAAAC	AGACCAGCGT	20880
GGCTGCCGGC	GGCAGTTTTA	CCTTTGGCTC	CATGACCGGC	TCAGGTTACA	TCGCTGCCTC	20940
CCGGGATAAG	ATGAAGAGCC	GCTTTGACTC	CGTTGCTGAA	CAAACCGGGA	TGTTTTCCGG	21000
AGATGGCGGC	TTCGATATCA	CGGTCGGCAA	CCACACCCAG	CTCGATGGTG	CGGTTATCGC	21060
TTCCACGGCG	ACGGCAGATA	AAAACAGCCT	CGATACCGGG	ACGCTCGGCT	TCAGCGATAT	21120
TCACAACGAA	GCGGATTATA	AAGTCAGTCA	CAGTGAATC	AGTCTGAGCG	GTGGTGGCAG	21180
CTTCGGGGAT	AAATTTACAG	GTAACATGCC	GGGTGGCATG	ATATCCGCCG	GAGGTCACAG	21240
CGGACATGCG	GAAGGAACGA	CTCAGGCCGC	AGTGGCAGAT	GGCACAATCA	CCATCCGGGA	21300
CAGGGACAAT	CAGAAGCAGA	ATCTGGCGAA	CCTGAGCCGT	GACCTGCGC	ACGCTAATGA	21360
CAGTATCAGC	CCGATATTTG	ACAAGGAGAA	AGAGCAGAGG	CGTCTGCAGA	CAGTGGGGCT	21420
TATCAGTGAC	ATTGGCAGTC	AGGTGGCGGA	TATCGCGCGG	ACGCAGGGGG	AACTGAATGC	21480
GTTGAAGCTG	CGCAGGATAA	ATATGGGCCT	GTTCCGGCGG	ATGCGACGGA	AGAACAGCGG	21540

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CAGGCATATC TGGCAAAACT GCGTGATACG CCGGAATACA AAAAGGAACA GGAAAAGTAT	21600
GGTACCGGCA GCGATATGCA GCGCGGTATC CAGGCTGCAA CGGCTGCACT TCAGGGCCTG	21660
GTGGGCGGCA ATATGGCAGG CGCGCTGGCA GGTGCTTCAG CGCGGAGCT GGCGAACATC	21720
ATCGGTCATC ACGCGGGTAT TGATGACAAT ACAGCGGCAA AAGCCATTGC CCATGCCATT	21780
CTCGGTGGTG TGACAGCAGC CCTTCAGGSC AACAGTGCGG CAGCAGGCGC AATTGGTGCG	21840
GGTACTGGTG AAGTGATCGC GTCAGCCATT GCGAAAAGCC TCTACCCGGG CGTAGATCCG	21900
TCGAAACTGA CAGAAGATCA GAAGCAAACGT GTAAGCACGC TGGCAACGCT GTCAGCGGGT	21960
ATGGCCGGCG GCATTGCCAG TGGCGATGTG GCTGGCGCGG CTGCTGGAGC TGGTGCCGGG	22020
AAGAACGTTG TTGAGAATAA TGGCTGAGT CTGGTTGCCA GAGGCTGTGC GGTGCGAGCA	22080
CCTTGCAGGA CTAAAGTTGC AGAGCAGTTG CTAGAAATCG GGGCGAAAGC GGGCATGGCC	22140
GGGCTTGCCG GGGCGGCAGT CAAGGATATG GCCGACAGGA TGACCTCCGA TGAAGTGGAG	22200
CATCTGATTA CCCTGCAAAT GATGGGTAAT GATGAGATCA CTACTAAGTA TCTCAGTTGC	22260
TTGCATGATA AGTACGGTTC CGGGGCTGCC TCGAATCCGA ATATCGGTAA AGATCTGACC	22320
GATGCGGAAA AAGTAGAACT GGGCGGTTCC GCCTCAGGAA CCGGTACACC ACCACCATCG	22380
GAAAATGATC CTAAGCAGCA AAATGAAAAA ACTGTAGATA AGCTTAATCA GAAGCAAGAA	22440
AGTGCGATTA AGAAGATCGA TAACACTATA AAAAATGCTC TGAAAGATCA TGATATTATT	22500
GGAAGTCTCA AGGATATGGA TGTAAGCCA GTTCCTAAAG AGAATGGAGG ATATTGGGAT	22560
CATATGCAGG AAATGCAAAA TACGCTCAGA GGATTAAGAA ATCATGCGGA TACGTTGAAA	22620
AACGTCAACA ATCCTGAAGC TCAGGCTGCG TATGGCAGAG CAACAGATGC T	22671

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT	60
ATCAGGGTTA TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGGCA ACTGAAACCC	120
GCTGACGGAT NANGTGTACA GTGGCATCAG TGGACGGM TT ACAGCATAAG TGCTTAAGGC	180
GCGTGACCAT ACAGMTACGG TCGCTGCAGA GAACAGGGAG AATATCATCC GGAACACGGT	240
GGCCATAAAC CGTAACACCA GGGGGCTGCT TTCCCCGGA GAGTGCTGG AGATGCATGC	300
GGACGTCTGA ACAGTCAGCA GGGCTGATTA ATGAGAATCA CGAGGAAATG AAGCGGGAGC	360
CGTACAGTGA GGATAAATTT AACGCCATAG CGGCTGTGGG CGGGTATAGT GCCAAGCAGA	420

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CTGCTTAAAG GCAGGTACTA CTTTCAGTGG CGCCTATGTT TCCTGGAATG TGGGTGTCAA	480
CTGGTAGTTC TGAACCCGGG CCTGAGTCAC CGGGGAGGCA GTTTTCGGTA TGAAGTAATG	540
ATTCGCTGCC TGTTTTTCTC CCGGATGGCA TAACTGACTG TTCCCGGGTA TTCCTGAAGA	600
TCTGAGAGGA AGAGTGATA TGCTGAATA TCGGATAAGG TCAATGCAGC TATTTATTGT	660
AAACGGTCGG GCTGACAGGG CGCAGGTGCG TCTGGAATGC GACGATGAAG CCGTTTTTGA	720
ATGTTATCTT CTTGCTGAAG GGAAGGGGA ACTGAAAGAA CTGAGCCTGT CAGAGCTGGA	780
AGAGCGGGCG CTGATGTATG CGGCAGACAG TTTCCGTTAT GAATGATAAG TCAGTTATAC	840
CGGTAATGGT AAACGGAGCC GGTATCCGGG ATACAAGGGG CAGAGAGTAT GCTGATTATT	900
ATTATGACCC GGGACAGATA TCTGGAATAT GGCCTGATGC GTATACTGAG CGGATATCAG	960
GTCACGACAG GCAGAGAGCT GTTTAATGCC GGAAAGCAAC GTCAGTCACT TCCCGAAGAC	1020
AGTTATGTGA TTCTCTGTGA CCGTAATCTG GAAAGGCTTA CATACTCTAT GTTCTGTGGG	1080
CGTCGGTTTC TTGTCATTCC TGTTTCCTCT GTGAGATGCC TGACAGATAT CAGGCAAACC	1140
ATCCGCCGTG GAGCGTGGCT GTTCGGACAT ACGGCAAGGC CACTGACCCG GACAGAGATG	1200
GTGGTGGTCT TCGGGGTTGT TTTCCATGAC TACGGGTTTA CCTTTCTGGC AGACCGGCTG	1260
GGGATAACCA TGAAGACGGT ATGTGCGCAT CTTTACAATG CGATGGAGAA AAATGGTATG	1320
CGCGGCGTCA GTATTAAATA TCTCTGCAAC ACCATAGACC GGTAAAAAGA TGGTTTTCTG	1380
ATAAAGGCTG TTGCGACGGG GATTTCTGTG CATGCTGTGT CACGGGCATC CCAGCTCTCC	1440
GGATAATTAA TGTTATGTAG TCAGGCGTGA TAAATTTTAT ATGGAACAGG TATGCGTTTT	1500
ATTTGTGATA ACAGTTAATG AGGTGTTTCC ATACACACTG AAGTTACCTG TAATATTAGC	1560
GGGGGATTTG AATGATGTTG CGTGTCTGCG ACCACTCGTT TATTCATGCA AATAAGTGGA	1620
CTGCTGGATC CACGGTAAGA GTACAGCGAG GGCCGTATTG ACGGGGATGT GTTATTCAGC	1680
GGGCAGTGCT ATGCGCCACG GAAGCAGTTC GCTGACACGG TTGACCGGCC AGTCAGCTAT	1740
GACGCCAAAC ACATGGCGAA GGTAGTTTTT TGGATCCTCG TCGTTCAGTT TGCACGTCCC	1800
GATCAGGCTG TACAGTAGCA CTCCCCGCTC ACCACCATGC TCAGAGCTGC GTATTACCGT	1860
GAAGGAGATC GGTGAGTAAC CCTCTGTGTC GGCACATTAT AGCCGTCACA TCGGATAACT	1920
GTTATCCTTC TGTTCTGATG TATTCTGGGA GGTGATGTTT CACTCCTGAT AAGAGCATT	1980
CTAATTACAG CTGCTTTTCG GATAACATTC GGGCAGTTTT CTTTAATTCT GAAGTCTGAA	2040
AGAGATATCA GTAATTGTAT TGCTTTTAAA CATTGTCAGT ATTTATTTGT CCAAATCGTT	2100
CACGTTTCTC ATAATCTTCC CGACAGTCAC CATCACAAAA CAATCCAGTC TTAACAGGTT	2160
CTCCGCAGTT ATAGCAGAAT CCTGTTTCAG GGAGTCTATT CCGGATACGA TTTTTTAGTC	2220
TGATGCTCAT GCTGAATTGT TCATTTTCAT AAGCAATATC TGCACTATCT GCCATAAACG	2280
ATCCTCTGAG GAGACCACAT CTTTATAACC CACCACCGAA ATATTACAAA GTAATACTCA	2340

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TTGTATAATC TTTAACCRGG GGCAGGATAA TTGTATCCTG CCCCT

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(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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CTTTCAGACC AGCGTTTCCT GTCAGGAGAT GAGGAAGAAA CATCAAAGTA TAAAGGCGGC      60
GATGACCATG ATACGGTATT CAGTGGCGGT ATTGCGGCCG GTTATGATTT TTATCCGCAG      120
TTCAGTATTC CGGTTTCGTAC AGAACTGGAG TTTTACGCTC GTGGAAAAGC TGATTCGAAG      180
TATAACGTAG ATAAAGACAG CTGGTCAGGT GGTTACTGGC GTGATGACCT GAAGAATGAG      240
GTGTCAGTCA ACACACTAAT GCTGAATGCG TACTATGACT TCCGGAATGA CAGCGCATTC      300
ACACCATGGG TATCCGCAGG ATTGGCTACG CAGAATTCAC CAGAAAACAA CCGGTATCAG      360
TACCTGGGAT TATGAGTACG GAAGCAGTGG TCGCGAATCG TTGTCACGTT CAGGCTCTGC      420
TGACAACTTC GCATGGAGCC TTGGCGCGGG TGTCCGCTAT GACGTAACCC CGGATATCGC      480
TCTGGACCTC AGCTATCGCT ATCTTGATGC AGGTGACAGC AGTGTGAGTT ACAAGGACGA      540
GTGGGGCGAT AAATATAAGT CAGAAGTTGA TGTTAAAAGT CATGACATCA TGCTTGGTAT      600
GACTTATAAC TTCTGACGAC ACTGCTCCTG AACGATAATT GCGTATATTC TGTAATTAAG      660
ATAATTGCAT ATCKTCTGCA ATTAARCAGA AATACCCTGC AGTCTATTAC TGCAGGGNTG      720
TCTTTTATCT GTTTACAGA NAATTT      746

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(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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TCTGTTTGTC GTTTTTTCCC CGTTGTAGCG GYTCTGCTCC TGGCTTCCCT GATAGTCAGC      60
CCGCAGGCGC CAGGGCCCCA GATTCCCCC CACAGTCCCG TTATAACTGA ACTGATGAGA      120
GTCTCCTCCC TGATAATTAC GGGAAACCGT CCCGTTGAGG TTATAATCCA GCATCAGTCC      180
GGGAATGCCG TCGTCCCAGC GTGAGGGAGG CAGCCAGGTG GCATCAGAAT ACTCAAGCCC      240
AGCTGCGGCA TATTGATGCG TAATACGCCC GCTCCGGTAT CAGGACGAAT ATCCACTCCC      300
GGCAACCCAT GAAAATCCGC AACTGACCA TCATGCCAGT AAACAACTTT ATCCAGAGAT      360

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TCTGCTGTTA ACCCCATCAG TCTGACCATA TCTGATGTCA GACAGGCCTG C 411

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 977 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TATTATCGCG CGCGCGCTGC ACAGGGGTTA TCTACATCTG CTGCTGCTGC CGGTTTAATT 60
 GCTTCTGTAG TGACATTAGC AATTAGTCCC CTCTCATTCC TGTCCATTGC CGATAAGTTT 120
 AAACGTGCAA ATAAAATAGA GGAGTATTCA CAACGATTCA AAAAAGTTGG ATACGATGGT 180
 GACAGTTTAC TTGCTGCTTT CCACAAAGAA ACAGGAGCTA TTGATGCATC ATTAACAACG 240
 ATAAGCACTG TACTGGCTTC AGTATCTTCA GGTATTAGTG CTGCKGCAAC GACATCTCTT 300
 GTTGGTGCAC CGGTAAGCGC ACTGGTAGST GCTGTTACGG GGATAATTTT AGGTATCCTT 360
 GAGGCTTCAA AGCAGGCAAT GTTTGAACAT GTTGCCAGTA AAATGGCTGA TGTTATTGCT 420
 GAATGGGAGA AAAAACACGG TAAAAATTAC TTTGAAAATG GATATGATGC CCGCCATGCT 480
 GCATTTTTAG AAGATAACTT TAAAATATTA TCTCAGTATA ATAAAGAGTA TTCTGTTGAA 540
 AGATCAGTCC TCATTACTCA ACAACATTGG GATATGCTGA TAGGTGAGTT AGCTAGTGTC 600
 ACCAGAAATG GAGACAAGAC ACTCAGTGGT AAAAGTTATA TTGACTATTA TGAAGAGGGA 660
 AAGCGGCTGG AAAGAAGGCC AAAAGAGTTC CAGCAACAAA TCTTTGATCC ATTAAGAGGA 720
 AATATTGACC TTTCTGACAG CAAATCTTCT ACGTTATTGA AATTTGTTAC GCCATTGTTA 780
 ACTCCCGGTG AGGAAATTCG TGAAAGGAGG CAGTCCGGAA AATATGAATA TATTACCGAG 840
 TTATTAGTCA AGGGTGTGTA TAAATGGACG GTGAAGGGGG TTCAGGACAA GGGGTCTGTA 900
 TATGATTACT CTAACCTGAT TCAGCATGCA TCAGTCGGTA ATAACCAGTA TCGGGNAATT 960
 CGTATTGAGT CACACCT 977

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTCTTAAGT CCGGCATTGC CACGCGTAAC CCCCACTTCA ACCGCATGAT TGAGCAGATC 60
 GAAAAAGTGG CGATCAAATC CCGCGCGCCG ATTCTGCTTA ACGGTCCAAC CGGCGCGGGC 120

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AAGTCATTTT TGGCGCGACG CATCTTAGAG TTAAAACAGG CGCGGCATCA GTTTAGCGGC 180
 GCKTTTGTGG AAGTGAAGT CGCCACCCTG CGCGGCGATA CCGCCATGTC GACGCTGTTT 240
 GGTCATGTAA AAGGCGCGTT TACCGGGGCG CGGGAATCTC GTGAAGGTTT ATTACGCAGC 300
 GCCAACGGGG AAATGTTGTT TCTTGATGAG ATTGGCGAAC TGGGCGCGAC GAACAGGCAA 360
 TGCTGCTGAA ACCCATTGAA GRGGAAAACC TTTTACCGT 400

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GTATGCGTTT TCATTAAGAT ATTCTCTGCT GTAGAGAAAC TTATAGCAAT ATAATCTGAT 60
 AATATCTTTT ATGTAAAATT TAAATAGTTC ACCTGTGACA GATATATGTT TTCTGCTCAG 120
 TAACTCCTGT GTATTAAGCC ATTCCCGTGA CCGAAGCACA CCCTTGTGAA AACTTTTTCT 180
 TACTTGCTTT GAGGCACGGC ATTGATGTAA TATTTTTGCG TCCTCAATAA TTCTCTTTCC 240
 CGTTTTATTT TTTGCAGCAT CTCTTACTCC ATAAAATATC TCCCGGTCCA GACTTTTGTC 300
 ATATTTACTG ATTATACGAC AAATATTCCT GACCCGACGA TTCTCTTTAT TTCGCTTCCA 360
 TAGCTTATAA TGATCATCGC ATAACCTTAA GGCATTTGCC TCATCAAATT CTGAAACAGG 420
 ATTACTGCAT TTTTATTCC GACAAATACC TTTGTTTTTA GCCATACTCT TCTTCCCGTC 480
 AATGGAAAAA TTTTCACACC CATATTACCT GAATGATAAA CCGGATTAGT GTGATCCGGT 540
 TCAGTGAAAT CAACAGGATA CCGGTATGCC ATTCAGCAAT TCTTCCCTCT CCGCGCAAGT 600
 GAAATCATAT CTGACGTTTC TTCCTGAAGA AATACGCCAG AAAATCCTTG AACATCTCCA 660
 CGGTGTTATT CATTACGAGC CCGTGATTGG CATTATGGGT AAATCCGGCA CCGGCAAGAG 720
 CAGCCTGTGT AATGCCATTT TTCAGTCCCG TATCTGCGCC ACGCATCCCC TGAACGGCTG 780
 CACCCGCCAG GTCATCGTC TTACCCTGCA GTCGGTGAA CGCAGAATGA CGCTGGTCGA 840
 TCTGCCCCGC ATTGGTGAAA CACCGCAGCA TGATCAGGAA TACCGAGCGC TTTATCGTCA 900
 GTTACTGCCG GAACTGGATC TGATTATCTG GATCCTGCGG AGTGATGAAC GTGCGTATGC 960
 TGCCGATATT GCCATGCATC AGTTTTTACT GAATGAGGGC GCAGATCCCT CGCGCTTTCT 1020
 GTTTGTTCTC AGCCATGCCG ATCGCATGTT TCCTGCTGAA GAATGGAATG CCACAGAAAA 1080
 ATGCCCCGCC CGTCACCAGG AACTCTCACT GGCGACAGTA ATAGCCCCGG TGGCCACCCT 1140
 GTTCCCTTCA TCATTTCCGG TACTCCCTGT AGCCGCACCT GCAGGCTGGA ACCTTCCAGC 1200
 GCTGGTGTCA CTGATGATCC ACGCGCTGCC ACCACAGGCA ACCAGCGCAG TTTATTCACA 1260

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TATCAGGGGG	GAAAACCGCT	CTGAACAGGC	CCGGAAACAC	GCACAACAGA	CTTTTGGTGA	1320
TGCCATCGGG	AAAAGTTTTG	ACGACGCCGT	TGCGCGGTTG	AGTTTTCCGG	CCTGGATGTT	1380
ACAGCTTCTG	CGTAAAGCCC	GGGACCGCAT	TATCCACCTG	CTGATCACAC	TGTGGGAGCG	1440
TCTGTTCTGA	CACACTCAG	CCGACAGATG	TGTGCTGGA	TTAACGAGCA	TTCTTCTTTT	1500
TATGAAATCA	TGCTTAAAAA	TCAGATAATT	ARAAGAATAT	TTTTTCTGCT	GCATTTTATT	1560
CCTGATTATC	CGGATGCGAC	ACATCCTTTC	AACATCATGA	TGCATAATAA	CATCATGAAA	1620
TAAAAGATGT	TTTCTTACGG	AGTGACATC	TATGTCTGAT	AATCGTTCCC	GGCATGATCG	1680
CCTGGCGGTT	CGCTTATCAC	TCATTATCAG	CCGACTGATG	GCCGGAGAAT	CTCTGTCACT	1740
AAAAACACTG	TCAGATGAAT	TTGGCGTTAC	AGAACGTACT	TTACAGCGCG	ATTTTCATCA	1800
GCGTCTGGTT	CACCTAGATT	TAGAGTACAG	AAATGGCAGG	TACAGCCTCA	GACGACAGAG	1860
CAGCCCAGGT	GCGATCCCTG	AAATGCTTTC	TTTTATACAG	AATACCGGGA	TCGCACGGAT	1920
ACTTCCGCTC	CGGAACGGAC	GACTGATAAC	CTGTCTTACC	GACAACCAGG	AGCCCTCTCC	1980
CTGCCTTATC	TGGCTACCGG	CGCCGGATAT	CACTGCAACG	TTCCCCGAGT	GTTTCTCGCA	2040
ACTCATCCTG	GCAATAAGAC	AGTGTATCCA	CATCTCTCTG	ATGACTGAGC	GATGGTATCC	2100
GTCACTGGAG	CCCTGCCGGC	TCATTTATTA	CAGCGGTAGC	TGGTATCTGA	TCGCGTTACA	2160
GAAGGGAAAA	CTGCAGGTCT	TTCCTCTGGC	AGATATCAAA	TCAGTCAGCC	TGACATCAGA	2220
ACGGTTTGAA	CGGAGAGGCC	ACATCCACAG	TCTGGTCGCT	GAAGAGCGTT	TTATCTCCGC	2280
CCTGCCACAT	TTCTCTTTCA	TCCATAAACT	TATCAACACC	TTTAACCTGT	GATCGCCGGC	2340
CTGCCAAAGC	CGTCCCGACA	GGTATGGAGA	CAATATGTTG	AACAGAAAAC	TAAATATACG	2400
GCTACGTCAT	TCCCTGAACA	GTCACTGCAT	ACCTTCCATC	ATTATCAATA	ACACCGTACG	2460
TTCATTTTCA	AGGTCACTCA	TGAATACCAG	AGCTCTTTTT	CCCCTGCTGT	TCACTGTGGC	2520
ATCATTCTCC	GCCTCCGCCG	GCAACTGGGC	TGTCAAAAAC	GGCTGGTGTC	AGACCATGAC	2580
GGAAGATGGT	CAGGCGCTGG	TAATGCTGAA	AAATGGCACG	ATTGGTATTA	CCGGCCTGAT	2640
GCAGGGATGC	CCGAATGGTG	TACAGACGCT	CCTGGGCAGC	CGTATCAGTA	TTAACGGTAA	2700
CCTGATCCCC	ACATCACAAA	TGTGTAATCA	GCAGACGGGA	TTCAGGGCTG	TTGAGGTGGA	2760
AATCGGACAG	GCGCCGGAAA	TGGTCAAAAA	AGCCGTTTAC	TCCATAGCAG	AGCGTGATGT	2820
GTCCGTTTTA	CAGGCATTTG	GTGTACGAAT	GGAATTCACC	CGCGGTGATA	TGCTGAAGGT	2880
CTGTCCGAAA	TTTGTCACAT	CACTTGCCGG	TTTTTCCCCG	AAACAGACGA	CCACTATTAA	2940
TAAAGATTCC	GTCCTGCAGG	CTGCCCCGCA	GGCATACGCC	CGGGAATATG	ACGAGGAAAC	3000
AACAGAAACC	GCTGATTTTG	GCTCTTACGA	AGTAAAAGGC	AATAAGGTTG	AGTTTGAAGT	3060
ATTCAATCCT	GAAGACCGTG	CGTACGACAA	AGTGACCGTC	ACGGTTGGTG	CTGACGGTAA	3120
TGCCACCGGC	GCCAGCGTTG	AATTTATCGG	AAAATAGCCG	GTATGTCGGA	CTGCCACCCT	3180

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GTTTTATTGC CCGAAGGCCC TTTCTCACGC GAACAGGCGA TGGCTGTCAC AACAGCTTAC	3240
CGCAATGTGC TTATTGAAGA TGACCAGGGA ACGCATTTCG GGTGGTTAT CCGCAATGCC	3300
GAAGGGCAGC TACGCTGGCG GTGCTGGAAT TTTGAACCTG ATGCCGGAAA ACAGCTAAAT	3360
TCGTATCTCG CCAGTGAGGG AATTCTCAGG CAATAAACGT CTTCATTTC AATCATCAGGC	3420
CGCGTCTTCT CCGGGAGACG CGGCCTTTTC GTTTATACCG CTAATTCATT CATAAGGAGC	3480
AAAGTATGCA ATTAGCCAGT CGTTTTGGTC ATGTAAATCA GATCCGTCGG GAGCGCCAC	3540
TGACACGCGA AGAACTGATG TACCACGTCC CGAGTATTTT TGGAGAAGAC CGGCACACCT	3600
CCCGCAGTGA ACGGTATGCG TACATTCCCA CCATCACCCT CCTGGAAAAT CTGCAGCGGG	3660
AAGGCTTTCA GCCGCTKCTT GCCTGCCAGA CCCGTGTGCG CGACCCAGAGC CGCCGGGAAT	3720
ATACCAAACA TATGCTGCGT CTGCGGCGGG CCGGACAGAT AACCGGTCAG CATGTGCCTG	3780
AAATTATTCT GCTCAACTCC CATGACGGTT CATCCAGCTA CCAGATGTTA CCCGGATATT	3840
TTCGTGCCAT TTGTACCAAT GGCCTGGTCT GCGGTCAGTC GCTGGGAGAA GTCCGGGTGC	3900
CACACCGGGG AAACGTGGTG GACAGGGTCA TAGAAGGTGC TTACGAAGTG GTGGGCGTGT	3960
TTGACCTGAT TGAGGAAAAG CGTGATGCCA TGCAGTCGCT GGTCTGCCG CCACCGGCAC	4020
GCCAGGCGCT GGCACAGGCG GCGCTGACTT ACCGTTATGG TGATGAACAT CAGCCCGTCA	4080
CCACTACCGA CATTCTGACG CCACGACGCC GGGAGGATTA CGGTAAGGAC CTGTGGAGTG	4140
CTTATCAGAC CATCCAGGAG AATATGCTGA AAGGCGGGAT TTCCGGTCGC AGTGCCAGAG	4200
GAAAACGTAT CCATACCCGG GCCATTACCA GCATCGATAC CGACATTAAG CTCAACCGGG	4260
CGTTGTGGGT GATGGCAGAA ACGCTGCTGG AGAGCCTGCG CTGATACCGT TTCCCTGAAA	4320
GCGCAGTCCT GTTCACGGCT GTCCCTTCCC CCAGACATTC CACCATTCTT TACTTTTTA	4380
TAAGGAATAA TCTCATGACA ACCTCTTCGC ATAATTCCAC CACACCTTCT GTTCCGTGG	4440
CCGCTGCATC AGGGAATAAC CAGTCTCAGT TGGTTGCCAC TCCCGTCCCT GATGAACAGC	4500
GCATCAGCTT CTGGCCGCAG CATTTTGGCC TCATTCCACA GTGGGTCACC CTGGAGCCCC	4560
GTGTCTTCGG CTGGATGGAC CGTCTGTGCG AAACTACTG CGGGGGTATC TGGAATCTGT	4620
ACACCCTGAA CAACGGTGGC GCATTTATAG CACCTGAACC GGATGAAGAT GATGGAGAAA	4680
CCTGGATACT GTTCAATGCC ATGAACGGTA ACCGCGCTGA AATGAGCCCG GAAGCTGCCG	4740
GCATTGCCGC CTGTCTGATG ACGTACAGCC ATCATGCCTG TCGTACGGAG AATTATGCCA	4800
TGACGGTCCA TTATTACCGG TTGCGGGATT ACGCCCTGCA GCATCCGGAA TGCAGCGCCA	4860
TTATGCGCAT CATTGACTGA AAGGGGCCGG AATAATGCAA CAGATTTCTT TTCTGCCCGG	4920
AGAAATGACG CCCGGCGAGC GCAGTCACAT TCTGGGGGCC CTGAAAACCC TGGACCGCCA	4980
TCTTCATGAA CCCGGTGTGG CCTTCACCTC CACCGGTGCG GCACGGGAAT GGCTGATTCT	5040
GAACATGGCG GGAATGGAGC GTGAAGAGTT CCGGGTGCTG TATCTGAATA ACCAGAATCA	5100

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GCTGATTGCC	GGTGAAACCC	TCTTCACCGG	CACCATCAAC	CGCACGGAAG	TCCATCCCCG	5160
GGAAGTGATT	AAACGCGCCC	TGTACCACAA	TGCGGCTGCC	GTGGTCTGG	CGCACAAATCA	5220
CCCGTCCGST	GAAGTCACAC	CCAGTAAGGC	AGACCGGCTT	ATCACCGAAC	GTCTGGTACA	5280
GGCACTGGGC	CTGCTGGATA	TCCGGGTGCC	GGACCATCTG	ATAGTCGGTG	GCAGCCAGGT	5340
TTTCTCCTTT	GCGGAACACG	GTCTGCTTTA	ACCGGTCACC	GTCACAATCA	CCTTCATATC	5400
ACTTCAGTTT	CTCTTTCTCA	GCTGTTTCTT	ACTTTCACAT	TCAGGAGGAC	TATTCTCATG	5460
AAAATCATCA	CCCGTGGTGA	AGCCATGCGT	ATTCACCGTC	AGCATCCTGC	ATCCCGTCTT	5520
TTTCCGTTCT	GTACCGGTAA	ATACCGCTGG	CACGGTAGCA	CGGATACATA	TACCGGCCGT	5580
GAAGTACAGG	ATATTCCCGG	TGTGCTGGCT	GTGTTTGCTG	AACGCCGTAA	GGACAGTTTT	5640
GGCCCGTATG	TCCGGCTGAT	GAGCGTCACC	CTGAACTGAA	TCAGGACGGG	CATTGAGAAG	5700
AGCAGAATTA	TCGCCACCAC	CGGACCATTG	TTAACCAATT	TTCTGTGAGG	ATTTTATCGT	5760
GTCAGACACT	CTCCCCGGGA	CAACGCATCC	CGACGATAAC	AACGACCGCC	CCTGGTGGGG	5820
GCTACCCTGC	ACCGTGACGC	CCTGTTTTGG	GGCAGCTCTG	GTGCAGGAGG	GTAACCGGTT	5880
GCATTACCTT	GCAGACCGCG	CCGGTATCAG	AGGCCGGTTC	AGCGACGCGG	ATGCGTACCA	5940
TCTGGACCAG	GCCTTTCCGC	TGCTGATGAA	ACAACGGGAA	CTCATGCTCA	CCAGCGGTRA	6000
ACTGAATCCC	CGCCATCAGC	ATACCGTCAC	GCTGTATGCA	AAAAGGCTGA	CCTGCGAANC	6060
GACACCCTCG	GCAGTTGTGG	CTACGTTTAT	ATGGCTGTTT	ATCCGACGCC	CGAAACGAAA	6120
AAGTAACTCT	CCAGAATAAC	CTTCTGCCCC	GGCCTGGTGC	TTTACCACG	CCACTTTTCC	6180
ATTTTTCATC	TCTGCATATC	AGGAAAATCT	TCAGTATGAA	CACATTACCC	GATACACACA	6240
TACGGGAGGC	ATCGCATTGC	CAGTCTCCCG	TCACCATCTG	GCAGACACTG	CTCACCCGAC	6300
TGCTGGACCA	GCATTACGGC	CTCACACTGA	ATGACACACC	GTTGCTGAT	GAACGTGTGA	6360
TTGAGCAGCA	TATTGAGGCA	GGCATTTTAC	TGTGTGATGC	GGTGAACTTT	CTCGTTGAAA	6420
AATACGCACT	GGTGCGTACC	GACCAGCCGG	GATTCAGCGC	CTGTACTCGT	TCTCAGTTAA	6480
TAAACAGTAT	TGATATCCTC	CGGGCCCGCC	GGGCAACCGG	CCTGATGGCC	CGCGACAATT	6540
ACAGAACGGT	AAATAACATT	ACCCTGGGTA	AGCATCCGGA	GAAACGATGA	AACTTTCCCT	6600
GATGCTGGAA	GCCGACAGAA	TTAATGTGCA	GGCACTGAAC	ATGGGGCGAA	TTGTGCTTGA	6660
CGTCGATGGT	GTAAATCTCA	CTGAACTGAT	TAACAAGGTC	GCTGAAAACG	GTTATTCACT	6720
CCGCGTGGTG	GAGGAATCCG	ACCAACAGTC	AACCTGCACA	CTACCACCGT	TTGCAACCCT	6780
TGCCGGCATA	CGCTGCAGTA	CCGCACATAT	CACGGAAAAG	GATAACGCCT	GGCTGTACTC	6840
GCTGTACAC	CAGACCAGTG	ACTTCGGTGA	ATCAGAATGG	ATTCATTTCA	CAGGTAGCGG	6900
ATATCTGTTA	CGTACCGATG	CGTGGTCATA	TCCGGTTCTG	CGGCTTAAAC	GCCTGGGGCT	6960
GTCAAAAACG	TTCCGTGCTC	TGTTATCAC	ACTTACCCGA	CGTTATGGCG	TCAGTCTCAT	7020

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TCATCTGGAT GCCAGCGCTG AATGCCTGCC GGGTTTACCC ACTTTCAACT GGTAACCAGG	7080
AACAACATGA AATCATTAA CACGGAAACC GCACTGGATA TTCTGATTGC GTGGCTGCAG	7140
GACAATATCG ACTGCGAATC GGGGAATTATC TTTGACAACA ATGAGGATAA AACGGATTCA	7200
GCAGCACTGT TGCCCTGTAT CGAACAGGCC AGAGAGGATA TCCGTACCCT GCGCCAACTG	7260
CAGCTTCAGC ACCAGAACCG GTGAGTCTCA CTCATCATCT CACTCACCAG ACTTCATTCC	7320
ACTSACGCCA GCCTGAACAC GGCTGGCGTT TTCATTTATC TGCAAAAAGG AATATCGATT	7380
ATGTCTGAAA TCACAGTCTC CCGTCCGGAA GTGGTCAACG AGAATACGGA CGTTATCTGC	7440
TCCACCTCAG TCAGGTACAG GTCAGTGGAA TATGATAATT TTCCGGAAAT CAGCGAAGCG	7500
AACATTCTGA GCACATTTGA ACAACTGCAC CAGAACAAAG ATGAAGTGTT TGAACGGGGA	7560
GTGATCAACG TCTTCAAAGG GCTGAGCTGG GATTACAAAA CCAACTCACC CTGTAAATTT	7620
GGCAGTAAAA TTATCGTCAA CAATCTGGTG AGATGGGACC AGTGGGGATT TCATCTTATC	7680
AGTGGAATGC AGGCAGATCG CCTGSGTGAC CTGGAAAGAA TGTTGCATCT GCTCAGCGGT	7740
AAACCGATCC CCGACAACCG AGGGATATC ACCATTAATC TGGATGACCA CATAAGTCC	7800
GTTCAGGGTA AAGGACGCTA TGAAGATGAG ATGTTTCATCA TTAAATACTT TAAGAAGGGA	7860
TCTGCACACA TCACTTTCAA AAGGCTGGAG CTGATTGACA GAATTAACGA TATAATAGCC	7920
AGGCACTTTC CTTCTGTGCT CTCAGCCTGA CCCCAGATTT GATTCCCTTT CGATATCAAA	7980
AGGGACTGCG GGTACAAAAG AGGGTACATC TTTACCAAAA CCAAACAAAA TAACTAATA	8040
TCAACATGAT AGAAGCATT CTTGATTCCG AGTCCGGCAC CAAATTCATA TAAACGGACC	8100
TCCACGGAGG TCCGTTTTTC GTTTCAGGAC GCCACGATTT AAGCGTCCTG CCGCCAAATC	8160
AATTCTACCG AACTCAACCA GATTCTCCCC ACATCACCAG CAATTTGCGG GCATATCCCA	8220
ATTCGGGAAA ATTTGTTTCT GAGCTATAGC GCTGACTGAC GTGAAATGTC GTGCGGCCCC	8280
GTGATGCTGT TGAAMGTCAA ATGACGTCAT CAGGAGCGTA ACGCACCCAT AAAGCACAAC	8340
ATCGGGCAGA ACGCCAACTG ATGAGATTTT CTGAATGAGA ACAAAGAGAA ATGTATCAGT	8400
CCGTTTGCTC ATGCAAAGAC TAACAATCCA TAAAATAGT AAGCGCTCCG GACAATTTTC	8460
CATGGATTAT TTTCTGAACA TTTTCTTTG GCAAAGATGA TGAATTTTGA TGGTAAGGAA	8520
AATTACTTCT GGTTCCTCAGT AAAATCCTTT CGTAATACTA TGTAATCAAG AAGTTTATGG	8580
CTAGTAAAAA TAACGTCTTG CATTCACCAA TAATATGTAA ATAAACCCAT CTATAGATGG	8640
AAAAAATAGG TTATGGAATT ATCATTGCAT CATTCCCTTT TCGAATGAGT TTCTATTATG	8700
CAACAACCTG TAGTTCGCGT TGGCGAATGG CTTGTACTC CGTCCATAAA CCAAATTAGC	8760
CGCAATGGGC GTCAACTTAC CCTTGAGCCG AGATTAATCG ATCTTCTGGT TTTCTTTGCT	8820
CAACACAGTG GCGAAGTACT TAGCAGGGAT GAACTTATCG ATAATGTCTG GAAGAGAAGT	8880
ATTGTCACCA ATCACGTTGT GACGCAGAGT ATCTCAGAAC TACGTAAGTC ATTAAAAGAT	8940

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AATGATGAAG ATAGTCCTGT CTATATCGCT ACTGTACCAA AGCGCGGCTA TAAATTAATG	9000
GTGCCGSTTA TCTGGTACAG CGAAGAAGAG GGAGAGGAAA TAATGCTATC TTCGCCTCCC	9060
CCTATACCAG AGGCGGTTC TGCACAGAT TCTCCCTCCC ACAGTCTTAA CATTCAAAAC	9120
ACCACAACGC CACCTGAACA ATCCCCAGTT AAAAGCAAAC GATTCACTAC CTTTGGGTA	9180
TGGTTTTTTT TCCTGTTGTC GTTAGGTATC TGTGTAGCAC TGGTAGCGTT TTCAAGTCTT	9240
GAAACACGTC TTCCTATGAG TAAATCGCGC ATTTTGCTCA ATCCACGCGA TATTGACATT	9300
AATATGGTTA ATAAGAGTTG TAACAGCTGG AGTTCTCCGT ATCAGCTCTC TTACGCGATA	9360
GGCGTGGGTG ATTTGGTGGC GACATCACTT AACACCTTCT CCACCTTTAT GGTGCATGAC	9420
AAAATCAACT ACAACATTGA TGAACCGAGC AGTTCCGGTA AAACATTATC TATTGCGTTT	9480
GTTAATCAGC GCCAATACCG TGCTCAACAA TGCTTTATGT CGGTAAAATT GGTAGACAAT	9540
GCAGATGGTT CAACCATGCT GGATAAACGT TATGTCATCA CTAACGGTAA TCAGCTGGCG	9600
ATTCAAAATG ATTTGCTCCA GAGTTTATCA AAAGCGTTAA ACCAACCGTG GCCACAACGA	9660
ATGCAGGAGA TGCTCCAGCA AATTTTGCCG CATCGTGGTG CGTTATTAAC TAATTTTTAT	9720
CAGGCACATG ATTATTTACT GCATGGTGAT GATAAATCAT TGGATCGTGC CAGTGAATTA	9780
TTAGGTGAGA TTGTTCAATC ATCCCCAGAA TTTACCTACG CGAGAGCAGA AAARGCATTR	9840
GTTGRTATCG TGCGCCATTC TCAACATCCT TTAGACGRAA AACAATTAGC CAGCACTGAA	9900
CACAGAAATA GATAACATTG TTACTGCTCC GGAATTGAAC AACCTGTCCA TTATATATCA	9960
AATAAAAGCG GTCAGTGCCC TGGTAAAAGG TAAAACAGAT GAGTCTTATC AGGCGATAAA	10020
TACCGGCATT GATCTTGAAA TGTCCTGGCT AAATTATGTG TTGCTTGGA AGGTTTATGA	10080
AATGAAGGGG ATGAACCGGG AAGCAGCTGA TGCATATCTC ACCGCCTTTA ATTTACGCCC	10140
AGGGGCAAAC ACCCTTTACT GGATTGAAAA TGGTATATTC CAGACTTCTG TTCCTTATGT	10200
TGTACCTTAT CTCGACAAAT TTCKCGCTTC AGAATAAGTA ACTCCCGGGT TGATTCATGC	10260
TCGGGAATAT TTGTTGTTGA GTTTTTGTAT GTTCCCGTTG GTATAATATG GTTCGGCAAT	10320
TTATTTGCCG CATAATTTTT ATTACATAAA TTTAACCAGA GAATGTCACG CAATGCATTG	10380
TAAACATTGA ATGTTTATCT TTTCATGATA TCAACTTGCG ATCCTGATGT GTTAATAAAA	10440
AACCTCAAGT TCTCACTTAC AGAAACTTTT GTGTTATTTT ACCTAATCTT TAGGATTAAT	10500
CCTTTTTTTCG TGAGTAATCT TAGCGCCAGT TTGGTCTGGT CAGGAAATAG TTATACATCA	10560
TGACCCGGAC TCCAAATTCA AAAATGAAAT TAGGAGAAGA GCATGAGTTC TGCCAAGAAG	10620
ATCGGGCTAT TTGNCCTGTA CCGGTGTTGT TGCCGGTAAT ATGATGGGGA GCGGTATTGC	10680
ATTATTACCT GCGAACCTAG CAAGTATCGG TGGTATTGCT ATCTGGGGTT GGATTATCTC	10740
TATTATTGGT GCAATGTCGC TGGCATATGT ATATGCCCCG CTGGCAACAA AAAACCCGCA	10800
ACAAGGTGGC CCAATTGCGT ATGCCGGAGA AATTTCCCTT GCATTTGGTT TTCAGACAGG	10860

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TGTTCTTTAT TACCATGCTA ACTGGATTGG TAACCTGGCA ATTGGTATTA CCGCTGTATC	10920
TTATCTTTCC ACCTTCTTCC CAGTATTAAA TGATCCTGTT CCGGCGGGTA TCGCTGTTAT	10980
TGCTATCGTC TGGGTATTTA CCTTTGTGAA TATGCTCGGC GGTACCTGGG TAAGCCGTTT	11040
AACCACGATT GGTCTGGTGC TGGTTCTTRK TCCTGTGGTG ATGACTGCTA TTGTTGGCTG	11100
GCATTGGTTT GATGCAGCAA CTTATGCAGC TAACTGGAAT ACTGCGGATA CCACTGATGG	11160
TCATGCGATC ATTAAAAGTA TTCTGCTCTG CCTGTGGGCC TTCGTGGGTG TTGAATCCGC	11220
AGCAGTAAGT ACTGGTATGG TTAAAAACCC GAAACGTACC GTTCCGCTGG CAACCATGCT	11280
GGGTACTGGT TTAGCAGGTA TTGTTTACAT CGCTGCGACT CAGGTGCTTT CCGGTATGTA	11340
TCCGTCTTCT GTAATGGCGG CTTCCGGTGC TCCGTTTGCA ATCAGTGCTT CAACTATCCT	11400
CGGTAAGTGG GCTGCACCAC TGGTTTCTGC ATTCACCGCC TTTGCGTGTC TGACTTCTCT	11460
GGGCTCCTGG ATGATGTTGG TAGGCCAGGC AGGTGTACGT GCCGCTAACG ACGGTAAGTT	11520
CCCGAAAGTT TATGGTGAAG TCGACAGCAA CGGTATTCCG AAAAAAGGTC TGCTGCTGGC	11580
TGCAGTGAAG ATGACTGCCC TGATGATCCT CATCACTCTG ATGAACTCTG CCGGTGGTAA	11640
AGCCTCTGAC CTGTTGCGTG AACTGACCGG TATCGCAGTA CTGCTGACTA TGCTGCCGTA	11700
CTTCTACTCT TGC GTTGACC TGATTGCTTT TGAAGGCGTT AACATCCGCA ACTTTGTCAG	11760
CCTGATCTGT TCTGTACTGG GTTGCGTGTT CTGCTTCATC GCGCTGATGG GCGCAAGCTC	11820
CTTCGAGCTG GCAGGTACCT TCATCGTCAG CCTGATTATC CTGATGTTCT ATGCTCGCAA	11880
AATGCACGAG CGCCAGAGCC ACTCAATGGA TAACCACACA GCGTCTAACG CACATTAATT	11940
AAAAGTATTT TCCGAGGCTC CTCCTTTCAT TTTGTCCCAT GTGTTGGGAG GGGCCTTTTT	12000
TACCTGGAGA TATGACTATG AACGTTATTG CAATATTGAA TCACATGGGG GTTTATTTTA	12060
AAGAAGAACC CATCCGTGAA CTTTCATCGCG CGCTTGAACG TCTGAACTTC CAGATTGTTT	12120
ACCCGAACGA CCGTGACGAC TTATTAAAAC TGATCGAAAA CAATGCGCGT CTGTGCGGCG	12180
TTATTTTTGA CTGGGATAAA TATAATCTCG AGCTGTGCGA AGAAATTAGC AAAATGAACG	12240
AGAACCTGCC GTTGTACGCG TTCGCTAATA CGTATTCCAC TCTCGATGTA AGCCTGAATG	12300
ACTGCGTTTA CAGATTAGCT TCTTTGAATA TGCGCTGGGT GCTGCTGATG ATATTGCTAA	12360
CAAGATCC	12368

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 833 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GCACGGCACT CTGATGTANC TTTTATCTGT TCCCAGTGGG AGCATGCCCC ACAACTGAGT	60
CATTAAGTGT GGAAGAACAG TTTTGTCCCC GCGTGAATC TCTCCCTTTC NAAAAACCAG	120
TATGTCGCCA TGCCTCGCCT TAATGGAGAG CGCTGAACCA TACCTTCTTT TTCCCAGTAA	180
TAACAGGTAA TAGCGTGCCT GGTAATCCGT TACCGCCAGC GCGTCCGCAA TTTCTGCGGT	240
TTTCCCTCCA TTATGCCTGT TCAGAAATYC CAGTATTTCA TTCTTCATAT ATTCACTCAT	300
CTCACTGTAA CAAAGTTYCT YCGAATAATA AAAATCATGC TTTCTGTTAT CAACGGAAAAG	360
GTATTTTTAT TCTCTGTGTT TGCTTTATTT GTGAAATTTA GTGAATTTGC TTTTGTGTTG	420
CTTTATTTGN ATGTGTGTCA CATTITGTGT GTTATTTTTT TGTGAAAAGA AAGTCCGTAA	480
AAATGCATTT AGACGATCTT TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA	540
GTGCATTCTT TTTGTTGGTG TTTTATTCTA GTTTGATTTT GTTTTGTGGG TTAAAAGATC	600
GTTTAAATCA ATATTACAA CATAAAAAAC TAAATTTAAC TTATTGCGTG AAGAGTATTT	660
CCGGGCCGGA AGCATATATC CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA	720
GTCATCAGTC GGTGAGGAAA TGCCTTTTTG CTGAATATAC GCGAGAGCGT AYTGTGCCCC	780
GGCTMTATGT CTGAAATGCA TTTTTTTTTA CTGATAGGTA TTTCTTCTCA TTC	833

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGCACCATCA CTGATACCAC CGGGACCCCG GATTTTATCC GGTCCCCGCG GACTGACAGG	60
GTTTGTGACA CCTGAGTCAT ATCCGATGTA AACTTCATTT TCACGGGTTG TACAGGAAAA	120
CTCCCTGTG CCATTGAGTT CTGATGTGTG CCCTTCGCCA CAACTCCAC CGTCACGGCA	180
CCAGTTGCAT CTGACGCCGA CCAACTGCTG AGAGCCATGC CGTTTCCGGC TTTGTGACA	240
ACGCATGCTG CAGTTCCCAG CGATGCGAAC TGGTCTGGCA TGCATTACG AACCAACAGC	300
AGTGGTGCTA CGTCCGGATG CAATTCGCAT GAGCTCCAAC CGCGGTTGTA AGTTCAGCAG	360
CCCGGGCCTC TGCCCCCGGC ACAGTCGCAT AAGTATTCGA TACCGTGCGA CACCATTACC	420
TTCAGGATAC GCCACGGACC CGTCACCCTA CGAAAACGCC GGAGCACCGG CAATCAGCAA	480
AGGCAGCAGT GATAAAAGAC TGATATATTT CCTGTCATTA TTTTTCATAT TAATTTAACT	540
CCTGATTAAC CGGTTTTTAT TGATATGAGA AAGTAATAGT TGCAATAGCC TTCACACTTC	600
CAGGTGTAGT TGCATCAGCA ATTTTTATAT AATTGGCTCT TAAATTGATA TGTGGATTTA	660
CCTCTCCCCCT GTAATCGGAG AAGTGCCATT GACTGCCATT TCCTTTCACA GGGGAGTCTT	720

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CACCATAGCT GATGGCAGTT ACATCACTGT CTTTATATAG CCTGATGCCA AATCCTTTTG	780
CAGTGGATTG ACTGCTTAAG GTCATATAT CTGTTCTGTT CACTGGCTGT GATGCATCTG	840
TCAATGTAGC ATAAACATCA ATTCCATCCG GGCATTGTAG GTGTATGTCA ATTTTACCTC	900
CCTGTATTTT TTTATACAAA GATGTGAACT GTGATTGATA TACGGTATTT AATGGCACCA	960
CATAGTTTTT TTGCCCCATG GTACATGTCT GACTCTGTAC CTGAATGCGC CCACCATTTA	1020
ACATAACAGG TGCTGTCAGT CCTTTATTAT TTAAACTTGT ACGTTTTGCT TCCAACAAAA	1080
TAGTACCAAG CTGCCTGGTG GGTATTGTTA TATATCCATT GGGTAATCTT CCCGTTGCGA	1140
CAAAAGCAAC AAACAAACGA GCTCCGAAGC TTGCTGTGCG ACCGTTATAA GTATTGGGGT	1200
TTGTATTGGC ACCTACAGGG TCAATATATA TACCTGAGCT ATTTATGGGG ACCAGAGGCG	1260
TTGCGGGCCA ATAGCCCGCC ATGCCAATAA TAATACCCAG TCCGGATACA CCAATATCAT	1320
AGATATCAAA ATCAGATGAA TCACGGCTGT TTCCTTGATG GAAAGTATAC GTAATACTTC	1380
CAATTTTAGG CAGTGCGGGT GTAAACTTTC CACGCATCAG AGCGATGGCA CCGCCATTAA	1440
AAACATACTG GTTACTTGTT CCCGCCAGCT CTCCTATCAC CCGGGGATAG GTATGGGCAT	1500
CAGCAGGACC AATCACAACA CCTGGCAATG TGGATGTATT AACCGCTATC TGCGAAGGCA	1560
CATAATCATC CGGACCCGCT ACCGCCAGCT TAGGGAGTAA AATTAAAAAC AATGGTATGA	1620
AAAAGATTCT TTTCATGTTT TTTCCTGATT AGGGTGCTGT ATACACAGAA CAGGAACGAG	1680
CTGAGATTGC ATATCATCTT TATTGTGTGC AACATGATAT ACAAATGAAC ATCTGTCTTT	1740
ATTATCTGGT CCCCATACAA CGCTGAGATG ACCTTTTTTCA GGGAGTCCCC TGGTAAATAC	1800
CTTCCCGGCC TGAGCGACAT ATCCGGCCAA CTGTCCATGT TCATCCAGAA CTTCAGAAGC	1860
CATTGGAGGG GGATTGCCAG TAGACATACG AATATCAAAT AACAGACTTC TTCCTGTTTT	1920
AGTGTCAAAT TTYACTAACG TGGCGCTATT AGCACGAGGA ATGATTTCTT GCTCCGTGCG	1980
CGATAATTCA ACATTCAAAT CTAAATTGGA GGGATCGATG CTAATTTGAT TTTTCTCATA	2040
GGGTGTAACA TAAGGAACAA TACCATTTC CCAAAAATCC AGACGACTAC CAGAGGCATT	2100
ATTGATGGCA GCCCCCTGAG CTCCTTCAGC ATGGATAATG GCAAAAGTAT CACTCAGGTC	2160
ATTACTCAAT GTCATCCAT AGGGGTGTGC GACCACCGCT CCCGACGCAC CAAATGACCT	2220
TTGATTATTA TTCTGAGTAT CATGCCCCGAC TGTTGTGGTT ATATTTACAT AAGGTGAACG	2280
ATAACCCCCA TTCATTGCAT AACCGGAAGG CCCGTTTTCC TGGCTGTTTC CTGAAAGACC	2340
ATAAGAGAAC TGATTATCCT CCCC GCCAGT ACCACTAATT GATGTCTGAA TACTATTTTT	2400
CTCTTCTTTG CTATAATTTA AAACAGTGGA AAACACCGGG CTTTGAACAC TTNCCTCCCA	2460
GAGGGAGAGT AAAATTAATA TAAAATCTGT CATCACGGCG TTGTTGCTCA TTATCTCTTG	2520
ACTGAGACAA TCCAATTTGA TAGCCGAGTT GTTTCAGAA GTTGCTGTAC CCCATCTGGT	2580
ATTCATTACG ACTTCCTTTA TGTCCCCAGT AATTATAGGT TGTTCCTGTT AAATACATCC	2640

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CACCCCATTT TTCACCTAAT TCCTGGTTGA TTGAAATCTG GAATTGATTC CTGGGACGAT	2700
AAAACGCTGT ACTTTTTTACA GAAACATCAT CAATAAACGC GTTGTGATTA GCTGATAGCG	2760
CATCCTTCAG ATGATAAAAA TCTTTTGATG AATAACGATA AGCGGCCAGA GTTATATTTG	2820
TGTTTTGAGG GCTGGGAATA TTGGATGGCT AATAACTTGG AGTNGCAGSA CTAATAAACC	2880
TTTACGGCG GTTACACCGG GAATACCNGG AAATGC	2916

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACCGCATCGC CAATCTCAGC GGCAGTGGTT TACATGTCTT CCGTGATGGA AGGTCATGGC	60
ATCAGCTACC TCCATCTGCT CTCCGTGGTC ATCCCGTCCA CCCTGCTGGC GGTTCCTGGT	120
ATGTCCTTCC TGGTCACTAT GCTGTTCAAC TCCAACTCT CTGACGATCC GATTTATCGC	180
AAGCGTCTGG AAGAGGGCCT GGTGAACTG CGCGGTGAAA AGCAGATTGA AATCAAATCC	240
GGTGCAAAAA CGTCCGTCTG GCTGTTCCCTG CTGGGCGTAG TTGGCGTGGT TATCTATGCA	300
ATCATCAACA GCCCAAGCAT GGGTCTGGTT GAAAAACCAC TGATGAACAC CACCAACGCA	360
ATCCTGRTCA TCATGCTCAG CGTTGCAACT CTGACCACCG TTATCTGTRA ARTCGATACC	420
GACAACATTC TCAAYTCCAG CACCTTCAA GCAGGTATGA GCGCCTGTAT TTGTATCCTG	480
GGTGTTGCGT GGCTGGGCGA TACTTTCGTT TCCAACAACA TCGACTGGAT CAAAGATACC	540
GCTGGTGAAG TGATTCAGGG TCATCCGTGG CTGCTGGCCG TCATCTTCTT CTTTGCTTCT	600
GCTCTGCTGT ACTCTCAGGC TGCAACCGCA AAAGCAYTGA TGCCGATGGC TCTGGCACTG	660
AACGTTTCTC CGCTGACCGC TGTTGCTTCT TTTGCTGCGG TGTCTGGTCT GTTCATTCTG	720
CCGACCTACC CGACTGCGT TGCTGCGGTA CAGATGGATG ACACGGGTAC TACCCGTATC	780
GGTAAATTCC TCTTCAACCA TCCGTTCTTC ATCCCGGGTA CTCTGGGTGT TGCCCTGGCC	840
GTTTGCTTCG GCTTCGTGCT GGGTAGCTTC ATGCTGTAAT GACCCATYGC GGGGCGTTCA	900
CGCCCCGCTT TCTTTCCCGC CGACTAACAT CCTTTCCCCG TCCGTTGTAT AGTGACCTCT	960
CTCTTGCGGT TCCATCTGTT CTTGCGAGGT GTTTATGCTT GATGAAAAAA GTTCGAATAC	1020
CACGTCTGTC GTGGTGCTAT GTACGGCACC GGATGAAGCG ACAGCCCAGG ATTTAGCCGC	1080
CAAAGTGCTG GCGGAAAAAC TGGCGGCCTG CGCGACCTTG ATCCCCGGCG CTACCTCTCT	1140
CTATTACTGG GAAGGTAAGC TGGAGCAAGA ATACGAATGC AGATGATTTT AAAAATACC	1200
GTATCTCACC AGCAGGCACT GMTGAATGCC TGAAGTCTCA TCATCCATAT CAAACCCCGG	1260

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AACTTCTGGT TTTACCTGTT ACACACGGAG ACACAGATTA CCTCTCATGG CTCAACGCAT 1320
 CTTTACGCTG ATCCTGCTAC TTTGCAGCAC TTCCGTTTTT GCCGGATTAT TCGACGCGCC 1380
 GGGACGTTCA CAATTTGTCC CCGCGGATCA AGCCTTTGCT TTTGATTTTC AGCAAAACCA 1440
 ACATGACCTG AATCTGACCT GGCAGATCAA AGACGGTTAC TACCTCTACC GTAAACAGAT 1500
 CCGCATTACG CCGGAACACG CGAAAATTGC CGACGTGCAG CTGCCGCAAG GCGTCTGGCA 1560
 TGAAGATGAG TTTTACGGCA AAAGCGAGAT TTACCGCGAT CGGCTGACGC TTCCCGTAAC 1620
 CATCAACCAG GCGAGTGCGG GAGCAACGTT AACTGTCACC TACCAGGGCT GTGCTGATGC 1680
 CGGTTTCTGT TATCCGCCAG AAACCAAAC CGTTCCGTTA AGCGAAGTGG TCGCCAACAA 1740
 CGAAGCGTCA CAGCCTGTGT CTGTTCCGCA GCAAGAGCAG CCCACCGCGC AATTGCCCTT 1800
 TTCCGCGCTC TGGGCGTTGT TGATCGGTAT TGGTATCGCC TTTACGCCAT GCGTGCTGCC 1860
 AATGTACCCA CTGATTTCTG GCATCGTGCT GGGCGGTAAA CAGCGGCTTT CCACTGCCAG 1920
 AGCATTGTTG CTGACCTTTA TTTATGTGCA GGGGATGGCG CTGACTTACA CGGCGCTGGG 1980
 TCTGGTGGTT GCCGCCGAG GKTACAGTT CCAGGCGGCG CTACAGMACC CATACGTGCT 2040
 CATTGGCCTC GCCATCGTCT TTACYTTGCT GGCGATGTCA ATGTTTGGCT TKTTTACTCT 2100
 GCAACTCCCC TCTTCGCTGC AAACACGTCT CACGCTGATG AGCAATCGCC AACAGGGCGG 2160
 CTCACCTGGC GGTGTGTTTA TTATGGGGGC GATTGCCGGA CTGATCTGTT CACCYTGCAC 2220
 CACCGCACCG CTTAGCGCGA TTCTGCTGTA TATCGCCCAA AGCGGGAACA TGTGGCTGGG 2280
 CAGCGGCACG CTTTATCTTT ATGCGCTGGG CATGGGCCTG CCGCTGATGC TAATTACCGT 2340
 CTTTGGTAAC CGCTTGCTGC CGAAAAGCGG CCCGTGGATG GAACAAGTCA AAACCGCGTT 2400
 TGGTTTTGTG ATCCTCGCAC TGCCGGTCTT CCTGCTGGAG CGAGTGATTG GTGATATATG 2460
 GGGATTACGC TTGTGGTCCG CGCTTGGTGT CGCATTCTTT GGCTGGGCCT TTATCACCAG 2520
 CNTACAGGCC AAACCGGGCT GGATGCGCGT GGTGCAAATA ATCCTGCTGG CAGCGGCATT 2580
 GGTTAGCGTG CGCCACTTC AGGATTGGGC ATTTGGTGCA ACACATACCG CGCAAACCTCA 2640
 GACGCATCTC AACTTTACAC AAATCAAAAC AGTAGAT 2677

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATCCTGATGA CGCCGTAAAT GTGCATTTGC CAGGATTGCC GCATAGAGGG CACGAAGAAA 60 -
 AGGTCCGTTG TCAGSATGTA TCCAGATGAT TCTGCCACTG AAACCTTCAG GGATAAGACG 120

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ATTGCCAACT GCCAGTCCTT TAAGGSCAGC ATTCAGCGCC TTACGCGGGG CATTCTGCTC	180
CAGAAATACG TATGCCAAGT GAGCGTGAC ATCAATAAAG TCATTCTCCT GTCGGGCAAG	240
GCGCCTGAGT TTGTTGATGT AACTTGTTTC GCTGATTTC TCGGCATCGT ATGCATCAAT	300
CAGTTCTTCA AACTCATCCA GCAACGAGCC AAACCAGGTT TCGGAAATA TGAAACAGCC	360
CTGGTTATCG TTCACTTCAA AGCGTAATTT GCCAGTCATA TTCTGAACCT GTAAAAAAGG	420
ATAGACCATA ATCTGCAGGC TATAAAAATT GTGGATGCCT GGCATCGGGT GTCCTTTTAT	480
TGTCCGGGAT TAACGTTGCC CATGATAATA CAGTGAATCC NGTTCTGTGG TAAGACG	537

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CGCTCGAGCA CCAGATTCAC TGACATGCGC AAATCATGT GTAAATCCTG TCTGGGCATC	60
TATCTCAAGT AACAGTTCCG TTAAATCTAC CGGTGGGAGT AGCTGTTTGA TCCGATTATT	120
TAGACGAAGC AATGATGGTG GCTCTTCCTG TTTCTCCAGA CAACTGATAG TCAGGGATGG	180
ATATTTACCT TCATTACAGA TATGAACTTC CGCATTCTTT TCAAATCGTG ATGCCAGGCT	240
TTCCAGGTCT CATCCAGCTG AATAGCCAGT TGTTGCACAC CTTTACGTCC ATCGACAGGA	300
TGTCCAGTG CCCGACAGAC AGGAATACGC TGAGTCTGCC ACTCTTCACC TTGCAACAAC	360
TTCTCGCGAG GATCTCCCCA GCGATCACTG TTTTCAAGCC CAGATGTCCC CGGCGGCGCA	420
RTGCATCCTG AAGGCGTTCC AGCAAACATA GTGAATAACC TGCACGCTGT ATCCCGTCCC	480
TCCGCATCGT ATACGAGGCG TTTCCAGGGA CCGGTGATAA TATGTTCAGC GCATCATCAA	540
GGATGCGCTT TTTCGAACCA TTCAGTTCTG CCAGATAATG AATCGCAGCC AGTACATGTC	600
ACCTGCCGGT GCCGCACGGA AATGCAGGTC CCGCAACACC GCCGGAAGAA AACGTTTAAC	660
CCGACCGTAC TGCTCAACCA TTTCGTCATG GAAATTATTG TTCTGTGGAC GAGCAAGTTC	720
ATTAACCTTG CTTACAGATT CTGCCAGTCT GTTTTTGGGT ACGCACTTGA AGATAACCTG	780
CCTGAGATCT GGGACATCTG TATTATCATC CAGCAACAAT GCACATGCCC GCGCCAGTAA	840
CAATGCGGCC TGATCAAGAT CTTTCAGTGT CCTGAGTCTT TTTTTTTGCC CGGTTTTCTT	900
TGCTTCGCGG ATAATGTCCA GAATTAGCAT ATCAAGCACA TCAACGGCAT CGTCTAATGC	960
CGTTATTTCC TGTGCTTTAA CGAATGCAGT AAGTACAGCA AGCTTTCTCT GCTGTGGCAT	1020
TCGAGCGATA TATTTTACCG ACGCCATGCC AGCATGAACG AGCCAGATTA CGCNTTGGNA	1080 -
ATGCTCAGGC AGACCGGGAA AAGTTCCAGT CGGGNAAAAC TCCAAGAA	1128

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(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGNTGATAAA AATCYTTTGA TGAATAACGA TAAGCCGCCC AGAGTTATAT TTGTGTTTGA	60
GGCTGGAATA TTGATGCTAT AACTTGAGTG CAGACTATAA CCTTTACGCG TTACACCGGA	120
ATACCTGAAT GCTGTTCTGG ACAATGTAAT GTCAGATGCT ATAGCACCCA GATGGGTATT	180
AAAGGCCAGG CCAGCTAACC CCGCTGTATA TCCTGAAGCT GTGGTAAGAC CACTGTTTAA	240
AGTAATATCA TTCGTCAGGC CGTATTGATA GGTGCCTTGT GCTATTAAAT CATTATATGT	300
TTTATTTCGCA TAACGATACT TTCCCACTGA CATTTGCCAG CGACTAAATC CGGGACGAAT	360
GAGTTGAGCA ACGGCCGCAA AAGGAACCGT GAACATTCGT GTCTGGCCAT TAGACTCTGT	420
TATCTTAACG AGAAGGTCAC CAGCATATCC ACTGGGATAT AAATCATTGA TGACAAATGG	480
TCCGGCTGGC ACCGTCGTTT CATAGAGGAT ATGAGCATTT TGATAAATGG TTACTTTAGC	540
ATTACTGTTA GCTATTCCCC GGACAGCAGG RGCATAGCCA CGTAAAGAAC CGGGTAACAT	600
TCGTTCATCC GATGCTAACC TGAATTTGTC TCTCAATGGG GCAAGGTCAT GCATTATACT	660
CGTATAAAAA TCCCCTAATG TGAATTGTGC TCTCAATGGG GCAAGGTCAT GCATTATACT	720
TGTTTCTATA TTCTGATATC CGGCAGGATA GCTATTATTC CAGCTCTCAC TGCCACGGTG	780
GCGCAAAGCC ATCCCCACAA ATTGAATCCA GCTTTTAATC CCAGATAAGT CTGTTTCGTTA	840
CTCGTCCCGG AAGAGCTATA CTGGTAATAG TTAGCATCAT AGTTTATAAA TGCTGCAGGA	900
ACACCACTTT GCCACTGAGA AGGGGAAATA TATCCTCTTG GACGTGTATT CAGCAGTGCT	960
GCGGGATTTC GATATTCAAC CTAAAGTCG ATAAGTCAAA ATTAATTCTG GCTGAAGAAA	1020
GCCCTGTTGA CGCCGGAAAG CAGGAGGTGT TTCCCGACAT AGTATCTTTG ACTAAATCAA	1080
TCAATGAAAG CAGCTCAGGC GTCAGGCATA ACGTCGGAGC ACCGGTATTG GCAGTACGTA	1140
AATACTGCAA ATCAGCCTTC CCCTCCATA CATTATTAAC ATAAATATCA GAATAATACC	1200
TGCCCTCAGG CACAGGGTTA CCATGACTAA AGCGGCGGAT ATCAATAGCA TTTATCCCTT	1260
TATCCAAATG CAAAACTCA GAATCAAAC CAGCCTCTTC AGCAGCAAAT GAATGGTTTG	1320
TTACTGTTAA CCCTAATGCA GCAAAAAGCA GAAGAGAACA ACGACAGTAA ATCAGGCATG	1380
ACAGATTATT AGCGTTCATT ATTACCTTAC TCCAGAACAG ATTCTCCTTG CTGATATCCT	1440
CCGTAATCAT TAACAATAAC CCAGGAAACT TTGCTGGTGG CGCAGTTCTG CCTTTAAGTG	1500
CAAATACTGT TGAAGAGAAA GGGGGAATCA TTCCACCATG TTCAACAGGC GTTAAGTGCT	1560

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TATTCTGCTC	AACTGCAATT	TTGTTGTAGG	TTATGTAATA	AGGTGTTGGA	TTAACTGCTT	1620
TAATTCGGCC	TTCCTCCTGG	TGCCAGGTAA	CTTTCAGATA	AGCATCATTT	GGTGTAACT	1680
TCAGGTGAGC	AGGACGAAA	AAAAATTTTA	TGCGACTACG	AACAGCTAGT	TGCAAATAAT	1740
TATTATTCCG	CTGCTCTGAG	TTATCGGAGT	CTTTTTTTGC	CCTGGGCTTT	GCTGGAATAT	1800
CCAGAACATT	TAGATAGAAA	AGAGATTCTC	GGTCTTTCGG	TAGTGACTCG	CCTGTATATA	1860
CAATTCTGAC	TGTTTGTCTT	GATTTAGAGT	CCATACGAAA	TATTGGCGGA	GTAATGATAA	1920
AAGGACGTGG	ACTGACTCAG	GGGGAGCTGC	TGCATCTCCA	TCGYCAACCA	GGACTGGACT	1980
AATGCCGAGA	TTTCATTGTC	ATTATTTNAA	CGTATGCTAA	TACTCTTTTG	AGTCGCCGGA	2040
TAAACAACAC	GGGTTCCCAT	GATAACTACA	CTACCCTGAA	CAACTGCAGA	TACAGATAGA	2100
GTAAAAA	ACAGCACAAA	CCTTAGCATG	GTATCTCCAG	AAGAAAGCAG	GGCAGTATTT	2160
CCTGCCCCAA	AATACAAAAC	CGTTTGTTAT	TCGTAGGCGA	TGGTATAATT	GA CTGTTGTT	2220
TTTACATTGC	CTGGAGTTGA	TGTCCCGGTC	GCATAATATT	GAGCCATATA	ACGTAATGTG	2280
GCATTACCAT	CCCCACCAAT	AGTTTCAGAA	T			2311

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TATTACCTGT	GATTTTTCCG	GGCGTAAATG	GAGTCCCTAA	AGTTATCGCA	GTCCCAATAT	60
TTCCTGCATT	ACTGTTATAA	AGATAAACGA	GTAACCCATC	AGAAGATGTG	TTTGATGTAT	120
TCTGAATAA	AATAGCATTG	TNATAAGTGT	TTGTTGCCGT	TATCGTAACC	TTTATTGTTT	180
CCAGATTATA	GGGACACCGC	ATATTCACAG	TAAACTCTTT	TTCGTGANTT	CCATTTTGAC	240
TCAGGGTCTG	AATCTCTACA	NCCTGCCAGT	CAACAGTTGT	GTTGCTTACA	GTACAGGCAG	300
GAATAATCAG	TTTTCTCTG	AAGGTCAGAT	TATCAACTGC	ATGTACATGC	TGAGACATTA	360
ACACTGCCCC	CAGCATTACC	GGAAGACACA	AACCTCTTAT	CTTTTTCATC	TGAAATATCC	420
TGTACAAAAA	TTTTGCTAAC	GATATGTCAA	TTCAAACGTG	GCTGTTGCTT	CATAATCACC	480
GGGTACCACA	CTCTTCGTCC	GCAGGGCTTC	CGGCGTTGCC	ACAACATACG	CGCCGAAAGG	540
AAGCTCAAGA	CTGTTTCCGG	TAACCTTTTC	CCCCTGGCCT	TTGTTATGGG	AGGTGCCGGG	600
TTTCAGCAGA	CTGCTGCCAT	CGGTGTCCAG	CAGTGCAATG	CCTAACCGGC	CAGCATTCAC	660
TCCGGTTACC	TTAGATGSC	CCGGGAGRCG	CYNTCTTCCG	TCCCCTTAAA	GGTCAGGGTC	720
ACAATTTTGC	CAACTGCTGT	TGCATGGCAG	TTTTCCAGCC	TGATGACAAA	CGACTCTGTC	780

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GGCGAACGTC CGGGCGGATA CCAGAAATCC CTGGACGCCC GGGTTTTGAA GACGACATGT 840
TTATTCAGAC TGTCACCGGA CACATGGCAG GGTCTGTCAA GCAGATTACC CCTGAATGCC 900
ACATCTGAGG CTATTGCCTG TCCGCGCAGAC AGTGCGGCAA ACAGTAAAAG AGCGCCTGTG 960
CTTTTTATCA TCACATTCCC TTAATCATAT TTTATGCTCA GACGCAGCAT GGCCGGATTG 1020
CTCCTGGCAT CAGAATACTC AACCTCTGT GCGGCGCTTT TCCTCCAGGC GGGCAAGCAT 1080
CTCCTCCTGG CGGCGGGTAA GCGGGGACA GTAAAAAA 1118

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTCGTGGGTG AAATCGTAGG CCGCGCTTTT TTGCTGATCG GCCAGTTGAT GAATAGGGTG 60
GCCAKGATCG GGATAAAACG TACAGGCAGC GATAAACAGA CAGCCCGGAT AGCGGTTGTT 120
TTTAACGCAC TCCGATAACG CCTGATAACG TGCCAGCAAC TTTTGTTCCG CGGTTTGCCT 180
TTCGTCCAGC ATCAGCTGAC GACGCCAGAC ATCTATCTGT TGGCTAAGAT AACGCAGCGC 240
ATCGTAGAGG ATTGCCTCTT TGTCTGGCCA GAAGCGGCGT ACTCGTCCAG TGGATAATCC 300
ACACGTTTAC CAACCATCTC CAGCGTGGTG TTGGCAATCC CTTGTAATTC TAATAATTTT 360
AGGGCTTCTC CCAGTACATC TTCACGTTGC ACGCTATTTT CCTCCGKCTT TCCCACTGCA 420
ATGTTTCGKTC ACGGTTGGCG ATCGCGCAA TGTGCGCTGG AAGGTTTCAG CATCCATAAA 480
GCCCCGTGACG CGTGCTTGTG GATGCTCCTG GCCTTGGTCC GGTCAAAAAA GAGAATTTGT 540
CCGGTAGGGC CAAGGATATT AA 562

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCATCGCTTT ACCCCAGAAA AGTTAAGCCA TATAATGTGA GGGATATAAG TCGTCGTATC 60
CGGTAAGTAC AGATAACCAC AACATAAGCT CATTAGTAA ATTTTATCTC TGAACAAACG 120
ACTATGGCAT GCTCATTTAT ACTATTCATA AGAAAGTGTG ATTATCTGTA AGCATTAACC 180 -
ATCAAATCAT ATAACCATAC TAAACTGGCG GATCATCAGC ACCATTAGCA GGTAACCTAT 240

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TGAAATTTTA TTATGTGTTT TTTGTTGATA ATTAATATGC AATATGAATT TGCTATTTTA	300
GAATCATGAA CACCATTTAA AATTACCATC ATTAACATCA TATAAAAATA TATTTTTACT	360
AAAACATGAA TTGTATATAT TTATTAGCTC AGGAAAATTA TCAGGGTTCA CCTTCAAATT	420
AACCTGAATG TTATGCTTAA TTTCACCCAG TAGTTCTTCA TGTGTAGATT TTATTATCCC	480
ATTATTATAA TCGATAAATG CACACATGTT TTTTATGAAT TCAAAACCTT TTCCTGTATA	540
CAGTTTAATG AATGCCACCA GAGCAAACAT TTCAAGATGT AGCCATAATG CTACGTTAGT	600
TTTTTGCAA GTATAAAAA TTGAATTCGC CACTTTTTTA CTTATTGCTC TTTTATACTG	660
TGATCGAGCA AGATTCAGTA GCGGAAGTCC TCGTTCAATA AATGAATGTG AAAAGACTGG	720
ATAAATTGAT GTCGGAAACC TTTCA	745

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGTTNATGC ATTTTCASAT TTTCCACTTC GTTCTGACGT TGCCTGCTT TGGCGTCATC	60
ATTACGTAAC GTATCGAGGA AATCGAGGTA GCCCTGATCA ACATCTTTGG TGACGTAGAC	120
GCCGTTGAAC ACCGAGCATT CAAACTGCTG GATATCCGGA TTTTCAGCGC GAACGGCGTC	180
GATCAGATCG TTCAGATCCT GGAAAAATCAA CCCGTCAGCA CCGATGATCT GGCGAATTTC	240
ATCAACTTCG CGACCGTGAG CGATCAGTTC CGTGCGCTC GGCATATCAA TACCATAAAA	300
CGTTCGGGAA AGCGAATTTT CGGTGCCGCA GAAGCGAGGT AACTTTCTT CGCTCCGGCT	360
TCGCGTGCCA TCTCGATAAT CTGTCAGAAG TGGTGCCACG	400

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGTCGACGAT GAGGCAGCCA GAGCATTAGA GCCGAAAGA AGGGATGATG CCATGACTGC	60
TGTTGCTATA AAATGTTTCA TATATTCTCC ATCAGTTCTT CTGGGGATCT GTGGGCAGCA	120
TATAGCGCTC ATACTAGGGG TTTGAGGGCC AATGGAACGA AAACGTACGT TAAGGAGATA	180
ATTGTTGTT TATATTTAAA TTTAGAGCTC TCAGTTCGCC TTTTAAAATA TCCTCTGGCA	240

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ACGTGAATGT ATAATGGCCC AACATATTGA TATGCCCGTG CATCAGGGGA GATAGCCGAG 300
 CGATATCTTC ATCTATAATT TCTTGGCCAT TACGGCGCAT CCAGCTCAAC GCTTCCTCCA 360
 TATAGAGCGT GTTCCACAGA ACCACTGCAT TAGTAACCAG GCCCAGCGCC CCCAGTTGAT 420
 CTTCTGCCCC TTCACGATAA CGCTTTCTGA TCTCTCCGG TTGTCCGTAA CAAATCGCAC 480
 GAGCCACAGC GTGCGKTCCT TCTCTCGAT TAAGCTGCGT CAGGATCCGC CGACGATAAT 540
 CTTTCATCATC AATATAATTG AGGAGATATA GCGTTTTGTT TACACGCCCT ACTTCCATAA 600
 TTGCCTGTGC CAGTCTGAT GGGCGCGAGC TTTTCAGTAA AGAGCGAATG AGTTCTGACG 660
 CATGAATTGT ACCCAACTTC AGGAACCAGC GGTTGCGATC ATCTCATCCC ACTGACTCTC 720
 CGCTTTTGAC AGATCTGCAT ATCCTCGGGC CAACTTATCC AGTACTCCGT AGTTTGCCGA 780
 TTTATTACC CGCCAGAACA CCGCCTCACC TGCATCGGCA AGCC 824

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 911 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ACAAATCAGA CCAGTTAACC AGTCAGTCGG TTTTATGATT TCACTCACTA TACTTTGTTT 60
 CATAAGGATT TCAGGATCTG CCAGACTGCG CAGAAATGAT GCTTACGAAT ACACAGTAAA 120
 GGCAATGTCA TTTCCGATAC AGAGCCTGAC ATTGCCATAA TGAGCTATTT ATCTGAAAAA 180
 CGACAGAATA TGATGTTTTA TCGTAACGTA ATTTTAAGTT CTCAACTTAT TGAGACATAT 240
 TGTCTTTTTT ACCCATGTGG TCATTTTTC TCCCATCCGT TTTGCTCATG TGTTCTTTCT 300
 CCATTTTCTC TTTATCCATT GCATTTTTC ACATACCATC CTTGCACATT TTATCATGCG 360
 CGCTGGACAT GCTGCCTTTT ACTTCATGTG TTTTATCCAT TGTGTCTGCT GCCTGAGCAT 420
 TGAACATGAA CAGCGCGGAT AGTACAGTTG CAGAAATAAT ATTTTTCATG GTTCTTCCTC 480
 ATTTTAAACA ATTGTATCAA CAACCACCAA ACCAGTTATA ACCCTGGTCT TCCCAGTACC 540
 CCCCCGGAAT ATGATTAGTG ACCTCTATAA CCTGAACATG CTTGGGGTTT TTATATCCCA 600
 GCTTAGTAGG GATACGTATC TTTATGGGAT AGCCATATTC TTTTGGAAT ACCCTGTTAT 660
 TCCATGTCAA TGTCAGCAAT GTTTGTGAAT GTAGTGCTGT CGCCATATCA ATACTGGTGT 720
 AGTAACCATC GACGCAACGA AAAGTACGT ATTTTGCCCG CATATCGGCA CCAATCAGCG 780
 TCAGGAAATG CCGGAATGGT ATCCCTCCCG ATTTTCCTAT TGAATCCAT CCTTCAACAC 840
 NGATATGACG GGTATCTGA CTCACATGCT GCATGTTATA CAATTCAGAC CAAAAACCAG 900 -
 TTACGGGTTA T 911

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(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

NGGGGCAGGA TAATTGTATC CTGCCCNGTA TATAATTCTC AGCACAGGTG TTGACTAAAG	60
AGCGTGAAAC TTTGCTATTA TGTCTTCGTA AGATTCACGG ACGGTTATAC TTGAGCCTGA	120
TTCTGTGAAG TAAACAACAG CAGAAGCATC GTTGCCTTTT TCAATGTATG AAACATTCCA	180
GTCATGGATA GCCACTGCGG GCTGACCATT ATCCCGACGG TCGTCTTAA TGAATCGCGG	240
AAGTAATTCT GCAATATCGT TAAAAACACC ATTTACGGTA TGAGTGATAC CACCAACGCA	300
ATGTAGATGA GTTGACTCCG GGGTATCATT GTCTGCTTCT GCAAAGAGTA TAGCTGTCTT	360
GCTAATTGTA ACAGGCGCCT GTGARCGGGA TAATTCGAGA GAAATAAACC CGGATTCTGC	420
CATAAAACT CCAGTTTGTG ATGTTATATC ATTTCATATG TTT	463

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTCTAACCTC TGACCAAAAA CAGAATTACG GTTGTTATGC TGCAGAACCT AATGACGTGC	60
AACTGGCGCG CTATTTTCAT CTTGATGAAC GGGATCTGGC CTTCATTAAC CAACGACGGG	120
GCAAACATAA TAGGCTGGGC ATTGCGCTTC AGCTCACCAC AGCCCGTTTT CTGGGAACAT	180
TTCTGACGGA TTTAACTCAG GTTCTGCCTG GTGTTCAACA TTTTGTCGCG GTACAGCTTA	240
ATATCCACCG TCCAGAAGTT CTCTCCCGCT ATGCTGAACG GGACACTACC CTTAGAGAAC	300
ATACTGCATT AATTAAGGAA TATTACGGCT ATCATGAATT TGGTGATTTT CCATGGTCTT	360
TCCGCCTGAA GCGTCTGCTA TATACCCGGG CGTGGCTCAG TAATGACGAC CGGGTCTGAT	420
GTTTGATTTT GCCACTGCAT GGTGCTTCA AAATAAGGTA TTACTGCCCC GAGCAACCAC	480
ACTAGTACGT CTCATCAGTG AAATTCGTGA AAGGGCAAAT CAGCGGCTGT GGAAAAAGCT	540
GGCCGCACTG CCGAACAAAT GGCAG	565

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGATGGCGTC CGGGGTGAAC GCCGGATAAG TTTAATTTAT CCGGTCAGGC AAAAGGCATT	60
AATCTGCAGA TAGCTGATGT CAGGGGAAAT ATTGCCCGGG CAGGAAAAGT AATGCCTGCA	120
ATACCATTGA CGGGTAATGA AGAAGCGCTG GATTACACCC TCAGAATTGT GAGAAACGGA	180
AAAAAACTTG AAGCCGGAAA TTATTTTGCT GTGCTGGGAT TCCGGGTCGA TTATGAGTGA	240
GTCACCTCCGG TGAGATGTCC GGTATTATTTAT CTTTTTTGTG AATCTGGTGA TGCCTGGAAT	300
GAAAGACAGA ATACCTTTTG CAGTCAACAA TATTACCTGT GTGATATTGT TGTCTCTGTT	360
TTGTAACGCA GCCAGTGCCG TTGAGTTTAA TACAGATGTA CTTGACGCAG CGGACAAGAA	420
AAATATTGAC TTCACCCGTT TTTCAGAAGC CGGCTATGTT CTGCCGGGGG CAATATCTTC	480
TGGGATGTGG AATTGTTAAC GGGGCCAAAG TA	512

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGCCGGTGC GGTTANTAGT GGCAGTGGTG TCTTTTGGTG TAAATGCTGC TCCAACTATT	60
CCACAGGGGC AGGGTAAAGT AACTTTTAAC GGAAGTGTG TTGATGCTCC ATGCAGCATT	120
TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC TTTCAAAAAG CTTCTTGAG	180
GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT TGGTTAATTG TGATATTACT	240
GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA AGCTGGCTTT TACTGGCCCG	300
ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG GTACGGGCAC AGCTATCGTA	360
NTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG AAGTGATGCT AATACCCTGA	420
AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTAA GAAGTCGTCA GCCGTTGGTG	480
CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT CAACCTGACT TATCAGTAAT	540
ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATCCGCTG TTTATTTCTC AGGSTATTTA	600
TCATGAGACT GCGATTCTCT GTTCCACTTT TCTTTTTTGG CTGTGTGTTT GTTCATGGTG	660
TTTTTGCCGG TCCGTTTCCT CCGCCCGGCA TGTCCCTTCC TGAATACTGG GGAGAAGAGC	720

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ACGTATGGTG GGACGGCAGG GCTGCTTTTC ATGGTGAGGT TGTGAGACCT GCCTGTACTC 780
 TGGCGATGGA AGACGCCTGG CAGATTATTG ATATGGGGGA ATACCCC 827

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CCAGGGGCCC AAAATCCGTG TATCCACCTT TAAAGAAGGC AAAGTTTTC TCAATATTGG 60
 GGATAAATTC CTGCTCGACG CCAACCTGGG TAAAGGTGAA GGCGACAAAG AAAAAGTCGG 120
 TATCGACTAC AAAGGCCTGC CTGCTGACGT CGTGCCTGGT GACATCCTGC TGCTGGACGA 180
 TGGTCGCGTC CAGTTAAAAG TACTGGAAGT TCAGGGCATG AAAGTGTTCA CCGAAGTNAC 240
 CGTCGGTGGT CCCCTCTCCA ACAATAAAGG TATCAACAAA CTTGGCGGCG GTTTGTCGGC 300
 TGAAGCGCTG ACCGAAAAAG ACAAAGCAGA CATTAAAGACT GCGGCGTTGA TTGGCGTAGA 360
 TTANCTGGCT GTCTCCTTCC CACNCTGTGG CGAAGATNTG 400

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CCGATTTTTTT GCGAAACGTT CCGCCTGGCA TCAGGATAGT TTGTTGTTA TCCAGTTCGG 60
 ATAGCGCATT GACGATATGC AGGCTGTTGG TCATCACCGT GATGTNATTA AAGCGCGAGA 120
 GCAGGGGAAC CATCTGCAA ACGGTACTGC CAGCATCAAG AATGATCGAA TCGCCATCAT 180
 GGATAAACT AACGGCAGCT TCTGCAATCA GCTCTTTCTT GTGGGTGTTG ATGAGTGTTT 240
 TATGATCGAT AGGCGGATCG GATTCCTCTT TATTCAACAC CACTCCGCCA TAAGTACGAA 300
 TGACGGTTCC GGCATGTTCC AGAATGACCA GATCTTTGCG AATGGKTGTG CCTGTGGTGT 360
 CAAATATTGC GCCATTCTTC AACCGAGCAT TTACCCTGCT TTGCAGATAC TCCAGAATGG 420
 CGGCCTGACG CTGACGAGTT TCATGGGCGT GATACCTGAT TTAGGTTCAA ATGATAACTC 480
 GCAAGCAGTA ACATCACACG NAATATCCAC GTTCAGTTAA GCGCCATGAT AGAGCATCCG 540
 TGATAGGGNC AGGGGNAGTC ACACGGCGTA ATCACCGC 578 -

(2) INFORMATION FOR SEQ ID NO: 39:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TGTTAGGTCA GGGCCACAG TCAAGCTTAG GTTTTACTGA ATATACCTCA AATGTTAACA	60
GTGCASATGC AGCAAGCAGA CGACACTTTC TGGTAGTTAT AAAAGTGCRC GTAAAATATA	120
TCACCAATAA TAATGTTTCA TATGTTAATC ATGGGGCAAT TCCTGATGAA GCCCCGGTTG	180
AAGTACTGGC TGTGTTGAC AGGAGATTTA ATTTTCCTGA GCCATCAACG CCTCCTGATA	240
TATCAACCAT ACGTAAATTG TTATCTCTAC GATATTTTAA AGAAAGTATC GAAAGCACCT	300
CCAAATCTAA CTTTCAGAAA TTAAGTCGCG GTAAATATTG GATGTGCTTA AAGGACGGGG	360
AAGATTTTCAT CGACACGTCN GCGTGCAATC TATCCGTAT	399

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CAGCCTCCGT TACCGGACAG CAAGGAGGCT GAATGGAGTT TACAGGATTT GCTTTTTTTAT	60
AATGTCTGGC CATGCAGTMA AACCGGACAG GTTTTATTAT CATGTGAGGT ATTCTGACAT	120
AAAATGCTGG ATTTTATTT TGTGACGAAT GCTGCAAAT TGCATCTGCA CTCTGATGTA	180
GCTTTTATCT GTTTCAGTGA AGCATGCCCA CAACTGAGT TATTAAGTTG TGGAAGAACA	240
GTTTTGTCCC GCCTGCATAT CTCCTTTCAA AAACAGTAT GTCGCCATGC CTCGCCTTAA	300
TGGAGAGCGC TGAACCATAC CTTCTTT	327

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGAGATGGGC ATGGAACTCA CTTCATAATA ATGCCTACCG AAGAAATATT AATAGATGAC	60 -
ATTTCCACGA GNGATAGCAA TAAAACATCA GAGCAGTCTT CTCGCTTAGA AAAAGCTTTA	120

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TTAGGTTTTTA CAAACACAAT GTACAGTGAT TCAAACCCCTC CTATTATAGC TCGTTTTAGA	180
GACTATCTSG AAGATGGTGA GTGCATTGAC AGAATTAGCG AATCAATTTT TTTTACACCG	240
CAAGAATTCA ATCTTGCGA TCACCACATT GAAGGATGGT TCAATGAATT TGGTCAATTC	300
AGTGGAAGT TTTT	314

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TCCCAAGATC TTTTGGCCG CAAATCCACA AAACCCGTCG TTANTGTCGC GCAGCCANTT	60
GCAGGCCGAA TTTGCACCGT TTTAGAAAGC GCGGTTTTGT AGAGCAGCAC GCAGTGAGAA	120
GCCACCGCGC CACGACCTAC GNGCNCGCGC AGCTGGTGTA ATTGCGCCAG ACCCAGACGC	180
TCCGGGTTTT CGATAATCAT CAGACTGGCG TTAGGCACAT CAACGCCGAC TTCAATAACG	240
GTTGTGGCAA CCAGCAGGTG TAGCTCACCT TGTTTAAACG ACGCCATCAC CGCCTGTTTC	300
TCGGCAGGTT TCATCCGCCC GTGTACCAGG CCAACGTTCA ACTCTGGTAG CGCCAGTTTC	360
AACTCTTCCC AGGTAGTTCC GCGCCTGCG CTTCCAGCAA TTCCGACTCT TCAATCAACG	420
TACAAACCCA GTATGCCTGA CGACCTTCAG TTATGCAGGC GTGGTGCACC GGGTGCAATG	480
GATGTCGGTA NNGCGGGTAT CAGGAATAGC GACCGTAGTC ACTGGGCGTG CGGCCTGGGC	540
GGCACTCCAT CTATACCGA GGGTATCGAG ATCGGGCATA CGCNTGCATT	590

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTGGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGGATA AATGCTTCAA	180
TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCTTT	240
TTTGCGGCAT TTTGCCTTGC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA	300
TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGGATCTG CAACAGCGGT	360

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AAGATCCTTG AGAGTTTTTC GCCCCGAAGG AACGTTTTTC

400

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATTCGGAAAG ATGCTTCTAN TTTTTTTAAG CACGTATAAA CTGTTAATTC AGGTTCAATG 60
CTACGAAATG CACTAGTTAT AACCTGTATT GAAGGAAAGA TCTTCTGATA CTCTTTCCAG 120
AGATCTTCAA GTCTGGCCAT GGAAATTGAC TTGGCTGCAT ATTCTAGGTC AGTGTTTATG 180
ATAGTTTCTC TATTCTCTCT GAATGCGGAA AAAAAAGCTT CATTCAACAA TGATAGTAAA 240
TCCCTGGGCC GGTAAAGGGT AAATTGCAAA CATCGCTTAA AACCATTCTT CCCTTTAAGA 300
TCATCCGCTG TGCATCTATC CCAAACCTCGT TGATCTTTCT CAATATCTAG CTAAATGCT 360
ACTTTCATTC TTTTAGCTGA CAGCATTAGG AGTTGTGCCC 400

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TAATGTTGAA GACAGAGATA TAATNTACAG CATCATCCCA CAAGGCAGAT ATAACAATAC 60
TTGACTGGGA TATGCAAAGC GATAGTGGGC AATTTGCTAT TGAAATAATA AAATCGATAA 120
TCGTTTCAGA TATAAATTCT GGAGGACGTT TACGTCTTCT TTCTATTTAT ACTGGTGNAC 180
ATGTTACTGC TGTTATAACT AAGTTGAACA ATGAGTTAAA GAAACATAC CGTAGCGTAA 240
TAAAAAATGA TGATAGTATT TTTATTGAAG ATAACATATGC ACTCGAACAA TGGTGTATAG 300
TTGTTATTAG TAAAGACGTT TATGAAAAAG ATCTTCCAAA TGTGTTAATA AAAAAATTCA 360
CTAACCTTAC AGCTGGGTTG CTATCCAACG CCGCACTCTC TTGCATTCTT GAAATAAGAG 420
AWAAAACCCA TGGGATATTA ACAAATATA ATAATAAATT AGACACTGCA TATGTTTCCC 480
ACATCTTAAA TTTAATAAAA TCCAAGGRGT CAAGGGCATA TGCTTATGAA AATGCTCATG 540
ATTATGCAGT AGATTTAATT TCTGAAGAAA TAAGATCAAT ATTGC 585

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

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ANTCATCCAA CTGGCCGATC AGCAAAAAG CGCGGCCTAC GATTTCACCC ACGAACTGTT      60
AACCACGCTG GAAGTTGACG ATCCGGCGAT GGTAGCAAAG CAGATGGAAC TGGTGCTGGA      120
AGGCTGTTTA AGCCGAATGC TGGTGAATCG TAGCCAGGCG GATGTCGACA CCGCACATCG      180
GCTGGCGGAA GATANTCNTT GCGTTCGCCC GCTGCCGTCA GGGTGGTGCA CTGACCTGAC      240
AGAAACACAG AAAAGAAGCG ATTTGCCGCA ATCTTAAGCA GTTGAATCGC TTTTACTGAA      300
ATTAGGTTGA CGAGATGTGC AGATTACGGT TTAATGCGCC CCGTTGCCCC GATAGCTCAG      360
TCGTAGAGCA GGGGATTGAA AATCCGTTGT      390

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(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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GGATGCCAGT GTCAGCGACT GGTTAAAGTG GTCGATATCG ATGAGCAAAT TTACGCGCGC      60
CTGCGCAATA ACAGTCGGGA AAAATTAGTC GGTGTAAGAA AGACGCCGCG TATTCCTGCC      120
GTTCCGCTCA CGGAAGTTAA CCGCGAGCAG AAGTGGCAGA TGATGTTGTC AAAGAGTATG      180
CGTCGTTAAT TTTATCTCGT TGATACCGGG CGTCCTGCTT GCCAGATGCG ATGTTGTAGC      240
ATCTTATCCA GCAACCAGGT CGCATCCGGC AAGATCACCG TTAGGCGTC ACATCCGTCG      300
TCCCCTGGCA AACGGGGGCG ATTTTCCTCC ATTTGCCTCA GTGGCTGGCG TTTCATGTAA      360
CGATACATGA CAGCGCCCGA CAAGATCCTG ATACTCTTTG GGTATTCAAC CGTTTCCAGT      420
GTAATTCGTC GTTACNAAC ATTGGCGTTA CAGGCGGGGC TGGCNGTNAC CCA      473

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(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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GAAGTGAAGG ATGGCTGTGG TTTCTCCATC GGTCACCAGC AGCAGTTNGC ATCATGGATT 60
 GCCTATAAAG TCGCGCCGTT CCTCGGNAAA AAAGAGGAGA GCGTTGAAGA CCTCAAATTG 120
 CCGGGCTGBC TGAACATTTT CCACGACAAC ATCGTCTCCA CGCGATTGTG ATGACCATCT 180
 TCTTTGGTGC CATTCTGCTC TCTTCGGTAT CGACACCGTG CAGCGATGGC AGGCAAAGTG 240
 CACTGGACGG TGTACATCCT GCAAACCTGGT TCTCCTTTGC GGTGGCGATC TTCATCATCA 300
 CGCAGGGTGT GCGCATGTTT GTGGCGGAAC TCTCTGAAGC ATTTAACGGC ATTTCCCAGC 360
 GCCTGATCCC AGGTGCGGTT CTGGCGATTG ACTGTGCAGC TATCTATAGT TCGCGCCGAA 420
 CGCCGTGGTC TGGGGCTTTA TGTGGGGCAC CATCGGTCAG CTGATTGCGG TTGGCATCCT 480
 AG 482

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GACGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA 60
 AAACCCTGSC GTTACCCAAC TTAATCGSCT TGCAGCACAT CCCCCTTTTCG CCAGCTGGCG 120
 TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCANCT GAATGGCGAA 180
 TGGCG 185

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAACGCTTCA ATACGCGCGA CCAGCTGGCG GCGCTCATA GGCCTAATTT TGGCGTCGGC 60
 GAGCAAATC CTTGTTTAA AGGTATTTTG CCAGCTGCCG TCGTCATATT GGCGAGCTTG 120
 CTGACGCGAC TGCGCAGGCA TTAAACGATC AGCACAATCC ATCGCCCGCA GCCAGTAAAG 180
 CGGATTGGTT TCGGTTGATT TACCTTGCA GCGCCAGATG TCGCTACATT CAGTAGAAAG 240
 ATAGTCAGCC AGTTGATAAA CCGGAATTTT TTCTTCTGCT GCGGTATCAA TGGCTGGCTT 300
 ATTGTGATTC TGCACGCAAC CCAGCAATGC CAGACATGGA GACCCTGCCA GCCACAGCCG 360
 TCGGGGCAAT AATCGTTGAA AAATGTGTG CATATTACC AGACTTAAAG CCTATCCCAG 420

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TGGGCGTAAT TGTTGCAGAC AGTCTGGACA TGGACAGCGC GGAGAAACCG GNAGCGTACA 480

TATCGTACGT G 491

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTGAACGG CAATTATTAT TTATCCATGC AACTTCAAGT TGCAGTATCG GAACATTAAC 60

TTTTCTGGGG TGAATATCAC TCTGATATCG TTTTTTGTAT GCGTNT 106

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTTATGTGCG GTATTGATGG CTGAAGCCTG TAATATCGGA CTGGAACCGC TGATAAAGCA 60

CAATATACCA GCACTGACCC GCCATCGGCT CAGTTGGGTG AACAGAATT ACCTTCGTGC 120

AGAAACGCTG GTCAGCGCCA ATGCCCCCCT GGTTGATTTT CAGTCCACAC TGGAGCTTGC 180

TGGTCGTTGG GGAGGTGGAG AAGTGGCATC AGCTGACGGC ATGCGCTTTG TCACACCACT 240

GAAGACCATC AACTCAGGAT CTAACAGAAA ATATTTTGGT TCTGGGACGA GGCATCACCT 300

GGTATAACTT CGTATCTGGA TCAGTACTCT GGGTTCCATG GCATTGTGGT ACCCGGTACA 360

TTACGGGRCT CGATTTTGTA CTGGAAGGAC TTCTTGAGCA GCAGACAGGG CTGAATCCAG 420

TTGAAATCAT GACAGACANT GCGGGTAGCA GCGATATTAT TTTCGGTCTG TTCTGGCTAC 480

T 481

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGGNCCGTAA TTCCCAACCA TTTGCCGAGG TCCAGNTTTT TCACCATGTT ACTCGGGATA 60

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GCCAAAACNG ATACCGATGT TGCCGCCGTC CCGGTGCGAG GATCGCGGTG TTGATACCGA	120
TCAGTTCGCC GTTCAGGTTA ACCAGCGCAC CACCGGAGTT ACCACGGTTG ATCGCTGCAT	180
CGGTCTGGAT GAAGTTTTTCG TAGTTTTTCG CATTTCAGGCC GTACGCCCCA GCGCAGAGAC	240
AATCCCGGAA GTTACCGTCT CGCCCAGACC AAACGGGTTA CCAATCGCTA CGGTGTAATC	300
ACCCACGCCG AGTGCATCAG AATCCGCCAT CTTAATTGCG GTCAGGTTTT TCGGGTTCTG	360
GATTTGGATC AGCGCGATAT CAGAGCGCGG ATCTTTGCCA ACCATCTTCG CGTCGAACTT	420
ACGGCCATCG CTCAGTTGAA CTTTAATGAC CGTCGNGTTA TNAACAACGT GGTGTTGGT	480
GACGACATAG CCTTTATCGG CATCAATGAT GACGCCGGAA CCCAGCGCCA TGAATTCTGT	540
TGCTGGCCGC CACCATTA	558

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CACCTGCGTG ACGTGACCGA CCTTTTCTCC TCGCTGNTTG TTTCCCCTAT CGTCGGCCTG	60
GTCATTGCGG GAGGCCTGAT ATTCCTGCTG CGACGCTACT GGCGCGGGAC GAAAAAAGCG	120
TGACCGTATT CGCCGCATTC CGGAAGATCG CAAAAAGAAA AAACGGCAAA CGTCAACCGN	180
CATTCTGGAC GCGTATTGCG CTGATTGTTT CCGCTGCGGG CGTGGCGTTT TCGCACGGCG	240
CGAACGACGG ACCAAAAGGG ATC	263

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTAACGCGTC TGGAAGATGG CCTGCCAGTG GGCGTCGTCG ATGTGGTCCA GGGGCTGGAC	60
GGTTGCCATT CCGCCAATAT CTCACCGGAC AACCGTACGC TGTGGGTTCC GGCATTAAAG	120
CAGGATCGCA TTTGCCTGTT TACGGTCAGC GATGATGGTC ATCTCGTGGC GCAGGACCCT	180
GCGGAAGTGA CCACCGTTGA AGGGGCCGGC CCGCGTCATA TGGTATTCCA TCCAAACGAA	240
CAATATGCGT ATTGCGTCAA TGAGTTAAAC AGCTCAGTGG ATGTCTGGGA ACTGAAAGAT	300
CCGCACGGTA ATAATCGAAT GTGTCCAGAC GCTGGATATG ATGCCGAAA ATTCTCCGAC	360

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ACCCGTTGGG CGGCKGATAT TCATATCACC CCGGATGGTC GCCATTTATA CGCCTGCGAC 420
 CGTACCGCCA GCCTGATTAC CSTTTTCACC GTTTCGGAAG ATGGCAGCGT GTTGASTAAA 480
 GAAGGCTTCC AGCCAACGGA AACCACAGCG CGCGGENTCA ATGTTGATCA CAGCGSCAAG 540
 TATCTGATTG CCGCCGGGCA AAAATCTCAC CACATCTCGG TATACGAAAT TGTTGGCGAN 600
 CAGGGGCTAC TGCATGAAAA AGGCCGCTAT GCGGTGCGGC AGGGACCAAT GTGGGTGGTG 660
 GTTAACGCAC ACTAACCGCT GAT 683

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGATGCAGG GAAAAACATT GATATTACCG GGGCAACGTG CTCGTCCGGT GGAGACCTTG 60
 GAATGTCTGC GGGTAATRAC ATCAACATTG CCGTAAACCT GATAAGCGGG ACAAAGTCA 120
 GTCCGGTTTC TGGCACACTG ATGACAACAG TTCATCATCC ACCACCTCAC AGGGCAGCAG 180
 CATCAGCGCC GCGGATAACC TGGGCGATGG CTGCAGGCAG AGATKCTGGG NTGTCACAGC 240
 ATCCTCTGTT TCTGCCGGGC ACAGCGCCCT GCTTTCTGCA GT 282

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGAACGGCC CCCCCACAG CCGTTAACA AACGGNTGCC CCGGCGATAA TCGTACTGAT 60
 AAGTTAACTC CAGCAGGCGG TTAATTGAAA GCGAACGGGA GGCTGATGCA TGTAATAAT 120
 CCCTTAAAC GCGACGGCAA CGCGCCAGTA AACCGTGAGA TGGTCAGGGG CAAGCCAGTC 180
 CGGGTAAACC AGAGGCAGTC CGGCAGTGAA CGAACCGGAA ACATGACCAC TGGTGGTGCT 240
 GAGCCCGGCA GCAGACCCCC ACAGCGTGCC GGACGAGTAC GGGTCATCTC TGTCAGAGTG 300
 CAGCCAGCCG CCGTCCAGTG CAGTCACTGC ACGGACTGTC CCCACATATG GCAGGGAGAA 360
 CAGAGACCAG GACAGCTCAT TTCGCAGATA ACCGCCGTTA TTACCGGAGA TATACTGCTC 420
 CTTAAAGCCA CGCACTGAAC TCTACCCCC GAGGCTCAGT TGTTCCACAC CATGAAGACG 480
 GTCCGCTGAC CACTGGGCAT AAGCGCTGGT CAGCCACCAC ACCCTGTCCG TGACGGGGCG 540

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CTGAAACTG GCACTCACCG ACCATTTCCG GAACTGATTT ACGGCGAGGT CTCCCCTTTT	600
CCCGTGGTCG CTTTCTGCGC CGAACCAGGG CATCCCCCGT GTGAATACCG GATTGAGTGT	660
TCCGACACCA CCCAGAACT TGTGTGTGTG ATTCANC	697

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4835 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TTGACTGAG CACCACAAAT ACTGGGTATC TCCCCAGATA GTTCATTGCG GTACAAGCAA	60
TATAGGTGCA GAAAGTCAAC CTGCTGCACC CTATTGGATA ATTATATATG GCCTTCAATA	120
AAGTTTGCGG TTGTCGACGT TGGCTATATC AGCCATTTCC AATGCATAGT TCTTTGGTTT	180
AGCACCATCA AGTTATAGAT TTGGGAATAG TTTCAACTGG TATTGATTGA ATTGGGTTTC	240
ATCGTCGATG ATTAATACTA TTTGTAAAGA CTTTATTGTT GATTTCCTAT TATACCACAA	300
ACCCAAACTG GTCTAGGTCA TCATTTGGTG TTGATAACGG GCTCTGATAA TTTCTGCTCT	360
TCTGCTATAC TGGGGATTAT GAAGAATATT AAGGCTGAGT GTATTGAGGT AGTGTCTTT	420
GAACCGACCA TTCATGACAA TATATTCTTC AATTCGTGAG TGATCCAGCA ACTGGTTGAA	480
TTTAAAACAC TGAGTGATGT TATCCTCTGT AATCGTATGG TTGCTGAACT AGTTGATGTA	540
GCCGATAAGG TTTATACCAG ATATCTTTTG GGGGGATTAG ATAACGTAGC CGCGGATAGC	600
AAACGAGATA GTTGAATTTT ATTACCGTAA TTTCTTCCAT TGAGAAAAGC TTATTTTCT	660
TGGTGGTATT CGCAGTTATG TATCTTCCAT AAAGACTTGG GAATATCTTG CTTGAAARGC	720
TATCTGGAGA TAGCCTTAGT TATTTGATAA ATATTTCAA TAGGAGGAGC CGTATGGCTG	780
TCATTTATAC CCTCACTAAA TCGTCACTTG TCAAGTCTGG TGGTCAATTA CATTGGAATA	840
TTGATTCGCC ATCAGAACAA CAGCCACAAA AGATCGTCAA TGGTCGGGTT GCGCTTCGGG	900
GATGGTTACT GGCAGATGTG GAAAAAGATC TCCGTGTTGC GGTAAATTT GAACATTTGA	960
CATACAGTTT TCCCTTCAAT ATAAAGCGCC CTGATGTTAT TTCAGCTATA CTGAAACAGC	1020
CACCTGAAAA ACATCAAAGA CTTCAATTGTG GATTTGATAT CAATGTCCCA TTTTCTACTA	1080
AAATAATTAT TGGCCTTGAG TCTGATGGGT TGATTACCTG GTTGGAAGAG TTATTATTTT	1140
TCCTGCCTGA TAATTGAATT AAGTATCTAT ACCGATAGTA TCGCGATAGA TATATTTTTT	1200
TACAGGATGA TAATTTGAGA ATCTATATAG CCGCTATTAT CAAGGATGAG TATTCAAGTT	1260
TACTTGAATG GATTGCCTAC CATCGAGTAT TAGGTGTTGA TGGSTTTAKT ATTGCAGATA	1320
ATGGCAGTCG TGAWGGTAGC CGAGAATTAC TATTTTCCCT CGCTCGCCTA GGTATTGTGA	1380

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CGATGTTTGA	ACAACCGACT	TTGGTGAATC	AAAAGCCACA	ATTACCTGCA	TATGAACATA	1440
TTTTACGTAG	CTGTCCCAGA	GACATAGACC	TGCTTGCAAT	TATAGATGCT	GATGAATTTT	1500
TATTGCCACT	TGAATCGGAT	ACCAATTTGT	CAGATTTTTT	TTCTGAAAAG	TTTCAGGATG	1560
AGAGTGTCAG	CGCTATTGCA	TTGAATTGGG	CAAATTTTGG	TTCTAGTGGT	GAATGTTTTG	1620
CTGAAGAGGG	GTTGGTTATT	GAACGTTTTA	CCTATCGTGC	CCCGCAATCC	TTTAACGTTT	1680
ATCATAACTT	CAAAAGCGTG	GTCAAACCCG	AACGAGTTAA	CCGCTTTCAT	AATCCGCATT	1740
ATGCTGATTT	GCGTTATGGT	CGATATATCG	ATGCATTGGG	TCGTGATTTG	ATTCTGCACC	1800
CGAGGCATGG	TAATGGGGTT	AGTGCTGAAG	TGACTTGGAG	CGGTGTCAGG	GTAAATCACT	1860
ATGCAGTTAA	ATCACTTGAG	GAATTCCTGT	TGGGCAAGCA	TCTGCGTGGT	AGTGCTGCCA	1920
CTGCTAATCG	AGTAAAGCAT	AAAGATTATT	TCAAGGCACA	TGATCGTAAT	GATGAAGAGT	1980
GCCTTCTCGC	TGCCGCATTC	TCAGAACAAG	TAAAAGCTGA	AATGGAACGA	TTAAGTGTGA	2040
AGTTGACTGA	GTTACCAGCA	GTTGAACCTA	TTCCTACTGG	TTCTTGTTTC	AAAAAAAAAA	2100
TGAAGAAATG	GATGGTTTGA	ATATATTGAG	CAAGCACTTT	GGTATTTATT	TCTGCTCTTA	2160
TCTACAGGTC	TGCTAATAAG	GATCTGTATC	CCCCAGGTGT	TACCTTGGAC	TGTAAGTTAT	2220
ATTATGTGTA	GCTATTGCGA	TTGGCAGCCT	CTGACATTGC	CAGACTCGTT	TTCTCTTCAT	2280
TCTGGTTGGC	TTCTGATTCG	GGGGCGCGTG	TTGACGACTC	AAACTCGAGG	TGAAACTCGT	2340
CTGCGCTGGC	AATGCGGACA	AGGAATATGG	CATGAACAGA	AGTTGCCGGT	CACTCGTCGA	2400
GGCACGTTGC	TGGAGCTGGT	TTATCTACCY	TCGGGAGCTA	GTCATTKGTC	TTTGCTGGCA	2460
AGTAATAAGG	GCGCTGAGTG	TAATGTTGAA	ATTACTCAGC	TTTGTGTGT	ATCCCGTGCC	2520
GAGAGTCTCT	GGCGTCGATT	GCGCCGGGTT	GTACCTTTTT	ACCGACGCTT	AACGAAGTCC	2580
AGACGCAAAA	GGTTAGGCCT	TTCATGGCAT	TTGTGGCTCA	CGGACTTGCA	GCAAGCTTAC	2640
CAACTTGTCA	GCAGAGTTCT	CGATGATAAA	CCACTCAATA	GCTATGATGA	GTGGCTAGCA	2700
GACTTCGACA	CCCTTGAACC	CGCCGAATAC	AAGCTGATTA	AGCGCCAGCT	GGCTCGCTGG	2760
GGCACATTAC	CACGTTTCTG	TTTGCATCTT	GTTGGCGTTG	GGGATGAACA	GAGCCGCCAC	2820
AAGACCCTGG	AGAGTATTCA	GGCACTCTGT	TATCCGGCAA	GCAATATAAA	CCTGCAGGAG	2880
CATGGTGCAT	ATCCAGAAAT	CTCCAGTCAG	TCAAGCGGCG	AATGGCAGTG	GGTGTGCTCT	2940
GTAGGGGCAG	TGGTTTCGCC	AAGCGCCTTA	TTTTGGGTTG	CCCACCAAGT	ACGCCAGAAT	3000
CCTGATTGTT	TATGGATATA	CGGTGATCAC	GATCTGCTTG	ACGAGAGAGG	TGAACGTCAC	3060
TCTCCCAACT	TCAAACCTGA	TTGGAATGAA	ACGCTGCTAC	AGAGCCAAAA	CTATATTAGT	3120
TGGTGTGGTT	TGTGGCGTGA	ACAAGGTGCT	GGCCGTGTTT	CCTTTGATGC	GGCGACATGC	3180
CATCAGTGGT	GGCTACAGTT	GGCAAAGATG	TGTGAACCGA	AACAGATAGT	CCATATTCCA	3240
TCATTGATGA	TGCATTTGCC	TGCAAGAGCG	TTGATTTTCG	ATGATTTTGA	GTCGCTGAAA	3300

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GATAAAGAAG ATTTACTGCC ATCAGGAGTG AGCATTGAGG CAGCACCTCA TGGTGTATGT	3360
CGTTGGCGCT GGCCGTTGCC AGCGCAATTG CCATTGGTTT CAGTGATTAT CCCTACTAGA	3420
AATGGTATTG CTCATTTACG CCCTTGATC GAAAGCCTGA TACAAAAGAC GCAATATGCC	3480
AATATGGAAG TCATAGTGAT GGATAATCAG AGCGATGAGG AGGAGACGCT TGCTTATCTT	3540
GCTCATATCG AACAGGTTTA TGGCGTTAGG GTGATTTCTT ATGATCAACC GTTAACTAT	3600
TCAGCCATCA ACAATCTGGC AGTGAGAAAC GCACATGGAG ATATGATATG TTTGCTGAAT	3660
AATGATACTC AGGTAATCAG TATTGACTGG CTGGATGAAA TGGTTTCTCA TTTATTACGC	3720
CCCGGCGTGG GTGTGGTAGG AGCAAAGCTG TATTACGGAA ATGGCTTGAT TCAGCATGCA	3780
GGCGATGCTG TCGGCCCTGG CGGTTGTGCA GATCATTTTC ATAATGGTTT GTCAGCTAAC	3840
GATCCTGGAT ATCAGCGTAG GGCTGTTAGT GCCCAAGAGC TGTCAGCTGT GACTGCAGCT	3900
TGTTTATTGA CTCATAAAGA GTTATATCTG GCGCTCGGAG GACTTGATGA AACGAATTTG	3960
CCGATAGCTT TTAATGACGT RGATTATTGT CTCAGAGTTC GAGATGCTGG CTGGAGAGTA	4020
ATCTGGACTC CCTTCGCTGA ATTGTATCAT CATGAGTCTA TTTCCCGTGG TAAAGATGTA	4080
TCAAAACAAC AGCAGATACG AGCGAAATCT GAGTTGCGCT ATATGAAAAA ACGATGGGCA	4140
TGTGCACTTA AACACGATCC AGCCTACAAC CAAAATTTGA GTTATGAACG TCCTGATTTT	4200
TCTTTAAGTA GAGCTCCTAA TATAGTATTG CCATGGATGA ATTAATTCGC AGGAACTAT	4260
TTAAGCCTTA TCGTAAATTA AATAAACAGA GTTATAGAAG TCCGCAAAGC TCTGAGATTA	4320
ACTTTGAACG ATTGTTTATA TTACATGAGG GAAAATCACC TACATTAGCC TATTTTGAAT	4380
CGGCTATTAT AAGTCGTTTT CCTGATGCAG AATGTCATTT TATCGACACA TTAGCATCCA	4440
CTGATATATT TATTCCTAGA GGATCTGCCC TTGTCGTCAT TAGATTCATC TCCCCAAAAT	4500
GGCAACAGCA CATAGAAAGA TATAACGACA GGTTTTCTCG AATTGTTTAT TTTATGGATG	4560
ACGACCTGTT TGACCCGACT GCACTATCTA CGTTACCAA AGAGTATCGT ACCAAGATAA	4620
TAAGGAGGTC GGCGGCTCAG CATCGATGGA TTACGCAATA TTGTGATAAC ATTTGGGTTT	4680
CAACTGCCTA TTTGGCTAAT AAATATGCAC ATCTTAACCC GGAGATTGTT TCTGCTAAAC	4740
CGTCACTGGC ACTCATTGAA ACACATCGAT CAGTAAAAAT CGCTTATCAT GGCTCAAGTT	4800
CTCATCGGGA AGAAAAATAT TGGTTGAGAC AAATC	4835

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

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GAAAAATGNC ATAACCGCAT TCCATCAAGC CCGTNAATAT CCGGACTTT CATTATTTC	60
TGAGGCGTAC AGGGAAGCAA TAACTGCTGG TCAGATATTG CTGTCTCCGG TACATTTACC	120
TGACACTGTA TTTTCCATC CCAGTTTACC GACAGGGTTT CCGCCGGCGT CACGCCACTC	180
AGCCAGSCAA GGCTTCGTG GSCCACCATG CCGAGTTCCC GGCTTTTTTC ACTGGTTACA	240
CTGGCACCAA ACGGGGGCTG AGAGCCATCA GCAAGACGCA GTATTGCAA CAGACGTTTC	300
CCTTTAAGCA CGCTGAATTT CCGGTAACCA ATGGCACCTT CTGTCAGCGC CGATTCCACA	360
ACAGAACGGG TTGCTTCCAC ATCATCCGT AAGCGCTTCA GGTCAACAGA GGTTGTATTC	420
CGGTAATAAC TGCTGATGTC AGTCAACACG CCGGTTCCCC AGCGATTTGT CACCACCTGC	480
CCGCCATCAA CCGGTACACC TCCCACACCA TCCGTGTCAA CAAGAAGACG TGTTCCACCG	540
GACATTCCCC CTGCATGTAA CGCCGCACCT TTTCCGGTAA TTGTTGCCCC ACCGGAAGCA	600
CTGACGCCGA AAGACGTATA TCCTTTCTGC AGGGATGCAA TATTCGCGGA CAAATTTGCC	660
AGCGGACTAC GATGACTGTA ATAGGCATTA ATCTGACGTT GCGATGTCAG TCCACCGCCA	720
CTGTTAAGGC CGGCGTTTCTG GCTGTAGCTG TCCAGACCGT CATTGAACGT GWCAGTGTAG	780
CCGGCCATAT TCACATAACG GTCATTACTC ATACTGCCAC TGTAGCTCGC TGTCCCCGTC	840
CCCCAGCGGC ACGGATATAC GCAGGTAAGC AGAATCNTTA TCACGCCCCA GATATTTAGA	900
CCTTGAGGCT GACAATCCAA CCGCCACACC CTGCAGTCCG AAAACATTAA AGTAGCGGTT	960
GACGCTCACC GTATAATAGT CCGTTTTCCG TATGTCCCAG TATGTCTGAC GGCTGTACTG	1020
CAGGTTAAAA GAGGTGTTCC AGTCCGCCAC GTTTTTATTG AGCGTAACGG TATACATCTC	1080
TTTTTCCCGA CTGCTGTAAT CATTACGGTA GCGGGCGTTC AGGTACTGCT CCATGGTCAT	1140
ATAGTTTCGC TCTGAGAAAC GATACCCGGC GAACGTAATG TCGGCATCCG CATTATCAAA	1200
CCGTTTGGAG TAGCTCAGAC GCCAGGATTT TCCCTGAAAC GTTCTCTCTC CCTCAATACG	1260
GGCTACTGAC TGCGTGATAT CAGCGGAAAG GGTCCCCGGC ACACCCAGGT CCCAGCCGGC	1320
ACCGGCTGCC AGTGCAATTAT AATCACCGGC AAGCACAGCC CCGCCATACA GCGACCACTG	1380
GTTACTGAGC CCCCAGGATG CCTCTCCGGT CGCAAATACA GGCCCTTCGG TCTCATGCCC	1440
GTATCCACGG GAACGACCGG AGACAAGTTT GTACCGGACC TGTCCCGGAC GCGTCAGATA	1500
AGGAACCGAG GCCGTATCGA CCTGAAAGTT TTCTTCCGTC CGTTCTGTTC AATAACCTCA	1560
ACATCAAGAC GTCCGCGAAC TGAAGTGTCC AGGTCCTGAA TACTGAATGG CCCTGCGGGG	1620
ACCATCGAGT CGTACAGCAC CCGTCCCTGC TGCGACACCA CAACACGGGC ATTAGTCTCC	1680
GCAATCCCGG TAATCTGCGG TGCATAAGCC TTCGCATTCT TGGGGCGGCA CATTCCGGGT	1740
CAGCGN	1746

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TGTACTGAGC ACGGCGAATA TCCAGTGTTC AAATTCCACT TTGCAGCGAC TGCATGATGT	60
CTGCGGCGCG GTAACAATCA GGGCATTACT GTGTTTGCTG GCGGCGATGG AGACAACCTC	120
ACGCCCCTA CCGACCGTGC CTTCCGCCTC TTCTTTAGCC GCCGTGAGCG TGCCGCTGAC	180
CTGCTTCAGC ACATCGACCA GATCTTCGGC TTTGCTGTAT TTGAGATAGA AAACCTGGCT	240
GTTGCCGCTG CGTTCCATTT CTGAGTCCAG CCGACGGATC AGGCGGCGCA TTTTGTCCCG	300
CGTGGCCGGG TCACCACTGA CAATCACACT GTTGGTGCCT TCGTCGGCGA CAATTTGAGA	360
TTTCAGCGTC GCAGSCTGCT TCTCGCCGCT GTTTTTAGTC AGGCTTTCCA GCACGCGGGC	420
GATTTCCGAA GCAGAGGCGT TATCCAGCGG GATCACCTCT TCAGTGCGAT TANCCGCGTG	480
ATCCACACGC TGGATCACTT CCGTCAGCCG CTCCACGACG GAGGCGCGCC CGGTGAGCAT	540
AATCACGTTG GAGGGATCGT AATTAACAAC GTTGCTGAG CCTGCGCTGT CGATCATCTG	600
GCGCAGAATC GGTGCCAGTT CGCGTACCGA AACATNACGT ACCGGCACGA CTTTGGTGAC	660
CATTTTCATCG CCGCGTATT GTCGCTGCCT TCACCAACCA GCGGCAGGGC TCGACTTTTCG	720
CGG	723

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TAGAGGATCC CCGGCGTTGC GATCGTCACG AACATAGACC CACAKCCGTC CGGTAGGTAT	60
TTACCCTGAC CCGGYTCCAG TACATTTACC GCGTGTCAT CGGCATGCAC TTTACCCGGC	120
ATCAGCACAT AGTGCTTCAG TTCATCATAC AGCGGGCGAA GCTGCTCTCC CATGATGTCA	180
ACCCAGCGCC CCATCGTATT GCAGTGCAGC TCCACGCCCT GGCGGGCATA GATTTCCGAC	240
TGACGGTACA GCGGCAGATG CTCGGCGAAC TTAGCCATGA TTATGCGGGC CAGCAGAGCC	300
GGACTGGCGT AACTGCGCTC GATGGGTTTT GGTGCTGCG GAGCCTGAAC TATACAGTCG	360
CACCGGCTGC AGGCCAGTTT TGGGCGAACC GTTTCGATTA CCCTGAACGC GGTGTTGATG	420
ATATCCAGTT GTTCAGAGAT GCTTTCTCCC AGCGGTTTCA GTTTGCCGCT GCAGACGGGG	480

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CATTGGGTTT	CTGCCGSGGA	GATAACCTGC	CTGTACCGG	GAAGTGTTGC	CGGAAGTGCT	540
TTSCGGACGG	GAGAGTCTGA	TGTTTTCGGC	GCTGTCTCTC	CGGJCATTGA	GGTGASTTGC	600
AACTGCGCCT	CACCAAGCCT	GTTCTGSGAG	TCGTTTATAC	GGTTTCTGC	CCGTGCGATC	660
TTCTTTTCTA	TCTTCTCGCG	GCTTTTCTGG	CTGCTGCGAC	CGAACAACAT	TCTCTGTAGT	720
TTAGCGACCA	GCGCTCTGAG	TGAGCTGATC	TCGCGGCATA	GGCGGTTATT	TCACCAGACA	780
GACGGACGAT	AACAGCCTGC	TGTGCGATCA	GCAGGGCCTT	CAGTTGCTCG	ATGTCGTCGG	840
GGAGTGTGTT	GTTCAATCCC	CTGTTTTATC	ACGGGTTATA	TCCGGATGCC	AGGCCGTTCT	900
GTCCGTTTGG	ATGTTGCCA	CGCGATCCCC	TCCAGTAGCA	TGGATAACTG	AGCTGSCGTC	960
AGGTGCACTT	TCCCTTCCCG	GSTTACCGGC	CAGACGAAGC	GGCCCCGTTT	CAGGCGTTTG	1020
GCGAACAGGC	ATAACCCGTC	ACGATCGGCC	CACAGTATTT	TCACCATTTT	GCCACTGCGG	1080
CCCCGGAAGA	CGAAGATATG	CCCGGAGAAC	GGGTCATCTT	TCAGCGTGTT	CTGCACCTTC	1140
GAAGCCAGGC	CGTTGAAGCC	ACAACGCATA	TCTGTGATGC	CAGCGATGAT	CCAGATTCTG	1200
GTACCGGTTG	GCAGCGTTAT	CATCGGGTAC	CTCCTTTTAT	TTGCGGGATT	AGCGCCCGTA	1260
ACATTTCCGG	AGTGAGAGGG	TCAAACAGTT	TTACCACACC	TGATTTAAGA	TGCAGCTCGC	1320
ACCGTGGGAC	GTTTCCGGGA	TCACACTCAG	GGCACTCATC	AGGCTTGTTA	CGCCAGAAGG	1380
GATTTGTAAC	TGSTCTGGTC	GGCTCTGGCG	TATCAGTCAG	AGCCACCGGG	ACAGGCATGC	1440
ATTCTGTAT	GTCATCATCG	CTCAGTAAGC	CGTCCTCGTA	CTGGCTTTTC	CATTTAAACA	1500
GCAGGTTATC	ATTGATACCG	TGCTCTCTGG	CGATCCGGGC	AACAACAGCA	CCGGGCTGTA	1560
ATGCCTGCTT	AGCCAGACGG	ACCTTAAATT	CACGGCTGTA	GCTGGCTCGC	CGTTCTTTTC	1620
GCCATGTGCC	TTCGCTGATT	TGAGGCTCTG	TTAATTCCTT	CTTTCTGTTG	GCATAAAGGA	1680
TGGCGTCAAG	CTGAGCTAAT	GAAACTGAAT	CGGGCAATGG	CCATGCGATA	CCGGATGCAA	1740
TAAATCGCTG	AAAAAGCGTA	TGTATTGTGG	AATGACTGAG	ACCTAGACGC	TGAGCGATGG	1800
CCCGGATGGT	CAGTTTATCT	TCAAATCTTA	AACGCAGAGC	ATCAGGCAAA	TAAGAACGGA	1860
AGCAGGGAAT	ATCTTTTTTT	GTCTGGGAAT	TCATCGTTTC	TGTCCATCTA	TATAGATGGG	1920
CGCGATTGTT	GCCAGACAGG	ACAATTTTCA	CAAGACGTCG	CAGATGGGGC	GCTTACCAGA	1980
AATGCGCGGG	TACGACAGTG	ACTCGTCAAA	TCTCAGTTGT	AGCACACGCG	GGATCAATTC	2040
CGGATTGTCT	GCCAGTACCG	CCTTTCGTGC	ATTCATCTTA	AATGTCCCTT	TACTGCAAAA	2100
ATGGACATTA	GATCGGAAA	CAGGAAAGGG	AGGCGAAAGA	CGGTTTAAAT	GAGACGGTTA	2160
CCATTGTGTC	GGGCTGTGTA	CGTTCTCCCC	GGACAGACAG	CCTCAGTTGG	TAGAATCTAT	2220
AAATTACTGC	TACTGATGCT	GCCGGGGAAA	GGCGTAACGA	AAAAACAGCC	TCCGTTACCG	2280
GACAGCAAGG	AGGCTGAATG	GAGTTTACAG	GATTTGCTTT	TTTATAATGT	CTGGCCATGC	2340
AGTAAAACCG	GACAGGTTTT	ATTATCATGT	GAGGTATTCT	GACATAAAAT	GCTGGATTTT	2400

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TATTTTGTGA CGAATGCTGC AAAATTGCAT CTGCACTCTG ATGTAGCTTT TATCTGTTTC 2460
 AGTGAAGCAT GCCCACAAC TGAGTTATTA AGTTGTGGAA GAACAGTTTT GTCCCGCCTG 2520
 CATCTCTCCT TTCAAAAACC AGTATGTCGC CATGCC 2556

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CAGTTAGTGT TAAAAAATNT CCTCTGCTNC AGAAATTACA CCCACCAATA TACAATNATT 60
 AATAAATTTT CGGTTGGGTT AGGTAATGGC TGGGATTCSA TAATATCTCT TGATGGGGTT 120
 GAACAGAGTG AGGAAATATT ACGCTGGTAC ACAGCCGGCT CAAAAACAGT AAAGATTGAG 180
 AGCAGGTTGT ATGGTGAAGA GGGAAAGAGA AAACCCGGGG AGCTATCTGG TTCTATGACT 240
 ATGGTTCTGA GTTTCCTCTG AATAAGATGA TGGATTATCT GACTGGCTGT TCATCAGTCG 300
 GATAATGATG AAAACTGATG AGCAACAGGT TGTGCGGGCA ATGTGCAGGA TCCGTCACCA 360
 AAGGGTGGAA GTTGCGGGCG ACTCAGATAA ACGGGTTACA TGAGCTATTT CTGGAGTTTG 420
 ACGAAGCCGT CTGGAAGGGA GAAGAGGCCA TTCCATTGAT GTCTCTGGAA AACATCTGTC 480
 AGTCGTGCTG CTGGAATAT TGATAGAGCA ATGGGAATGG TTATCCAACA TTGATGAACA 540
 TATTGTATAT TTACAGAAAT TTTTAAAAAC AGGACTCAGC AGGTTAAATC GTGTAAAAAT 600
 TACTCATGAA TACCATTATG GGCTTACAAA GCGATGTGST TAAGCAGATC TTATTCAGGC 660
 CTGTGCAGCG TAGGATTACA ATAGGATCGA ATAACGCCAT ACAGGGGAAT GGGAGATAGG 720
 CTGATTCATC CTGTGGCTAT AACCAGGAGC ATATCGGGAA TCMANTATGT TACCCAGAT 780
 GGAACACCAT 790

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10906 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCGGCCGCAG TACTGGATCT CTTTGCGGCA TGACGATGAG GGGGAGAGAA ATAACTTAA 60
 CCCAGTCATG GCAGATGAAG AACAGGCTTA CGTAAAAGGG TTATATGAAG GGATTATGCT 120-
 GATTGGTAAT ATAATCAATA AGCCTGAAGA AGCTAAAGCG TTAATCAAGG CAACTGAAAA 180

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TGGCTGCAGA ATGGTGAGTA ACCGCTGCA ACTTCTACCC GAAGAGCAGC GTGTTGCTGC	240
CTATATGGCG AATCCTGAAT TGACCACTTA TGGTTCCGGA AAATATACAG GATTAATGAT	300
GAAACATGcT GCGGCAGTAA ACGTCGCCCC TTCCACCATT AAAGGTTTCA AACAGGTCTC	360
GATAGAGCAA GTCATTGAAT GGAATCCTCA GGTAATTTTT GTGCAGAATC GTTATCCTGC	420
TGTAGTGAAT GAAATACAGT CAAACCCACA GTGGCAGGTA ATAGATGCTG TCAAAAATCA	480
TCGTGTTTAT TTGATGCCAG AGTATGCCAA AGCATGGGGC TATCCGATGC CCGAGGCTAT	540
GGGGaTTGGG GAATTGTGGA TGGCGAAAAA GCTGTATCCA GAAAAATTCA ATGATGTTGA	600
TATGCATAAA ATAGTCAATG ACTGGTATAG AACGTTTTAC CGTACTGATT ATCAGGGTGA	660
AGACTAATGC GAGTGCTTGC TGCGGGCAGT TTACGCCGGG TATGGAAATC ACTTGTGTCA	720
GAGTATCAGG CCGATAATAT ACAGTGTGAT TTTGGACCAG CGGGTATATT AAGGGAGCGT	780
ATTGAGGTGG GTGAGGCATG CGATTTTTTT GCATCAGCCA ATATGACTCA CCCACAGATA	840
TTAATGtCCG CAGGanGAGC ATTGTGTATT AAACCTTTTG CCAGAAATCG TTTGTGTTTG	900
TATGTTCCGG CGAATAAATT CAATGAGAAT GACGACTGGT ATTCTTTATT AAATCGGGAA	960
ACATTGCGAA TCGGAACATC AACGGCGGGA TGTGATCCAT CTGGTGATTA CACTCAGGAA	1020
CTGTTTGAAA ATATGGGGAG TGTCGGTGAA AAAATAAGGC AACGGGCTGT AGCATTAGTT	1080
GGGcgGGAGG CATTGTTTTT CTCTTCCAGG AAATGCGATA gcAGCGCAGT GGTAAATTGA	1140
AAATGATTAT ACTGATCTGT TCATCGGTTA TGCCAATTAC GCTCCTGGCT TGCAATCAAT	1200
TGATTAGTA AAAGTTATAG AAATACCGGA ACCTTATAAT CCGATTGCTA TCTATGGATT	1260
TGCCTGTCTG ACCGATAATG CCCTGCCACT TGCCGACTTT ITAGTTTCAC CTGTTGCCAG	1320
AGGTATACTT GAACAGCATG GGTTTATGCC TCCAGGTACG TTATAGCCCC CTGTCTTACA	1380
GCTGtCTCTT gATCAGATCT CCTGATCAAG AGACTTCATC ACCAGGTAAC CCTCAACCAT	1440
ATCCTGCATA TCCTGAAGTC TGAACCAGCC ATCCACATA ACTACCCAAC CGGGGCGGCC	1500
TGTGCGTTTG CTGTCATGCC ATCGCCCCAG TTTGCCAGT TTCAGACAGG CCCATTTACG	1560
TGTCGGCGTC TGTGACGGAA GCGGTTTTCC TTCCAGCTTA ACCCACAGCA GTTTCCACTC	1620
TGTCGGCGTC AGTATTTTCT TACAGCTGTC ATTTTGTGTT TCTTCACTGA TACCTCCCTG	1680
CCGCAGGCCa GCACCCGTAC CGCGATAAAC GCCTTGATAA CCACCATGCG CTCAAGGTTA	1740
TCCCGGGTCT GCATTGCGAG CGATTCCACA CATGTACCAC CACTTTTCCA CGCCTTGTGG	1800
TATTCTCTA TCAGCCaGCG TCGCTCGTAA TGGCTGACGA TACGTCGCGC ATCGGCGGCA	1860
CTCGCCACTT TTTCTGACGT CAGCAGATGC CAGCAGGCAC CGTCCTCTGC CTGCTCCCGC	1920
CAACAGACAT ACGTGAGCGG GAGCGCCTGG CCGCTGTTGT CGGGATTTTT TATGCTGAcT	1980
TCGTTGTAAC TGATGAACAT CCGGGCctgg CGGGCTGCCC GCCCGCCTTT TTGCATCACA	2040-
TTCAGCGTGT GGCTTCCCGC GGTTGCCAGG ACTTCCGGCA GTTCGAAGAG CTTGCCGGGT	2100

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GCTTCTTCCA GCCGGCGATT CTGTGCAGCA CGCACCACGA AGCGCTGTCC GTGGCTGACT	2160
TTATAATGCA GGTAATGCTA GATATCCGCT TCCCGSTCAC AGACAGTGAT TACCCGTTTC	2220
TGTATCTCCC CCAGCCGTTC GGCCATACGC TCCGAAGCCT GCTGCCAGCG GTAACTTTCT	2280
TTTTCTTCAT AGGGACGTTC TTTTCGCTGG TGCTTAACAC CATAGGTgtC CGTGACCCGA	2340
CTCCAGCGCT GCTGTTCGAT AAGACCGACT GGCAGGGCGC TGTCGGGGGC GTACATCAGG	2400
ACAGAGTGAG CCAGCAGCCC GCGCGTCTTC GGGTTAGTGG TGGTATTCCC CAGGTCATCA	2460
GATGCCGTAC TGTGGCTGAA GTTAATGGTG GTGGTGTCTT CCAGTGCAGAG GAGCAGCGGA	2520
TGAGCCTCAC ATGCCCTTAC AGTGGCGGTA AATCCGGCTT CGGCAATGGC TTGCGGGGAC	2580
ACAGACGGGT TACGTATCAG GCGGTACGCA CCTTCAACCT GAGCAGTGGA CTGGGATGAT	2640
TTCACAATAG AAAGACCTGC ATGCTGAGCG AGAGAAGAGG TCAGTGACAC AAGGCGTCGT	2700
GTACGACGCG GATCACCGAG ACGGGCATGT CCAAACCTGCT CGTTAGCCCA TGAATAACAA	2760
TCAGAAAGTA CCATAACAGA GTCGAATAAA ATGAAATATA AGAGAAGATC AACGGGTGAA	2820
GAAAAAGTTC AAAAAATGGC TACCGGGGAG GAAGGAAAGT ACCGGATGGA AAGAGCCCCC	2880
CTAAAGCAGA CTGACAGACA TCACAAATCC CCGGGGGGGA CTTGTGTATA AGAGACAGGT	2940
CTTACAGGGG GAGCGTCCGT CTTTTTATCA ACATCAGGCA ATGACATAAC ATTATGAACA	3000
AGCTCACAAAG TCTGATGGTT AAATTTTATA ATGCTCCTTA CTAAGACCGT ATTTTTTCAT	3060
TCTGAGATAG AGTTTTTCC GCGGGATTTG TAAATATTCA GCAACCTCAT TGATACGCCC	3120
CTGATGGATA TTAAGTGCCT CTGTGATTAT CTGTCGCTCA GCGTCCTCCA CTCGTCTGTC	3180
AAGCGGTGTC GGGGTTCGA CGTGCATCAA CGGATTTGCT GTTTCTGCCA GCGGTAATAC	3240
TCCTACAGTA AATAGTTCTG CTGCATTGGC CAGCTCTCGC ACATTATTTG GCCACATGCG	3300
GCGCATCATC TCTTTGAGCA TCTCTTTTCC CACTTCCGGA ACAGGATGGT TAAGCCGTTG	3360
ACATGCTTTA CAAAGGTAAT GGCAGAACAG TGGTTCAATA TCATCGGGGC GTTGAGTTAA	3420
TGGCAGGCAA GCGATTTGTG TCATTGCAAA GCAGTAATAG AGCTCCGCGA TGATATGGTT	3480
GCTGGCGGCC AGCTCGACCA GCGAAGTGTC TCCAATACCA ATCAGGCGAA AAGGTCGGTG	3540
TTCTTGCTT TGTAAC TGAA CCAGATGGTA CTGCTGTTCA CGCGTCAGGT GTTCAGGATG	3600
GCTGAGCACT AATGTTCCCC CCTGAGCCAG CGCAATGAAA TCATTAAGCT GTGGTGCATT	3660
GTCTGGTGTC AGCTCGCGGT AGATAAATTC GCCTTGTGCA TTACGTCCAA ATTGGTGCAG	3720
ATAACGTGCA CCGGTCATCC GTCCTGTGCC TGGGGCACcG TAGAGCCAGA CGGCAATATC	3780
TGTTTCAGAC AACTGCTGTA AACGTGCGG ATACTGATTT ATCCATTAC TTCTCCCTAT	3840
CAACTCCACC TGCAACGTCT GTTGGCAATA CTGACGACGC GCAATGATTG ATTGACGCTG	3900
GCGTAgcGDC TCTTCAACCA GAGAAAGCAA TTTGCCGGGA TCAACCGGTT TTTGCAAAAA	3960
ATCCACGCG CCTTTTTTTTA CCGCATCAAC TGCCATTGGC ACGTCGCCGT GCCCGGTaAT	4020

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AAGCAGAATG GGGATCTGTT GATCATCTCG GTGAAATAAC ATCATCAAAT CGATACCAGA	4080
GCAGCCAGGC ATACACACAT CACTTAGCAC AATACTGCG CAGTCTGGTT GATCCACGT	4140
CTGCGCCTCA AAAGGATTGT TACAGGCAAA AACCCGATAG CCTGACTGTT CAAGTAACTG	4200
TGTGTAGGCG TCCAGCACGT CAGCATCATC ATCAATCAGC AGAATCGAAT ATTCACTACT	4260
TAGCATCTTC CACATCCGTT AGTCTGAATT GCAGTACCAC ACAGGCATTG CTGGTCATCG	4320
TTGATGCCAG CCGTAATTCA CCTTTCATTT GCTCCATCAA CGACACACAA ATTGAAAGAC	4380
CAATACCCAG TCCTACTTCT TTAGTGGTGG TAAACGGCTT CAATAACGAA GGCAACAATG	4440
CCTCAGGCCA GCGCGGGCCA TTATCGCCAA TGAATACGTT CAGCGTTTTA CCCTGCATTT	4500
GCCAGTTAAC GGTAATGACA GCGCCTTGCC CACAAACATC AAGCGCATTC GCCAGTACGT	4560
TAACCAGTAC CTGCTGGGTT CTGACCTCAT CGCCTGAAAC TGTGGCTGTA CCTTGCGGCA	4620
GAACAAGCGT AGCTTGCAAA GGGCGATGAC GCATGGCCAG AAGTTCCCAG GCCGCACTGA	4680
ACATCTGTGC TAAATCAACG GAATGGAGTG ATATTTCCAG TTCGGCGCGC CGGGTAAACT	4740
GCCGTAGTGA ACGGATAATG GCGTCAATGC GACCAATCAC CCCTTCGGCT TTACCAAGCA	4800
TCATGCTGGC CTGTTCTGTC TGGSTCTGTT cAaTGcCTGC GGGCTGTAAA CAGATACATC	4860
GACAGCGCAT TTAGCGGCTG ATTGATCTCG TGGGCCAGCG TGGTCATCGT TTGCCCGACT	4920
AnCCGCaGct TCGCTGTCTG AATCAGTTCT TCCTGGGTGG CTCGCAGATC GGCTTCTATC	4980
ACCTTTTCGAT CGGTAATTTT TTGTTCAAGT TGCTGTTTTT GCACATTGAG CTGCCCAGAG	5040
GTATGGCGTA ATAATCCTGC AATTCTCCCC AGTTCATCAT TCCCATAAAC AGGAATAGCC	5100
GTTTCCGTGC CTCCAGACC AATTTCACAA ACGGCTGAT TCAGTAGGGT AAAGCGTTTC	5160
ACCAACCGTG AGCGGATAAA ATAATGGTTG AATACCCATG CCAGCAGTAA CGCCAGTGcT	5220
GTCGCCACCA GGATCAGCCC ACCgctAACG CGAACAATTT GTTCCATTCT TTGATTAAAC	5280
ATCTGCATTT GTTGATGAGT ACTGCGcAAGT GCGCTTCCAG TAACGTTCTG AAGCGACCCA	5340
GTGTGCTTc CCTGGTGCGA CTGGCATCCT CTAAGGCTTT TTGGGCGGTG ACATATTAC	5400
GCATCGTAGC CGGCATTTTG TTTTTTACGA TTCCCATATC CAGCAATTCA TCGATAGTCT	5460
GCCTCAGGGT AATGGTGCCA GGCCAGTCAT CCAGCATACG TATATTTTCA TCTGCCGTTT	5520
TTTTTCAGATT TTCAAAATAA CGGAGATGAG TTTCCACCTG TGTGTCGTCA TCACGTCCTG	5580
ATTTGAGTTC ATTGAGTCTG TCACGCAGAT CGTCAACAAT CTGATTTTCA ATGCGTGCCA	5640
GGGTATAAAC CTGCTGCTGT TCATTTTGCA CTTACGAGA TCGCTTCAGG TATTGCGCCG	5700
TATCGCCyTG TCGGGAGGCG ATTTGATCCA GCAGCGTTCC CTGCTGCCAG GTGAAATCCT	5760
GCACTAAAGA ATTAAGCTCG GTAGTAAAT CATCGTGTA CCAGTCAATC CTCGCTGATA	5820
GCTCACTCAC CTTTTCCCGT AGTAAAAACA TGTTGTAAAG CGCACGATCC AACTCGGATA	5880
ACAGTGATCG ACTGTCCTGC AAAAtGACCG TCAGTTGTTG GCGTTCCCGG GATGACAGCC	5940

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CCCGACTAAG CCGTTCTATG GTGTCGAGAT GCTGAATAAT CTGGGTACGA AGTTGCAATC	6000
GCACCGTGGT GTTGGGAGCC TGCAAAAATT CATTTAGCTG GTCTACCACC AGATTACAGGT	6060
TCCCTTCAAT AAGGAAAGCA GAGTGAATAC GGGGAAAATA CTCATCCAGC GAGTAACGAA	6120
TTTGTGAGCT TTGTTTCATG CATGAATACA GACTGACACT ACTGACAATC AGGGTCAGAA	6180
GTGCCCCCAT CAGAAATGCG CAACGTAAGC TGGTACTGAT ACTGACCTGT CTTAAACGCT	6240
GCCACAGCGT TATGTTTTTC ATTCAGCTC TTCCAGTTTT TTTATCGCCA GCGCTGGTT	6300
ATTCAGAAAC CAGAGTTGCC ATTCCATCAT TTGCTGCTCG GCAAAGCTTT TGTTCATCGAA	6360
CTGTGCCAGC CAGACGGGAT CTTCACTGCT GGCCGCTGCA ACGGGCACTT GTGTAAACAG	6420
TGCACGTATT TCTGGTAATG GTTTCTTCAG ACGTGCCTCG GACTGTGCA GCGCTCGCCA	6480
GGCATCTTTT AGCTGTGCTA ACCGAAAGCT AATTGCCGTA TCAAACAAGC GCTGCACCAG	6540
ACGCTGACGT TTCAGGATAA GGTGATAATT CAGCGGGGGT TGATTCATCA GGAGCTGTTG	6600
TTGCGTTGCC CGCGGATTGT CTGCGGCAAG TGGTGTCAAC GGATATTTTC CTGTATTGGC	6660
ATCGGCCAGA ATACGCTGTC CTTTCGGACT TAACAGGTAG TGAATAAAGC GACGGGCTGC	6720
ATCGACGTGT GGGCTTTTCC TGAGAATTGC AACGTAGGTG GGGGATACCG CAGACCGGGG	6780
GAAATAGGTA AAAGAGAGAT GGGGGTCATT TAACAGTAAA TTAGCATAGT TATCGATAAC	6840
GGGGCCGGCA ACGCCGAGTC CGCTTTTTAT TTTATCTCGT ACGCCAAAAC TCGGGGAGGA	6900
GATTGTCACC AGGTTTCCTG CACTTGTCAG CAACGTTTCC CATCCTTTCA CCCAGCCTTT	6960
TTGCTGTAGT AATGACTCAA CCATTAAATG GTTAGTATCT GAACGCGACG GACTACTCAT	7020
CAATAAAGCG TCCTGATAGA TCGGCAAAGC AAGATCGTCC CAGTCAGCAG GGGCAGGAAG	7080
GTGTTTTACA GAAAGCGCCG GACGATTAAT GAGCAGACCA AAACCTGATA TTGCTACTGC	7140
AACGGAGGTT GCACGGATCG ACTCCGGCAC CAGGTTTTGG CTTTCTGCGG GTGCATCATC	7200
AAACGGGGCC AGTTTCTGGT GCTCCTGAAG GTGCTGGAGC AGCATTGGTG ATGAAGTCAG	7260
GATAAGATCG ACGTTTTCTA CGTTGGCCGT ATCAAGCAAC TGTTCAGTG AGGCACTGGT	7320
GCGGTTAAGC GTACGGATCA TTACCGACTC AGGCTCTGTT TGCCAGCGCT GTATTATCCA	7380
CGCGGTAGCT CCGGGTGAGA ATGTGGTGGC CATCACCAGT TCATTTCTGT GAGCCCTGAC	7440
GGCCCCGGCG TCCATCAGCA ACAGTAAAAG AATCATGGTT TTGATGCCGA TTTGCGACCA	7500
GCTAAAAAAT CGGTTTGTGA TCCAGGTCAT AAATATTAAT ACACCGCAA AATCGCATTG	7560
AGACAAAAAT TACCCGTTTC AGACATTCGT CTGATAACAC GTCTGCTCAA AGAGACCGTT	7620
AATATATTAA TCAGAGATTA CCCGATAATC AGCATGAGAT TTGTTAATAT CCGCACATGC	7680
TAACAACAAA CCAGATAAAG CATAAATCTA CCTTGCTAT GCATCAATAA AATGGGTCAA	7740
AAACAGGCTT TGATTTTATT ATTTTGTGTC AATTGTGACA CATTTTTTCA GTTTGATGTT	7800-
TCATYTCAAT TATATGACTC TCATTGTCAG AATACTCCTG ATGTTTCATAT CAATATAAAA	7860

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TACAGGTGAA GACATGTTAT CAATATTTAA AACGGGGCAA TCGSCGGATA GTGTTCCGGT	7920
GGAGAAAATT CAGGTGACAT ATCGTCGCTA TCGTATGCAG GCGTTACTTA GCGTATTTCT	7980
GGGGTATCTT GCATACTATA TCGTCGCTAA TAATTTCACT TTATCGACGC CTTATCTTAA	8040
AGAGCAATTA GATCTCAGCG CCACACAAAT TGGCGTACTG ASTAGCTGTA TGCNTATCGC	8100
CTATGGTATC AGCAAAGGAG TGATGAGTAG CCTTGCCGAT AAAGCCAGTC CGAAAGTCTT	8160
TATGGCGTGT GGGCTGGTGT TATGTGCCAT CGTTAACGTT GSCCTGGGAT TCAGCACTGC	8220
ATTCTGGATT TTTGCGGCAT TGGTTGTTCT GAATGGTCTT TTCCAGGGAA TGGGCGTTGG	8280
TCCTTCTTTC ATCACTATTG CTAAGTGGT CCCTCGCCGG GAGCGTGGTC GGGTTGGTGC	8340
TTTCTGGAAT ATCTCTCATA ACGTCGGTGG TGGTATTGTT GCGCCTATTG TTGGTGCCGC	8400
TTTTGCCCTA CTCGGCAGCG AGCACTGGCA AGGTGCGAGC TATATCGTTC CGGCCTCGCT	8460
GGCTATCGTT TTTGCGGTAA TTGTGCTGAT TCTCGGTAAA GGTTCCTCAC GTCAGGAAGG	8520
TCTACCTCT CTGGAAGAGA TGATGCCGGA AGAAAAAGTC GTCCTGAATA CCCGACAGAC	8580
GGTAAAAGCA CCAGAAAACA TGAGCGCCTT TCAGATTTTC TGCATTATG TATTACGCAA	8640
CAAAAATGCC TGGTATGTCT CACTGGTTGA CGTATTTGTA TACATGGTGC GCTTCGGGAT	8700
GATTAGCTGG TTGCCTATTT ACCTGCTGAC GGTGAAACAT TTTTCTAAAG AACAAATGAG	8760
CGTCGCGTTT TTATTTTTTG AATGGGCCGC AATCCCTTCC ACGCTACTTG CCGGTTGGTT	8820
GTCAGACAAA CTGTTTAAAG GCGTCGTAT GCCATTGGCG ATGATTTGTA TGGCGCTGAT	8880
TTTCATTTGC CTGATTGGCT ACTGGAAAAG TGAATCGCTG TTTATGGTGA CAATTTTTGC	8940
TGCCATTGTT GGTGCTCTGA TTTACGTTCC ACAATTTCTG GCTTCCGTTT AGACTATGGA	9000
GATCGTTCCC AGCTTTGCTG TTGGTTCTGC AGTAGGCTTA CGCGGTTTTA TGAGCTATAT	9060
CTTCGGTGCG TCTCTGGGCA CCAGCCTGTT TGGTATTATG GTCGATCATA TTGGCTGGCA	9120
TGGCGGATTT TATCTTCTTG GCTGCGGTAT TATTTGTTGC ATCATTTTCT GCTGGTTATC	9180
ACATCGTGGT GCAATTGAAC TTGAACGTCA CAGAGCCGCA TATATAAAAG AACACTGATT	9240
ACCTTCCCCA GGGCCGTCTC CCTGGGGAGT GGAGTATATT ATGATTTATA AGATATCTGG	9300
AAATCAGAGA TTAATATGGA AATTTTATAA GACTGATTAC AATAAATGGA GATGGTATTG	9360
TCATGAGAAA AATGGATATC TTTTGTCTCA ATCAGATAAC GCATATAATT CGCAATTGTT	9420
ATGCATTGAA AATGCTAAAA AACAGGGATA CTCAGACGAA TCGGTCTTGC CACTTTTTCT	9480
ACATATTTCC TATATTCAGG AAAAAGGCTG GAAATGGTAT CAATGTTATG ATTGTGGATA	9540
TATTGTAAAA GAAACCTCTG TTTTTTTTTC GACATACCAG GAATGTGTCA ATGATGTTAA	9600
AAGGAATATA CTAGCATCTA TGTGTAGTGG TTGTAGTGGC ACAGTAAATT TGGCCACCTG	9660
ATTAAAGGTG ATATTCTCAC CACAACATAA AACACAAGA AAACAAAGCG TACCTTCTCT	9720
CCTGAGTTTA AACTGGAATG CGCCCAACTT ATCGTTGATA ACGGTTACTC ATACCGGGAA	9780

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GCTACTGAAG CTATGAATGT TGGTTTCTCT ACTCTGGAGG CATGGGTACG TCAGCTCAGA	9840
CGGGAACGTC AGGAGATCAC GCCTTCTGCT GCAGCACCAC TCACATCAGA GCAGCAACGT	9900
ATTCGTGAGC TGGAAAAGCA GGTGCGTCGT CTGGAGGAAC AAAATACGAT ATTAAAAAAG	9960
GCTACCGCGC TCTTGATATC AGACTTCCTG AATAGTTACC GATAATCGGG AAACTCAGAG	10020
CGCATTATCC GGTGGTCACA CTCTGCCATG TGTTCAGGGT TCATCGCAGT AGCTACAGAT	10080
ACTGGAAAAA CCGTCCTGAA AAACCAGATG GGCTGTATTA CACAGTCAGG TACTTGAGCT	10140
ACATGGCATC AGCCACGGTT CGGCCGGAGC AAGAAGCATC GCCACAATGG CAACCCGGAG	10200
AGGCTACCAG ATGGGACGCT GGCTTGCTGG CAGGCTCATG AAAGAGCTGG GGTGGGTCAG	10260
CTGTCAGCAG CCGACTCACC GGTATAAAGC TGGTGGTCAT GAACATGTTG CTATCCCTAA	10320
AAGCAACAGC AAACAGCGAC CACTGGGGAG CCCTGCATTG CGGGATTGTA TTGTTCAGCG	10380
GGCCATGCTG ATGGCGATGG GGCCGAGGAG AGTGATTTTC ATACGCTCTC ATATGGTTTT	10440
CGACTTGTC GAAATGTCCA CTACGCGATC CGCACGGTGA AACTGCAACT CACCGACTTC	10500
AGGGGAAACT CGGGGCCGCT GGGTAATCTC ACATAAAAGT TCTTCGGTGT CATAAACAAC	10560
GAGAGTATTT GATTCTTTTA TGGTGGCCTG GTGCAGAGCT GCCCTTTCCC AGGACCTCCA	10620
TATAATTTTT GTAGCGGCAG TCAGTGGCAC ACTCAGTTAA CTACTTTCAC TTCAGTGACT	10680
TTGAATGAGT CAGGGCTGCC GTTAAAGGTG TTAATGAAGG CTTGTATTTT CCACTTCTGG	10740
CCTGGTTCAA GATTGGATGC TGTGTCGATT GTTTGACCGA TAACGACTCC ATCTTTTAAN	10800
AGATTAAATT TTACATAAGC ATTTTGTACA ACAGAGTTTG ATTTATTTNC AGCATAACCC	10860
ACAATTGCCT TCGTCCCACT TGGGGTGTTT TCCACATGAA GGTTAG	10906

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ATGGTTATTT TTATTTCTCT CACCTTGCTT CATTTGAAAT AAAAACATAT GCATACGACG	60
CTGCCATTGA GCAGAAAAAT ACAGGAATTA ATGTTATGAG TTAACCATAA TACCTGTGTT	120
ATGAATATCT GACATAAACA AGAACAATTC ATATCTTCTG TATTCAGCAG AATAATAAAA	180
GTTCTGCTGC CATTCTCAAA CTTATTCTTC GGAATACGTT GTTTCATGAA AGAAGGGGCC	240
GGAATAAAAG CTGGTCACCG TAATGCTAAT ATTAATGCAG ACTACCGCCT TCTGGAATTA	300
ACAGTCATCA ACCAGCACAA ACCATTAGCA ATCAAACAAA TTTTAATTAA CAAAATTTTA	360
GCTAATACAA TTACTGCATT AACCCTCTG CAGTTTGCCT TCTCAATAAG TTACAGATGC	420

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CAAACAATAC TCTTTTATAT GTTATAACAT AACACAAACA ATAAATAAAG AACAGACGGC	480
ACTCCATTTT TCCACGTAAG TGAGCCATCA GAATCGCTTA TGAATGTGTA CGGCAGACGT	540
ATACTCGTGT TTTACTGCAG CAACCGGAGC AAAAGTTGCA CTTCCACAGC CTGGGTTAAG	600
TTTTTCATGC TTGTGGGCTC GTCTCCCTC CATTTCACCC GCGGGCAAAC AAGGCCATCT	660
TTTGTCTGGC CACACAGCAG ATGGAGAGTC GAATTATGCT GTCTGACGAC ACCGGGAACA	720
AATATGCCAT GCCTTCGCAC AATGAACCCG GGCATCATCG TTTTATCTTT ATAATCGAGA	780
CAGGTATGAG GGAAAGTCGG ATGATAAGCA GATAGTGAGT GAGGCGCTGG AACATGCGCG	840
TCTGGCAAGA GAAGTGTAC AGGTTACCTG ATGATATGGG GCAACCTGAT ATCTACTTAC	900
TTTTTTGCCT ACTCTCTTAC TTCATGCCAG CAGCGAGGGT ATCGACATTG TGTTTGAACG	960
CTGCCGTGTA GGTAGCAGCG AGGCCGCTAC TGTCGGTAAG TGCTTCCGGA TAAAGCTCTC	1020
CTCCCGCTTG TGCACCACTG GCATTGGCGA TTTGTTTCAC CAAACGGGGA TCTGTCTGGT	1080
TTTCGATAAA GTACAATTTT ACGTGCTCTC TCTTAATTTG ATTAATCAGT TTCGCCACAT	1140
TTTTACTGCT AGCTTCCGAC TCAGTGAGT ACCCCACTGG CGACAGAAAG CGAACCCCGT	1200
AGGCGGCAGC GAAATACCCA AACGCATCAT GACTGGTCAG TACTTTACGT TTTTCTCTTG	1260
GAATAGCAGC AAACGTCTGC GTGGCGTAAT TATCCAGTTG CTTCAACTGC TGGATATAGC	1320
TGTCACCCTG TTTTCGATAA TCGCTGGCGT GCTCCGGGTC TGCTTTGCTC AGGCCATTGA	1380
CAATGTTGTG AGCATAGACA ATACCGTTTT TCATGCTGTT CCAGGCGTGC GGATCAGTGA	1440
TGGTGATCCC ATCCTCTTTC ATTTTCAGTG TATCTATTCC GTTAGACGCG GTAATTACCT	1500
CACCTCTGTA GCCAGAGGCT TTCACCAGAC GGTCCAGCCA TCCCTCCAGT CCCAATCCAT	1560
TGACAAAGAC AACATCCGCC TGTGCCAGCG TTTTGCTGTC TTTCGKCGAC GGTTCAAATT	1620
CATGTGGATC ACCATCCGGT TGCACCAGAT CAGTGACATG AACGTATGGG CCGCCAATCT	1680
GGCTGACCAT ATCGCCCAGT ACCGAGAAAC TTGCCACCAC ATTCAACTCT TTTGCAATCA	1740
CCAGTGGGCT CACTAGTAGG CTGGACAGTG CCACAACCAA AATGGACCGT TTCATCTTTC	1800
CTCCTTCATC TCGTTGCTAT GTGTAAAAAC ACTTCTTGTC AGCGACATCT GCATAACATG	1860
CCGCCATTAG AGCCAAACAG AACTGAAAAG CAGAAAAACA GAGTGCTCGT GAGGATGACT	1920
GCAGGACCTG CAGGCAAATC AGCGTAATAA GACCAGATCA GTCCAACCAG ACTGGCGCAG	1980
GTACCAATAC CCACTGCAGC TAACAACATG ATGGACAGAC GTTGA CTCCA GAAACGCGCG	2040
CTGGCAGCCG GTAACATCAT AATACCGACT GTCATCAGGG TGCCAAGTAG CTGGAAACCT	2100
GCCACCAGAT TGAGTACCAC CATTGACAAA AACAGGCACT GGATCAGCGC CCGCGACCGA	2160
CGTGACAGAA CTTTCAGGAA AGTGACATCA AACGACTCAA TCACCAGCAC CCGGTAGATC	2220
AACGCCAGTA CCAGAACCGA ACCGGAACTA ATTATGCCGA TAGTGATCAG AGCATTGGCG	2280 -
TCAATAGCCA GAATGGAACC GAACAGCACA TGCAGCAGGT CGACACTGGA GCCACGCAAA	2340

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GAGACCAGGG TGACGCCAAG TGCCAGCGAG CCGAGGTAAA ACCCGGCGAA ACTGGCGTCT	2400
TCTCTCAATC CAGTGCGGCG GCTGACCACA CCAGACAACA TCGCCACAGA CAGCCCGGCA	2460
ATGAAGCCAC CGACTCCCAT CGCAACCAGC GACATGCCCG ATACCAGGTA GCCAATTGCT	2520
ACTCCCGGCA ACACCGCATG GGACAGTGCA TCACCGATCA GGCTCATACG GCGCAGTAGC	2580
AAAAAACAGC CAAGTGGCGC GCGGCTCAGG GTCAACGCCA GACATCCGAC CAGCGCCCGA	2640
CGCATAAAAC CGAAATCGCC AAATGGCTCG CACAACAGGT GCAGTAACAT CATGGCAGCA	2700
GGCCCTGCTG CGGTGGCGTG GCTGCAGCCG TGAGGGAATG GAGTATATCG GCACTTCTCC	2760
CCCATCGGTG GCCTTCCGCA CTGAGCATCA GTACATGAGG AAAGTATTTT TCTACCTGTT	2820
CCATGTCATG CAACACCGCA AGAATTGTAC GTCCTTCCAG ATGTAGCTGC CGAATAACAA	2880
CCAGCAGAGT ACGGATAGTC TGAATATCAA TGCCAGTAAA TGGTTCATCC AGCAGAATAA	2940
CCGACGGCTG CATCACCAGC AGTCGTGCGA ACAGTACGCG CTGTAACTGA CCACCGGAAA	3000
GTGTGCCGAT GTGCATCGGC GAAAATTCTG TCATACCGAC GGTATCCAGC GCTTCGATAG	3060
CTTTTTTTTCG CCATAGACCG GAAATACGAC CGAACATCCC GCTGTGTGGA ATACATCCCA	3120
TCAGCACCAAG ATCGTTAACA CTCAGTGGAA ACTGGCGATC AAATTCAGTC AATTGGGGCA	3180
AATAACCTAA CTGGCGTTGC CCCTGCGGTG CCATGCAGAA GCAACCACCC AGAGGTGGCA	3240
GCAGACCGGC CAACGTTTTA AGCAAGGTGG ATTTACCTGT GCCATTCGCT CCGATAATGG	3300
CAGTCAGTGA ACCGGTGTCA AAACATCCAT TCAGCGTACC CAGCGGGTGC TGTCCCGAAT	3360
AGCCAAATGC CAGTGAATGT AATGCGATCA TGTCAGTACC ACCGCCCAGG AAATAAGAGT	3420
CCATAACAGT ACCAGCAGCA CACCGACGAT ACCCAGTCGG GCTATTGCGG AAAAAGCATA	3480
AAGACTGACC ACAGTATCCC CCATCAAAAT TGTTATAGTA TAACATTATT GCTTTATGGG	3540
TGCCGATGAT AGGTAAGAAA ATGTGTCATG GCTTCTGCAG CGTAAGCATA CAGCGAGAGC	3600
AGTATTGACA GGGATGCGTT AGTCATTTAG CAGTGTAATG CGCTAAATAG NTGCGCGGAA	3660
TAGTAGATCA CTTTGAGGGT ACTCAGCCCG GATTGTGCGC TCTGATCAAT CGCCAAATCA	3720
AAACAAATCA CCAACCGAAC TGAGCAATGC CGATCATAGC ACCAATTTCC CGTGACGAAC	3780
GACACCGGAT GCAGAAAGCC ATCCATAAAA CACACGATAA AAATTATGCC CGCAGACTGA	3840
CTGCCATGCT GATGCTGCAC CGGGGCAACC GTATCAACGA CGTTGCCAGA ACGCTCTGCT	3900
GCACCCGTTT ATCTGTTGGA TGCTGGATTA ACTGGTTACT AAAATCATTC CCTGCCGGGC	3960
GTGCCCATCG CTGGCCATTT GAGCATATCT GCACACTGTT ACGTGAGCTG GTAAAACATT	4020
CTCCCGACGA CTTTGGCTAC AAGCGTTCAC GCTGGAATAC AGAACTGCTG GCAATAAAAA	4080
ATCAATGAGA TAACCGGTTG CCTGTAAAT GCCGGAACCG TTCGCCGTTG GTTGCCGTCT	4140
GCGGGGATAG TGTGGCTAAG GGTGTGCCA GCTCTGCGTA TCCGTGACCC GCATAAAGAT	4200
GAAAAGATGG CAGCAATCCA TAAGGCACTG GACGAATGCA GCACAGAGCA TCCGGTCTTT	4260

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TATGAAGATG AAGTGGATAT CCATCTTAAT CCGAAAATCG GCGGTGACTG GCAGTTACGC	4320
GGACAGCAAA ACGGGTGATC ACGGCGGGAC AGAATGAAAA ATATTATCTG GCCGGAGCGC	4360
TGCACTGCAG GACAGGTAA AGTCAGCCAT GTGGGCGGCA ACGGCAAAAA TTCGGTGCTG	4440
TTCATCAGTC TGCTGAAGCG GCTTAAAGCG ACATACTGTC GAGCGAAAAAC CAGCACGCTG	4500
ATCGTGGGCA ACAACATTAT CCACAAAAGC CGGGAACAC AGCGGTGGCT GAAGGAGAAC	4560
CCGAAGTTCA GGGGCATTTA TCAGCGGGT TACTCGCCAT GSGTGAACCA TGTGAACGG	4620
CTATGGCAGA CACTTCTCGA CACAATAATG TGTAATCATC AGTACCGCTC AATGTGGCAA	4680
CTGGTGAAAA AAGTTCGCCA TTTTATGGAA ACCGTCAGCC CATTCCCGTA GGGGAACATG	4740
GGCTGGCAAA AGTGTAGCGG TATTAGGAGC AGCTATTTAG GAGAACAGCT CGCTGACCCG	4800
GTTGACTATG ACTCAAGCCC ATGACGAAGA TAGCTTTCTG GATCAACATC GTTCAGTCTG	4860
CACGTCCCAA TCCAGCCACC AGCCACCAGC CACCAGCCAC CAGCCACCAG CCACCAGCCA	4920
CCAGCCAGGC TACAGTGCCA TCCCGACCTC CCCACGTAAA CCCAGGGACA GGCTAAAGGC	4980
AGAAAATGGG GAAGGCAGTA TGA CTCTCCG TGACACAGAT GCGGGTACCT GATGGGAGTG	5040
AGATCATCTT CCCCTCCCGG TCAGTTCCCG GATCAACACC GTGAGCAGCT CTGGCGAAGG	5100
TTTTTCCAGC GTCATTTTAC CGTAACGAAA TTCAACCTTA CAGGAACTGG CACAGACTGT	5160
GCACTAAGTG GCAGTGGATA AAAGCGGAGT AAGAGCCGCC ACAGGCTCTT TCTGCTCATC	5220
AGGCATTATC TCAACAGGTA ATAATTCAAC GCCAGCGCCA GAAGAGGTTG TTACCGGAAG	5280
ACGCCGCGCC CCCCTTCGTT CAGCCAGAGC CTGAGCCATT TGACCAGGAG GTTATCATTG	5340
ATATCGTGTT CCTGGTCAAT ACGGSCAACA GAGGTGCCTA CGACGTTTTT TCAGTTCGGT	5400
TATCTATTGA CTTAACTCTT TGGCCAGTAA TGCTGCAGCC CCCGTGCCAT GAATAAACGA	5460
GTGGTTCGAG ACCACGCAAC ATGCAACATC ATTCAGATCC CCCGCTAATA TTACAGGTAA	5520
TTCAGAAATCA GCAATACTTT TCCCGACCAT TAAAAGTTCT GAGTCACGAT CAGTTGACTC	5580
ATCACTTTCA GTCGGGCTCG GTGGAACAGG ATGAAGACAA TGTAATCTTA TTCTCAAACC	5640
TTCTGGCATA TGA ACTATCA TATTCATGGA GGAATTTCC TTGTCCACTA AATACTGTAT	5700
TTCTGCATCA CTTAAAATCA TCCAGGAATA TACATGCATG CCATATAAAT TTTCTTTCGG	5760
GCATTTTCAGG GAGTATGGAA ACACTTCATC CAGAGGTGAT AGTTTCTGTT CCCACCATAA	5820
GTTTGTTTCA AGAAGAACAA GTATATCAGG TTTTCTTTA TTTATAAGTT CAAGAATGGG	5880
TATATATTTT TTATTGGTCA TAAGAACATT GAATACCAGT AACTTTAAAC CCAGAAATCC	5940
ATCAGAGTCC TTTATTTCTT TTACCTGCTT CTTGCCAATT ACTGTATAAG GAATTATCCA	6000
TACCAACTGG TAAGCGACAC AAATTAAACT TATTATCCCA ACAAACAACCT CTGTAAATAA	6060
GTCAAGAAAA ACAACAGACA GAAAAACATT CAAAGTACAC AGCAAAAGTA TCTGTAGTCG	6120
GGGAAAATCC CATCCCCGA CAACCCATGA TGTATTACCG GAAACAGGGA TAAAAGTTAT	6180

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GACTGCCAGA AGGATAGCAG TAAAAATAAA AACACAAGTT ATCACAAATC GTCCTTGTT	6240
CTGAACCGGA ACACAAAAC TGCATATACG TTTCAAAAGT AAAAATACAC TGCTGCCACA	6300
AGATTTACAG CGTAACCGGA CAGCATATCC TGATTACGSA CAATCCATGA AACCGCCTCA	6360
CCAGAAGCGT CCATCACATC CGTTTTTTCC CTGTTTTATA TTCCCCGAAA CATTTTATTT	6420
TCAGGAATCT CCGGGCCTTT ATCCCGCATC ATTGCAAAAT GGCATCTGAA TCGATCATGA	6480
TTTGGCATCC ATCTCCGATC ACAGTTTGGC ATCACAATCG ATCAGGATTT GGCATGCTTC	6540
CGATCATTGA TTAGCATCCT GCCAGTCACT CCGGGAATTA ACTCTTTTCG CCACAGTCTT	6600
CATTGCCGTG TTTAAACCAA TGGAGACGGC AATGTCCAAA AAGAGAATAT CCAGGAGCAC	6660
TATGGATACC TGTTTTAAGA TCCTTCAGCT CAAGTTCGAC CAGAAGCTGG CTAACCGTTG	6720
TATCGGACTT GCAAAACACC AATGGGGATT GATCTCTATT TTGCGACACA GACGCATTAT	6780
CAATACATCG ATGGTGCGAT CAAATACCTC AGTGGTCTCA CCGTGGATCA AATCCAGCAA	6840
TTGCTCACAG ATTAAGACTC GTCGGGAGTT TTGAGCCAAC ACCAGCAGTA ACCCATATTC	6900
ACCTTGAGTG AAATCTACAG GCTGTTGATG AGCATCAACC AGCACGTAAC GGTCCGGGAT	6960
CAAGTGCCA GCCGTAAAAA AAACCACTCT ACTACCCTGC TCGACCTAAG CCTCGGCGTT	7020
CAGCCGCCTG AACGGGTATG GCAAGGGTGA AAAGAAACAG CATCCCCACA GTACCGACCA	7080
GACGACAGGA TGATGCTGGA ACAGAAAGCA TTCGCACCTC TCTTAGAATT AGACAGTGCG	7140
TACAGGATAC GTAAGACAGG GTGACGGGGC GGCGATAAAC TCTATTTACA AAGCTGAAAA	7200
TTTTCTGACG ATGAAAAACT ATTCAACAAG GTTATCTGAG GCGTTAAAT AACAGCTCG	7260
ATTAACGACT AACTTGAGGT GAATATGAAT TTAAAAATA TAATTTTAAG TACTGTTTA	7320
TCAATCGCTA GTTGTCATGC CCTGGCTGTA GGTAATTCTC CAAATAGCGC TATCTAACCT	7380
TCATGTGGGR AAACACCCCC AGTGGGGACS AAGGSCAATT GGTGGGGTTA	7430

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGATTATTCT GGCTCAGATT CATTTTTTCAT CAGTCGCTTT CCCCTATAAA CCGTAAGGTT	60
CCATAGTGTC GACGCTCTCG CTTAATTCCC ATATCGTCGA TAGTCTTATT AGCCGCTTCT	120
GTCAGGTCAG AAAAAGTATC ACGCTTCTTT GGGAGTTCAA GTCAGATTTC TCGCCGTCGG	180
GCGATGCGCT CAAAATGTTT GTCTGTATGG GGTCGCTTCA TCACGTCAAG CCATCGCGCT	240-
GCCGCTCTCC GCCAGAGTAC AAGCTCTTCC AGTTGTTCTG CTTTTATCT TATCTGTGGC	300

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GATGCAGTAT CCTCCTCCGT TTGTGTAAAT CGTTGAGTGG TGAATCACGC AAAGGGGCTT	360
CTTTTTTCTG ATCTATCCCC ATATTCTTTA GCGTTCTGGT CGCAGCATCT CTGATGTCGC	420
AGACACTGAA CCTTTGTATT TTCCATGATC TTGTGGAGTT TTCGATACAT CTGCTCCGAT	480
GCTGGGTTAT AAAGATCCGC TCTTTATCAT CCTTGGCTTG TGTAAAGCAAT TCTCCCCAAC	540
GTTCTGCTGC ACGCCGCCAT AACTCTCTTC TTTCCAGTTC CTCAGCTTTT TCATCATGTA	600
CCATTGCTGT ATCCCCGTTT ATCCAGTCTG AACCGCACCG GGTTTCCTGG AGAATGTTTT	660
CTCTGTGAAC TCAGGCTGEC AGATCATCGT TTCCGATGGA AGCATAATAA GCTTTTTCTG	720
CTTCTGCCGG ARGAAATATGG CCCAGCTTTT CCAGCAATCG TCGATTGTCA TACCAGTCCA	780
CCCACGTTAG TGTGGCCAGC TCCACTTCTG TCCGTTTTTT CCAGCTCTTA CGGTTATTAC	840
CTCCGTTTTG TAAAGACCAT TGATGCTCTC CGCCATTGCG TCGTCATACG AGTCGCCTGT	900
ACTCCCTGTT GATGCCAGTA ATCCGGCTTC CTTAAGCCGT TGC GGACACA TAATGAGAGC	960
CTTTATCGCT GTAATTGTCA ACGACGGATG AAAAGTGATC CACTTATATC TCCACCAACG	1020
GCCCAATATT GATCCACCGT TTTACTCAGG ATTAGCTTCT GCTATAACCC CGGCCTTTCG	1080
TTTCTGTCTG AGTCGATAGC TTTCTCCTTT GATTTGAACG ACATGTGAGT GGTGTAAGAT	1140
ACGGTCCAGC ATCGCTGAGG TCAGTGCTGC ATCACC GGCG AACGTTTGAT CCCACTGCCC	1200
GAACGGCAGA TTGGATGTCA GGATCATTGC GCTCTTTTCG TAACGTTTAG CGATGACCTG	1260
GAAGAACAGC TTTGCTTCTT CCTGACTGAA CGGCAGATAG CCTATTTCAT CAATGATGAG	1320
CAGGCGGGGG GCCATTACTC CACGCTGAAG CGTCGTTTTA TAACGGCCCT GACGTTGTGC	1380
CGTAGATAAC TGAAGTAACA GATCTGCTGC TGTGTGAAG CGAACTTTGA TACCTGCACG	1440
GACTGCTTCA TAGCCCATCG CTATTGCCAG ATGGGTTTTT CCCACACCTG ATGGCCCCAG	1500
TAATACGATA TTTTCATTAC GTTCTATGAA GCTGAGTGAG CGTAACGACT GGAGTTGCTT	1560
CTGCGGTGCT CCGGTGGCGA ATGTGAAGTC ATACTCTTCG AACGTTTTCA CCGCCGGGAA	1620
GGCTGCCATT CGGGTATACA TCGCCTGTTT ACGTTGATGA CGTGCCAGTT TTTCTTCATG	1680
AAGCAGATGC TCCAGGAAGT CCATATAACT CCATTCCCTGG TCTACTGCCT GTTGTGACAG	1740
CGCAGGCGCT GCGCTTATAA GGCTTTCCAG TTGCAACTGC CCGCGAGCG CCATCAGTCG	1800
TTGATGTTGC AGTTCCATCA TCACGCCACT CCTCTGCAGA ATGAGTCGTA GATGGAGAGT	1860
GGATGATGCA GGGGGTGTTT GTCGAAGTTC ACCAGATTTT CATCAAGATG CACGTCATAC	1920
TCTTTTTTCT CCGGAGCAGT GCCAGCATGG ACTGCTGTCT TCGAGCCAGC GATCGCAGGG	1980
ACGGGCCTGG ATTGTTTCAT GCTTTCGTTG GTTAGCGACA TCGTGAGCC AGCGCAGACC	2040
GTGGCGGTTG GCTGTTTCAA CATCGACAGT GATCCCCATC GGGCGCAGGC GAGTCATTAG	2100
TGGGATGTAA AAAGTGTTAC GGGGTGACTG CACCATCCGT TCCACCTTAC CTTTAGTCTG	2160 -
TGCCCTGAAG GGGCGACACA GTCGGGGAGA GAAGCCCATC TCCTTGCCGA ACTGCCACAG	2220

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CGAAGGATGG AACCGGTGCT GACCGGTCTG ATATGCGTCA CGTTGCAGAA CCACAGTTTT	2280
CATATTGTCA TACAACACTT CGCGCGGCAC ACCACCAAAG AAGCGGAACG CATTACGATG	2340
GCAGGTCTCC AGCGTGTCAT AACGCATATT GTCAGTGAAT TCGATGTACA GCATTCCGGCT	2400
GSTATCCGAGA ACAGCAACGA ACACGTGAAG CGGTGAGCGA CCATTACGCA TAGTGCCCCA	2460
GTCAACCTGC ATCTGTCGTC CGGTTTCAGT TTCGAACCGA ACGGCAGGCT CCTGCTCCTG	2520
AGGAACCGAG AGAGAACGAA TGAATGCCCT GAGAATGGTC ATTCCGCCAC GATATCCCTG	2580
GTCTCTGATC TCGCGAGCGA TTACCGTTGC CGGGATTTTG TAAGGATGAG CATCGGCGAT	2640
GCGTTGACGA ATATAATCCC GGTATTCATC CAGGAGTGAA GCAACAGCAG GTCGCGGCGT	2700
ATATTTTGGC GGCTCAGATT TTGCCTGCAA ATAACGTTTA ACCGTATTGC GGGAGATCCC	2760
CAGTTCTCTG GCAATCGCCC GGCTACTCAT TCCCTGCTTG TGCAGGATTT TAATTTCCAT	2820
AACTGTCTCA AAAGTGACCA TAAACTCTCC TGAATCAGGA GAGCAGATTA CCCCCTGGAT	2880
CTGATTTTCA GCGTTGGGTG TGGATCACTA TTGCACCGTT CGTGACAGTA ATGGATTGTG	2940
TCAGACGGAC GACGGGCCCCA TAACGCCTGC TCCAGTGCAT CCAGCACGAA TGTTGTTTCC	3000
ATGGACGATG AGACTCGCCA TCCCACGATG TATCCGGCGA ACACATCAAT GATGAACGCC	3060
ACATAAACAA AGCCCCGCCA TGTGCTTATC CCGGTAAAT CAGCTACCCA CAACTGGTCC	3120
GGGCGTTCTG CGATGAACTG ACGGTTTACA CCGTTGCATG CGGCAACAGC TTTCCGGCTG	3180
ATTGTCATGC GAACCTTTTG CAAACCCCAT ATATTTTACA CGATACCGTT CAACGGTAGT	3240
GAACCCACCA TCACCGCTCC CGGTATCCCG CTCATGCTGG TATACCCAGA CATGCAGGGG	3300
TTCCAGCGTA CAGCCAATCT TTGGGGCAAT GGAACAAATT GACGCCCACT ACGAGTCATA	3360
CGACTTTCCA GAACAATACG GAGCGCCCGC TGACGGACCA CCAAAGAGCC GCCATTATTC	3420
TTATTACCTT TAACTAATAA TGCCAATTCA GACCCAAACA CGGCATCATT CGCTTCAGCC	3480
TCTGCGCCAT TAATTAATGC CAGGACTTGG TCAAGAAAGC GTTGCGCTTC GTTTACATCT	3540
GTTGCTTGTC GCAGGTAATA AGGTATTCGT TCAACAACT CGGAACGTGA TAAAGGCTGA	3600
TGCTCCAGCA AAACCTCAAG CATTGCGGGC CGCAACAAAC GACGCTCAGC ATCAACATTG	3660
GGAAACTTAA CCTCAATGGC ATATGTGGCA AAATACTTAA GTTGCTCCTT AAGCCCCAAA	3720
TTAGGCATAA GAGAATCAAT TGAGCCAGAC GCCACTGCAG CGCTTGATTC AATTGTTTCT	3780
ACATACTCGT AGGAAGGTAC AACAACATCT GGAGCCAATG TTTTAAGCTC ATGGAGTTGA	3840
CGGATAATCG GGGATAGAAC CTCATCAGGA TTAAGTGAACC AATCAGTGGA CCAAATACGG	3900
CTAATTCTCC ACCCCAAACG CTCCAAAACC TCTTGACGCA AACGATCACG GGCAGATTTA	3960
GCTGAATGAT AAGCCGCACC ATCGCACTCT ATACCCATTA AGTAACAACC CGGATCTTCT	4020
ACCGACAGAT CAATAAAGAA TCCTGCAACC CCACCTGAGG TTCACACTCA AACCAGCGT	4080
GATTGAGTGC TTCCATTATA GCAACCTCAA AGTCACTATC CGGAGCCCTG CCCGTATACG	4140

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TCGTGAGGGA ATCTAATTTG CCACTTTCGG CAAACTGTAA AAAACCTTTC AACGAAATAA	4200
CACCAAATTT ACTGGTTTCA CTCGTCAATA CATCTTCAGA ACGCATTGAA CTAAACACAT	4260
GCATCCGTTT CTTTGATCGA GTTAAAAGCA CATTCAAGCG GCGCCAGCMA ACATCGGAAT	4320
TGACAGGCCU AAAGCGTTAA TAAACCTTTC CACCATGCTC AGAAGGTCCA CAGGTAAAGG	4380
AAATAAAGAT TACATCACGC TCATCACCTT GAACGTTCTC AAGTTTTTTC AAAAAAGTG	4440
GCTCTTCCAT GGCATATAAG CCATCAATTG CATCGTTAAA TTCAGTGCGA TTTCGGCGCA	4500
ATTCATCAAT AGCGCGCTCA ATCTGATCGC GTTGCTTGGA ACTCATGGCC ACTACCCCAA	4560
GAGATTTCATC CAGCCGGTGT TGCGCATGAT GAAGTACAGC CTCAGCAACT GCTTGGGCTT	4620
CTTCAATATT GTGTTGATTA GAGCAACGAC CTTTGTATAC ATAAGTAAAT TTGATTCCAT	4680
ACTCTGGAGA CTCAGCATTT GGAGAAGGGA ATATCACCAA ATCACTGTTA TAAAAATGGC	4740
GGTTAGAGTA TGCAATTAAC TTTTCGTGTC GTGAACGATA GTGCCAATGC AAACGTCTCA	4800
TAGGAAACAG TGGCAAAGCA GCATCCAAAA TGCCGTCAGT ATCACTTAAA GCCGCGACAT	4860
CATCGTCATC TTCTCCGGCG GAACTTCGAT CTGAAGTGCG ACACTGAATT TGGCCACCTG	4920
AACAGAGGTG ATATGCTCAC CTCAGAACAA CACAGGTGCT CCAATGAAAA AAAGGAATTT	4980
CAGCGCAGAG TTAAACGCG AATCCGCTCA ACTGGTTGTT GACCAGAACT ACACGGTGCG	5040
AGATGCCGCC AAAGCTATGG ATATCGGCCT TTCCACAATG ACAAGATGGG TCAAACAACT	5100
GCGTGATGAG CGTCAGGGCA AAACACCAA AGCCTCTCCG ATAACACCAG AACAAATCGA	5160
AATACGTGAG CTGAGGAAAA AGCTACAACG CATTGAAATG GAGAATGAAA TATTAAAAAA	5220
GGCTACCGCG CTCTTGATGT CAGACTCCCT GAACAGTTCT CGATAATCGG GAAACTCAGA	5280
GCGCATTATC CTGTGGTCAC ACTCTGCCAT GTGTTCGGGG TTCATCGCAG CAGCTACAGA	5340
TACTGGAAAA ACCGTCCTGA AAAACCAGAC GGCAGACGGG CTGTATTACG CAGTCAGGTA	5400
CTTGAGTTGC ATAACATCAG CCATGGTTCT GCCGGGGCAA GAAGCATCGC CACAATGGCA	5460
ACCCGGAGAG GCTACCAGAT GGGGCGCTGG CTTGCCGGCA GGCTCATGAA AGAACTGGGA	5520
CTGGTCAGTT GCCAGCAGCC TGCGCACCGT TATAAACGAG GTGGTCGTGA ACATGTCACT	5580
ATCCCGAATC ACCTTGGGCG GCAGTTCGCA GTGACAGAGC CAAATCAGGT ATGGTGCGGC	5640
GACGTGACGT ACATCTGGAC GGGGAAACGT TGGGCATACC TTGCCGTTGT TCTCGACCTG	5700
TTTGCAAGGA AACCGGTAGG TTGGGCAATG TCGTTCTCTC CGGACAGCAG ACTGACCATC	5760
AAAGCGCTGA AAATGGCCTA GGAAATCCGC AGTAAACCAG CCGGGGTAAT GTTCCACAGC	5820
GATAGTAATA ATGCCGGTAT CAGTTTTTAT CATCACTCTG TTTGCTGTTT AACCAGACTG	5880
GTGTGATTAC TGATGCAGTG AAGACCTTCC CGCATCCTGA CTCACACAGC GATCGACCCT	5940
TTGTGTCTTG CCCTGGACCT GTCGGTTGCC GGAAGCGCCT TCATGCGAGG CGTCTCCTCA	6000
CCGATGCGCG TGACTCAAGA AGGGCCTGAC GGTGTGTCTC GTTACTGTCC TGTCCGGGTT	6060

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ATCTGTCTGG AGATTCAACT CTGTTTCTCTC ACAGGAGCTC TGTTATGGCA GGTAAAGTTA 6120
CGGAAACCGC TGTTGTGGGT GCGTGGATA CACATAAAGA TCTGCACGTT GCCGCTGTCTG 6180
TAGATCAGAA CAATAAAGTT CTGGGGACCC AGTTTTTCTC CACAATACGG CAAGGTTACC 6240
GGCAGATGCT GGCATGGATG ACTTCGTTTG GGGCATTAAA GCGAATTGGT GTTGAGTGTA 6300
CTGGCACCTA TGGATCAGGT CTGCTTCGCT ATTTACAGAA TGCCGGGTTA GACGTTCTTG 6360
AGGTGACTGC GCCAGATCGG ATGGAGCGAC GCAAACGGGG TAAAAGTGAC ACGATTGATG 6420
CTGAATGTGC CGCTACGCC GCATTCTCCC GAATAAGAAC CGTCACACCC AAAACGCGCA 6480
ATGGCATGAT TGAGTCTCTG CGGGTATTAA AACTTGCCG AAAACAGCA ATATCAGCCC 6540
GCAGAGTCGC TCTCCAGATT ATCCATTCCA ATATTATCTC TGCCCCGGAT GAATTACGTG 6600
AACAGCTCAG AAATATGACG CGCATGCAGC TCATCAGGAC TCTGGGATCC TGGCGGCCTG 6660
ATGCCAGTGA ATACCGCAAT G 6681

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TATTCGCGCA TACGCGTTGC ACATGTTCTT TTGGCGAACG ATCATCGGCA ATACAGAGTT 60
CCCAATGGGG ATAGCTTTGA GCCAGGACAG AATCCAGACA GGCACGCAMG TAGATCTCCG 120
CTGGATTATA AACAGGAATC ACAATAGATA TAACTGGAGG GTGAGTCATA CTGGCAAGCA 180
TCAGACTCAC CWCTTCKTTG CCAGGCAACG AAGGTAATTC CACCGTTTCT ATCCATTCTT 240
CATAACCGAC AGAAGACGGG GTAACGCTGA ACGTYTCGTT ATAGAATGCT TGCAGGCGCT 300
CTATTGACAT ATCGCCATTG TSCATCAATA TGGATTTTWT GATTTTTTCT AGCGGCATGT 360
CACGATAGCT TTGGTGTTCT TTTTGAATGC GAGCCAATAG TGCAGACTCG ACTACTTTCA 420
CATCAACAGC CGCTATTTCA AACTGATTAA TTGCAAATTT TGCTGCCTGT TCTAATGGAT 480
CAAATCGTAA TGCACAAGAG GCGATTCCAG ATAGAACAAC GACTGACGCT GACCGCTCGT 540
TTATATGGCA ACGTTACTGT TTCAAACCTCA TTGAACCCTT TACCTGTATC CAAATRTAAC 600
TTAGCTAATC CTTGCTTTGG TTGGGCAATT AATAGAGATA TTAAATTGAT ACCATCCCTT 660
GCTAATATTT GAGAGCTGCT CCAAATCAAT AATGAAAAAT GGATCATTTT CCTCTGCAAC 720
CCAACTTTGT GAATTATCTA TATCTATCGA GAGCTGATTT GTTGCCAGAT AGGGCAGCAC 780
AACTGTATTT TGCATTTTAC TCACTGCAGG AGAAACGTCC CATGCTTCGC ATGGTTTCTT 840
ACCAAGTAAC ATCCCAT AAC GCTTAAATG TTCTCTTGCT GACAACCCGG TCTGTTTCAC 900

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ATCCAAATAG TTATGCAGAT ACCAATGTTT ATCAAAGTGA GCTAGCAACT CGTCTTGGTG	960
ATTTTAAACC ATCACTTTTA TTCTCCCTTA TTGACAGGCA GGCAACTGCG CTGCTCAAAC	1020
TTCCCATACA TAATGTAATG AAGCAGCGGA TTAATGCCTC CTTGGGCCAC ATCCGSATAG	1080
GTTTGCAAAT ACCAGCGAGT ATCAAACCTC TCACTAGGGC TATAACCTTT ATCCGCCCCC	1140
ACGCTAATAA AATGCTCAAG AGCTGAGAGC CCAGTGTCTG CAACCTCTGG GTAGCGATGT	1200
TGATACCAGA GTTCATCAAA CAATCCTGAA GCGGCAANTA CTCCGCGGCA CTCTCTGTAG	1260
CTGTTGTTCT GGATGGAGTC TCCTCCTTAA ATGTTCTGCC AAGAGCACGA ACTGGGGCTG	1320
TAATCTTCCA AGAGACGGTT CT	1342

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CGAAGGAAGC AGTNTGCNGC CTGCGCTGGC GGAGTTGCGC CTGTTCCAC CGATGATGCT	60
GTACATGAAT CCTCCGGCGA ACAGAGCGGT GAACTGGAAA CCATGCTTGA ACAGGCCGCG	120
GTCAATCAGG AACGGGAATT TGATACCCAG GTGGGGCTGG CGTTAGGGCT GTTTGAGCCG	180
GCGCTGGTGG TGATGATGGC GGGCGTGGTG CTGTTTATCG TCATCGCCAT CCTCGAGCCG	240
ATGCTGCAAC TGAACAATAT GGTGGAATG TAATTTACGG AGTTATCACA TGAATTCGTT	300
ATCCCGCACA CAAAAACCAC GGGCAGGTTT TACCCTGCTG GAAGTGATGG TGGTGATTGT	360
TATTCTTGGC GTCCTGGCAA GTCTGGTGGT GCCTAACCTG TTGGGCAACA AAGAGAAARC	420
CGATCGGCAA AAAGCCATCA GCGATATCGT GGGCTGGAG AATGCGCTGG ATATGTACCG	480
ACTGGATAAC GGGCGTTATC CGACCACTGA GCAGGGGCTT GAGGCGCTGA TCCAGCAACC	540
GGCCAATATG GCGGATTCCC GTAACCTACG TACCGGTGGA TACATTAAAC GACTGCCAAA	600
GGATCCGTGG GGCAATGATT ATCAGTATCT CAGCCCGGGT GAAAAAGGGC TGTGATGT	660
TTATACCCTG GGGGCAGATG GTCAGGAAAA TGGGGAGGGC GCTGGCGCAG ATATCGGTAA	720
CTGGAATTTG CAGGAGTTTC AGTAATCAGT GCCTGAACGC GGATTCACAC TTCTGGAAAT	780
CATGCTGGTG ATTTTCCTTA TCGGCCTTGC CAGTGCGGGC GTGATACAGA CGTTTGCAGC	840
CGCTTCAGAG CCGCCTGCGA AAAAAGCGGC GCAGGATTTT CTGACTCGCT TTGCGCAGTT	900
TAAGGACAGG GCAGTGATCG AAGGGCAAAC ACTCGGTGTG CTAATCGACC CGCCTGGCTA	960
TCAGTTTATG CAGCGTCGTC ACGGACAGTG GCTACCCGTT TCTGCGACCC GCTTATCGAC	1020
ACAGGTTACG GTGCCAAAAC AGGTGCAGAT GCTGTTACAA CCCGGCAGTG ATATCTGGCA	1080

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GAAGGAGTAT GCGCTGGAGC TGCAACGTGG TCGCCTGACG CTGCACGATA TTGAACTGGA	1140
GTTGCAAAAA GAGGCGAAAA AGAAGACGCC ACAGATCCGT TTTTCGCCTT TTGAACCCGC	1200
CACGCCGTTT ACGCTGCGCT TCTACTCAGC GGCGCAAAAC GCATGTTGGG CGGTAAAACT	1260
GGCACACGAT GGCGCGTTAT CCCTCAGTCA ATGTGATGAG AGGATGCCAT GAAGCGTGGA	1320
TTTACCTTGC TGGAAGTGAT GCTCGCGCTG GCGATTTTTG CGCTGGCTGC CACGGCGGTG	1380
TTACAGATTG CCAGCGGCGC GCTGAGTAAT CAGCACGTTT TTAGGAAAA AACGGTAGCG	1440
GGCTGGGTAG CTGAAAACCA GACCGCACTG CTCTACCTGA TGACCCGCGA ACAACGGGCG	1500
GTCAGGCACC AGGGCGAGAG CGATATGGCA GGAAGCCGCT GGKTCTGGCG AACCACACCA	1560
CTGAATACCG GTAATGCGCT	1580

(2) INFORMATION FOR SEQ ID NO: 68:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTTAACCATT ACCCAGCATT TGGTAGTTAA ATAGTCGTTA AAAGCATAAA ACATGGACAT	60
TGTGCCATCC CAGCTAAAGC ATCCATTACC GCCTGACAGG GATAAAAATA AAAAAGCAGG	120
GAACCATTTT TTCATCAGAA ATCACTTCCG TAATTACAGT TATTCATTTA GGTATGACTC	180
AGTTATAAAT CATGCTCATA CTGGCCGTGG TCTGGRAATC CCCGCCATTC AGTATCCCGC	240
TGCCATTACG AAAGGGCACT GAAGTAAAGG TGAACGTTGA ACGTGCTGTG TCCAGACCTG	300
CTGTCACTCC GTAACCATTT CCTGAACCAT TACCTAATAT AAGAGGTGTT GACATTCCTT	360
TTCCCTGATA CAGCGCTATA CCAAATGAG TTATATTTGT TGCCAGTACA TTATTCTGAC	420
CTCCTCCCAT AGTATTTCCC GTAACTTTTA TCCAGAGAGA GCCACTCTTA TACGGACAGG	480
ATATGCTTAT GGTTTTTGTG ACTTCACCAC GTGAGTTGTC CACGTGCTCA GGATTAATAT	540
TCCCAAAATC AACAACAATA TTCTGCCCCG TATTAATGGT GCATGGGGGG ATATAAACAT	600
TCCCCCTGAT GTTAATCTGC ACATCAGCCA GTACAGCGAC CGATGTCAGA AGCAACGATA	660
TAAATAATGA TAAACGAATC ATTCCCCTCC GGAGAGCGGT ACAGAAAACA TTTTATTTTA	720
CGAGATATAA AATTAACGTA TTTTAGTTGA TACTATTACG AATATGATGC AACCAGCGTT	780
GCTGTTGCAG AGAAAGGACC GGCTATCAAA TTCTGCATAT TCCCTTTATA TCCAAGTTG	840
GCATGAAGTG ATATAGTTTT ATCTGCATTA TTACCTGTGA TTTTCCGGG CGTAAATGGA	900
GTCCCTAAAG TTATCGCAGT CCCAATATTT CCTGCATTAC TGTTATAAAG ATAAACGAGT	960
AACCCATCAG AAGATGTGTT TGATGTATTC TGAACAAAA TAGCATTGTT ATAAGTGTTT	1020

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GTTGCCGTTA TCGTAACCTT CATTGTTCCC AGATTATAGG GACACCGCAT ATTCACAGTA	1080
AACTCTTTTT CGTGATTTCC ATTTTGACTC AGGSTCTGAA TCTCTACATC CTGCCAGTCA	1140
ACAGTTGTGT TGCTTACAGT ACAGGCAGGA ATAATCAGTT TTCCTCTGAA GGTCAGATTA	1200
TCAACTGCAT GTACATGCTG AGACATTAAC ACTGCCCCCA GCATTACCGG AAGACACAAA	1260
CCTCTTATCT TTTTCATCTG AAATATCCTG TACAAAAATT TTGCTAACGA TATGTCAATT	1320
CAAACGTGGC TGTTGCTTCA TAATCACCGG GTACCACACT CTTGCTCCGC AGGCTTCCGG	1380
CGTTGCCACA ACATACGCGC CGAAAGGAAG CTCAAGACTG TTTCCGGTAA CCTTTTCCCC	1440
CTGGCCTTTG TTATGGGAGG TGCCGGGTTT CAGCAGACTG CTGCCATCGG TGTCCAGCAG	1500
TGCAATGCCT AACCGGCCAG CATTCACTCC GGTTACCTTC AGATGGCCCG GGAGGGCGCC	1560
TCTTCCGTCC CCTTAAAGGT CAGGGTCACA ATTTTGCCAA CTGCTGTTGC ATGGCAGTTT	1620
TCCAGCCTGA TGACAAACGA CTCTGTCGGC GAACGTCCGG GCGGATACCA GAAATCCCTG	1680
GACGCCCCGG TTTTGAAGAC GACATGTTTA TTCAGACTGT CACCGGACAC ATGGCAGGGT	1740
CTGTCAAGCA GATTACCCCT GAATGCCACA TCTGAGGCTA TTGCCTGTCC GGCAGACAGT	1800
GCGGCAAACA GTAAAAGAGC GCCTGTGCTT TTTATCATCA CATTCCCTTA CTCATATTTT	1860
ATGCTCAGAC GCAGCATGGC CGGATTGCTC CTGGCATCAG AATACTCACC CTCCTGTGTC	1920
GCCCTTTTCC TCCAGGCGGC CAGCATCTCC TCCTGCCGCC GGTCAGGCCG GCACAGTAA	1980
AAGGTATCAC CATCGTGTAT AACAAGATGG TCACAGCCGG ATAGCTTACG GTCAGGAAGT	2040
AAAGCACTTC CGCTTCCGGG ACCGGTTACC AGTGAGCCGG AGACTGTCAT CGCAACGCCC	2100
CGTTTTCCGG GCTGAAGTGC ACCACCGTCC CCACATCCTG CCAGCCTCAG CATCAGAGGT	2160
GCTCCGGCTG CCGCAGAGTG ATTTTCCGGC CGGAGGYTTA ACGGCACCTC ATTACTCACC	2220
AGCGTGCAGG GTGAGGACAG CAGTGCACCA CTGACGGTCA GGCTTCCGGT GCGTCCCCC	2280
CGTTCATTTA TCCGGTAATG ACGCAACTCA TCTGCAGTAA AGACGTCATC GTATATACCC	2340
CGCTCTTCAG CCCGCAGGAA AGTATGGATG AAACCACTCA GCGACAGTGC AATAAGATAC	2400
AGTACTGCTG TTGTTTTATT CACAACCATA ATATCCCACC CGCATTTAAC CGTTATTGCG	2460
GTACATTATT TCTCTTTTTT CACAGAGCAA CGGCTACCAT TACAGATAAA CGACAGTACC	2520
GGGCGACCAC CATAGTCATT AATATAAGAC AGATAAGGGG TATTATAATT TGCCGATTTT	2580
ACTGTCTGCT CTGAACGGGG AGACAGCATC ACGGTTTCAA ACTCACCTTC CTCTGCCTGC	2640
TTTTCACTTC CTCCCAGACC AATAACAGTG ACATAATAGG GCGTTGGGTT TTCAATACGA	2700
TACCCACCGC TGACTTTGTT CAGAATTAAC TGGTCTCGCC ATACTTCATT TGGTCTGGTT	2760
TTAATTGCTG CCGGGCGATA AAAAAGCTTT ATTTTGGTCT GTAAGGCTAT CTGCAGTACA	2820
TTGGCCTTTT CACTCCTCGG CGGTATTTCC CTGAGATTAA AATAAAACAG TGATTCCCTG	2880
TCCTGAGGAA GTTTACTGAT ATCCGGTGTG GTACTCAGCC TGACCATGCT TTTGCGACCC	2940

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GGCTCAAGGC GCTGAACCGG AGGGGTGGCA ATAACCGGCC CTGTAATAAT TTTTCCTGA 3000
 TTTTCATTTT CTATCCATGC CTGAGCAAGA TAGGGCAGTT GTTGTATC ATTGGAGATA 3060
 TCAAGCGTCA TTGACTTCTC ACTCCCGTCA AACACCGCGC GGGTTCTGTC CAGCGAAACA 3120
 GCAGCGTCTG CCCC GGATAT AACAAACAGG GGGATGGCAG CCATCAGAAT CTTTTTTCGA 3180
 ATCATACTTA ATTTCCACAT TCTGTAATTT CACCTGGTCC GGAAATGGC ATAACCGCAT 3240
 T 3241

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AACGTGGATC TCCAGCTGAT CGGTGCCGTA TTCCAGGTCG TAAGTTTCAC TGATGGTTTC 60
 ACGCGGCAGT TTGCCCCGTT TACGGACCGG TACAAAGCCA ACGCCCAGAC CCAGAGCTAC 120
 CGGAGCGCCA AACAAGAAGC CACGCGCTTC GGTGCCGACA ACTTTGGTAA TGCCCCGATT 180
 TTTGTAACGC TCAACCAGCA AGTCGATGCT GAGAGCGTAA TTTTCGGGTC TTCCAGTAAG 240
 CTGGTGACAT CGCGGAAAAG AATGCCGGGT TTTGGGTAGT CCTGAATGCT TTTGATGCTA 300
 TTTTGTAGAT ACTCAAGCTG CTGTGCATCG CGGGKCATAA GTGTATGCCT GCTTGTTACG 360
 TGGGTACTCA CGGCGCGTTT TTAAACGTAT CAAAAGTT 398

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CAGTTNCNGT TCTCATAGAC AGATTGATAA AATCGTAAAC AGCCCCTAGC ATTCCCGTTT 60
 CCTTTGCACA CATATTCAGG CACGGGGATA AAGTATAAAG AATGTCGTAC TGCTGCTACC 120
 AGAGCAATAT TCCCCCTGA TGGCCGTATC AGAGATAGTA TGCCGGTATT TTGCGGGTGG 180
 TTCCCGTCAG GTTATCGTGT ACCTCCACGG TCGTAGTCAC CACCGGCATT CCGGCYTTTC 240
 TCAGCCTCAA AACATCAGCT GCAATACGCT GACTGCCGAA CCAGAACAGG CCGTCCAGTG 300
 CAGTACCAG CAACCCCGCC TCCAGCGCAT GCTTCAGCCG TTCACGGGGC GCTTTCACCT 360
 CCCGGGCAAT CTGCTGGTAT GCGATGATG TGTTTTTCATT CCAATCACC CGGCGAATAC 420

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GATGAGACAG	ATGATACCGG	TATGATCCG	GCACACCGGA	AAGGCTGGCC	TTCAGGCTGT	480
ACACGCAGCC	AAATCGTTTA	TCATTGAACA	CCACATTTTT	CTGGCTGATG	CCCCATTCTT	540
CACGCAGCGC	GGCAATCAGT	TGTGGTGTAC	GGGTAAGCAA	CAAGCGAAAA	GGCAGTTCAA	600
AACTGGTGAC	ATAATCCACA	TTCAACAGGG	CAATGCGAAG	TCGTCTTCT	GGTCCGGCTT	660
CTGTCTGCCG	GCACTCCTCC	AGGACATCCT	GCCACTGCAG	GCGAAGACGG	GAAGACTCAT	720
TCAGTTCTGT	AAAGCAGTAT	TTATCCGCCA	GATAGTCAAT	TCGTGTATGC	ATACTGAAGA	780
GTATTCCGTA	TAAAGATTCA	GCTGGCAAAA	CTTTATCAGT	CTGTAAAAAC	TAACGGAAGA	840
GTCGATATTT	CTCCCGACAA	TCACCGGATG	ATTGTTGCAA	TACCTCGTGG	CATCAGAGAC	900
TGAACAGCAG	TTTTTAACGC	AACGTATTGC	TCTGATGTAT	CAGGCCGGAC	AACCCGAAAA	960
CAGCCTTCCA	CCCGGCATTG	TCCGCCAGCG	CTTATCACCG	GCCAGGTCTG	TTGCAGTAAA	1020
TCCGCCACTT	GCGAACATGC	TTCATCAACT	GTGACACTGG	CCCGCGGATG	GCAAATGCTC	1080
GTCTGGCTGA	GCAGCAACAG	GCATCGCATT	GTTGCTCCTC	TATGTTGTTC	CCGCAACCAG	1140
CGTAATACCA	CCGGCGAGGA	TGGACAGGCA	GTGTGATTAC	GCTCCGTAAT	ACGTTCTGTG	1200
ACCCGTCGGT	GAAAGGAACT	ACAGAATGTC	TGAATCTGTT	GCCCGTTGAT	GTATCCTTCT	1260
GTCGAATGAA	GTGTGAAGTG	GATTGCCAGC	AGATGCGGCC	AGTGATCCAC	CGCCTGCTGA	1320
ACAAAACGCC	GGATTTCCCC	CGGCTCTGAA	AGTAAGGCTT	CGGTTATTTG	CACTATTTTA	1380
TCTCTGTTGA	ATTTGGTTAA	GTCGGTGCAG	ACGCATCAAC	ACAAGTACGG	TTCGATGCAA	1440
ACAGCTGTGA	CTGGCAATAT	GAAAGGAATG	ATGAATCAGT	CAGGATGACA	AAGTGCCGGC	1500
TGACCGGAGG	GGACGCAGGA	AGATTACCGG	GGGGACCAGC	ACCAGGGAAC	AGCGCCACAA	1560
TACCAGCGCT	GACACGTTGA	ACATTGCCAG	CGTACCGGTA	TCACAACACG	TTTCATACTT	1620
CTGCCCCCGT	GATTCTTCGA	TTCGTTACTG	TATCTACTGT	GACACTTCGC	TTTTATACCT	1680
GCGGCTGGAT	CGGCCCGGCT	TGATGAATCT	TCACTGATCA	GCTTATAAAA	CCCTCTGTCT	1740
GTCATACCGG	TGAAACTGGT	GATATAGTTC	ATGTCAATCA	GGGAATTATC	GGCACGCAGA	1800
AATACGCTGT	CGTGGCTTGT	TGTAGTCAAC	ATGGTCAGAA	TGTCTCTGT	GAGATTTATG	1860
AAGATTGTGC	GAATGCGGGG	AATCTACTGA	GCTGTGCTTT	CAGAACTGGC	CTGTTACGGG	1920
AKRSCAGGGA	TTACCGGCGG	GGTAACGGGC	TTCCGGATCA	TACACACCAC	GATTATCGCG	1980
GACAAAATCA	CTGAACGCCC	ATATCACCTC	TTTAAGTATG	TCTTCGCAGC	CCGGTACATG	2040
ACGATCCAGC	GCCACATCCC	GAGTGGTACT	ACTTTGATGC	GCCCGGTGAC	ACAAAGCCCCG	2100
GATTGTTCCA	GACATCCTGA	ATCAAACGCC	CCAGATTAGG	GGCGTCGAAA	TATGCCTCTC	2160
TGACCATTAT	ATTCCGGTGT	ACAGGTAGCA	GGTCAGAAGT	GACAATGCGT	CACCTGACGT	2220
TAAAAGTCAC	TACACCCAAG	ATGACGTTCA	ACAGCACCAT	GCGATTCAAT	GTAAGCCCCG	2280
GCTGTCTGTT	CCAGTACACC	AGGCTCAGCG	TTGTATGTGT	TAGCTGCATC	AAATACCAAC	2340

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GACAGCACTT CAGGATACAC AACCAGATGT GTAATGGAGT TATCTTCACC CAATACTTTT	2400
CCCCACGCCT GCTCAATCAG ATTTCTGAGA ACCACCACCT CACGACTCTT ACACCAGACA	2460
TCGTTATTAA GTAGCAGCAC CATAAGATAA GGAGTGGTAT CGTTAGTCAC AGCCTCCCTA	2520
CTCCAGAGAT AATATAAAGG GGTGGGCTCA ACAGATTTAT CTTTACGTCG CTTACACTGC	2580
AAATATTAG AAATGAGTCT ATGCAGTTCA CCAGTAAAAT CCGCCATCAG AGAGGGAATG	2640
GCCTTATTAA TACCAGGGCA AGGTATTAAT TTAAATTGTA ATAATTTAAT TTCAGGATGT	2700
GTGGCTGCAG CCCGATACAG AGTTGCAAGG ACACACTTTT GCCAGAGGGC GTTACTGGAA	2760
AGCTTAACGT TTGATTCTGT ATACATAATA AATCACCTTA CAGTTACAAC AGGTCAAAAA	2820
CCGCTGTAGC CAGAGTTACG CTGGCCTGAT GCTTTAGTAC CGGGCTTCGT CAGATAATCC	2880
AGACGCTCCA ATAAGCGCTG ATACTGCTCA GGGAAATCAG GATCATGAAT ATCCTGGATG	2940
TCACGTCCAT TAGCAGGGAA ATGAATAACG CAGCCCCCTG GATTAACAAT GCAGAAATCG	3000
TCCTGAGGTA CTGATCAATA CGGAGAGGAC TCTCGCGTGT GGTTTATTGA CACCACAGTG	3060
CAGATTCGGC GAATCCGCGA TCACGGTGCG ATTTCTGTTCC ACAGCACACA ATCATGACCC	3120
CGGGTTTTAT TCAGGTAAGC AGGATTGCGG ATATCCGGTG TCGCGCCTTT CTGTCACGAA	3180
CGGGGTAGGT GCGAAACACC GGATAAAATG CAGGCTGGCA ATACCTCTGA ACGCCCTGCG	3240
CAGAGCGGAT ATTTTGATT AAGTACTCGC ACCTCCGCAG TCCTGAAACA AGTCTGGCTG	3300
GTAGCTGTAA ACAGACTTCG TACATGTTGC TCTGGAATAG ATCCCCGTGC CACAGGCTTC	3360
GCAGAACTTT TTCCCGGAA AATGCTGCCC GCACATCACA CAATGCCACT CCAGCACGAC	3420
CGGTAATGGC GATAGAAACA TCGCCATATC CTCAATGTAA GGGTGGGACT TTTCCGGATT	3480
CAGACCACG CAGGCCGCCT TCTGTTGCGC GCTCAGGGCA TGTAATCGT GCTCAAACCA	3540
CGCCCCCTGA GCATCTGTCT GCAAAATCAA CCGACCACGA CAGGAAAGGC AGAAACAATG	3600
CCTGATATTT CTGCTAAGGC TGAGGCCGCA CTGATAATGT GTTACCCCGG CGTGATCCCC	3660
AGCCCCGTTT TTATACCGTT CATTACAGCCA CTCCCTCCTC ACTGAAGTGC CCTGTATGGC	3720
AGTGAGTGCA GTACCGCTCC CCATAATAAT CGTGGTGACA TTGTCTGCAG TGCCAGCTGG	3780
CTTTACGCAC CACGGGTAAG GCATCCGGTA CGAATTTCTG CAGACGCTTA ATCAGTTGTA	3840
TTTCTCTGCG CTCCGGTCTG ACATAAGGGC ACTGTTGACC GTGCTCCGTC AGCCCGTCGT	3900
CAGTGTGTTT AAACCAGGGA AGTTCAGTGT CGTATTGCGG ATGGTATCTG AGCGCACTGC	3960
CGCAAAGGTG GCAGGTGTAG CGGTCGTAAG GTGCAGTCTG TGCGGTACGG GCAGCGGTCA	4020
GACGTCCGTT GCCATCAAAT GCGAGAAAAG ATTTTGCGTA CATAGTATAT GTTCCTTACC	4080
GCCAGACGAC ACGCAGGCGT CAGCGTCCCT TTACGGGCAG CGTGGGCAGG GTGTGAATGG	4140
CGGTACAGTT AAGGGGGGGG TGGAAAATGG GCGGGCTGTT GTTACAGCAC TGTGGATGTC	4200 -
ACATCATGGC GTACCAACGT AAAAAATAAT CAGCAGGCCC GGATACATCG TTGTCGCCGG	4260

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ACATCAGCCC	GTCTGCTGG	TTTTGCCGGG	CTCAGCCCCG	ACTGCAGCCG	AAATTACGCT	4320
CACCAGTGGC	GTGAGCTTTG	GTATGTTCT	TCGCCAGATA	GTGAGCACGT	TCCAGCACCT	4380
GCTGAAAGCC	AGTGTATCA	CCGCGTTCCA	GCCACACCGC	CGGCGTGTCA	GGAAAATGCG	4440
CCAACGTGGC	ATAAGGCCCG	GCATCCACCC	CCAGGGCACT	GCACCGAGCN	TGWTTAATCA	4500
TCCCGGCCAG	TGACCCCGGA	TCGCGGTAAT	CGCCGGCAGC	ACACCAGGTA	TCCCGGTTGA	4560
CCAGCAGCAG	GAGGTGATAG	TGTTTTTTGC	CCCTGAGTAC	CCCGAACTCC	CGGGCCCAGG	4620
CGTAATGCAG	GGTGGTGGGA	TGCACGCGTT	TACCTTCAGC	NCGTTACGCT	TCTGTAAGC	4680
GTCGATTCGG	GCTTTCAGGG	CATTGATGAA	GCGGGATATC	ACAGCCGCGT	CCGTAGCTGC	4740
CGGTACATCC	GGGAGACGCA	GATCAACCCG	AAGTGCCGTC	AGGCGGGGAT	GAACATTGAG	4800
TGCGTGCCGC	ACCGTCTCAC	GAATACGTTG	CTGCCAGAAG	GGGTTGTATT	TGTAGGTCAT	4860
GGTTAAATCT	CCGTATGGTT	CATACGGAAT	AGCCACGTCG	TAAAAAATGC	GCAGAGCCCC	4920
TGACGTGGCC	ACCGACAGAA	CACGGCCTCA	GGCGCGTTGT	GATAACCCAG	CTATCGTTTTC	4980
CGGACTGACG	GTTGAATTTT	CTGCGTTGTT	TTCTTAATGT	AAAAAACCTG	CTACGGGTAA	5040
GGCTGTGAGG	AGGAAGTGAT	GGTGATACGC	AAAAAGAAGT	GCAGGGACTG	CGGAGAAGCG	5100
ACAGAGCATA	ACACGGTATG	TTGCCACAC	TGCGGTTCTG	TCGATCCCTT	CGGCTATTAC	5160
CGCAATACAG	ACAGAATATT	CACCCTCCTG	ATGGTCCTGC	TGGTTGTGGT	TCTGCTGATG	5220
ACGGCTGCGG	TCAGCGTGTA	TGTGCTGTGG	TAGTCGGAGG	GGCAGGGAGC	AGACGATGAC	5280
GTAAAATATC	TCCGGTGCTC	AGATATCACG	GCCGGTCAGA	CCGCAAACCA	ACGGTTAATC	5340
GTAACCGGAT	CAGGCAAATG	TGTGATTAGC	CCCCTGGCGC	TCATACCCGC	ACCGCAGACC	5400
ACCTTAAGTA	CTTCCCGCCC	GACACCATTC	CCTGCTCCCG	GATAATTTGT	TGTCGCTATA	5460
CCGCTTAACA	TCACCGATAC	CACACCGGCG	CAGATAGCAC	CGGATTCATT	GTAGAGATGA	5520
CTTAAGGTTC	AGGTAACATA	TTCCAGACA	GAAGCGGGAA	CACGATCGTA	AAGTTTGTTT	5580
ATGGTCAGTT	CTGCCAGCCG	GTGATCAACC	GCAGAGTTGA	AATTTTCCAG	CTCCGCCGGG	5640
GTGAGTTTAT	ACCGTGCGTG	GGAAATCACT	TTTTCCAGTG	TCTCCCGGGA	TGAACAACGA	5700
CGGAACTGAT	ACAGCCAGTC	TTCTTTGGTT	TTTACTTCCA	TTCGTCTCTC	GTTACTTTAT	5760
GCTGCGGTTA	ACAGGATGCC	GTGAGTATAC	CGCATGCAGA	CACTCTCCCG	CTCCCCCGCT	5820
TGCTGCGATA	CAACTTAACG	TTTCCAGGAAT	CCAGTCATCG	CACCGGGAAA	GGCTTTCTGG	5880
TGACAGGAAA	CGTCAGGAAC	AGGAGTTTCT	CAGACTCCCA	CTCATCGGAT	CAGGCTCAGA	5940
CAGGATTATT	AATACGCTCA	GTTATGTGT	CATATACAGG	GCATCGGGGA	TGAATATATG	6000
GGTATAACTC	AGAGCCTGTA	CTACAGCTTT	CACTGCTGAC	TGATTTTACG	TATCAGCGTT	6060
CATGTATCTG	CACTCTGATA	TAGAATACTT	CTACCGGAGC	TACTCTTACG	TTAGCTCACT	6120 -
CTCACATCAG	GCAACATCAC	TTATTGAGCT	CACTTACCTC	TTACCACTCA	CTACTTCTTT	6180

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ATATTTATAA TATCAATCAG ACAGCCTTAT CCCCCCGGTA ATATCTGTTG CTTCCCGCC	6240
AGCCACAGGC TTATTCACCA CAACCACCTC CGATAACAAC TCTGCAATTA TCAGAACGCC	6300
TGCTTCTCTC CCTGTCTCA CGAAACTAT CCCCTCTTTA TCGCGCGTGC GTGCGGAAGC	6360
ATCTTTTCGC AACAAACCACC CGGGATTCCG CTACGGCTCT GCCATCGCAA TCCCCCGTT	6420
TATCTCCGGA CAGCCACATT CCCGATTATT TTTTACGTTT CTCCCCGGTT GTTATGCCGG	6480
TGAAGGTGGT GCGTCGTTTT CATCACCACA CCGGTTGCGA TTAACAACAT CCGGAGGAAC	6540
ATTCTCATGA CCACACCCTT TTTACTGATG GATGACCAGA TGGTCGACAT GGCGTTTATC	6600
ACTCAACTGA CCGGCCTGAG CGATAAGTGG TTTTACAAAC TCATCCAGGA CGGAGCCTTT	6660
CCGGCCCCCA TCAAAGTGGG CCGCAGCTCC CGCTGGCTGA AAAGTGAAGT GGAAGCCTGG	6720
CTGCAGGCGC GTATTACACA GTCCCGTCCG TAATTTCTGC CCCTTATCCG TTCACCCGCA	6780
GCAGACGCCT CCCCAGGCTG CCGTTGACAT TCTGCTGCCT GTTTTATCCC CGTGAGGAAT	6840
ATGAAAATGA AACACAGTA CCAGACCCGC TACGAATGGC TCCACGAAAG CTACCAGAAA	6900
TGGCTGACCG GCTTCAMCCG GCACGCCGTA TCCTGGGGCG TGTGTCATCC GAATATCTAC	6960
TATTTCCATA ATCTGACGCC CCGGTGGGTG TCATTCAACG GCGAACAGTC GGAGATTGCC	7020
ATTGTTCCCG GCAGTCTGCA CCGGCTGATT TATGGTCATG ACAAACGGGC CATGCCGCCC	7080
CTGGATGATG ATCTGGTGGT GAATTTATGC ACCAGTGAGA ATCTGCTGGT TCATCATCCG	7140
ATGCTGGAAG GCATTCTGCT GTCTGAGTGC ACGCGCCTGC ATAAAAAATC ACTGGCGAAC	7200
AACTGATCA GTATATTCCG TCAGTTTGAC GGCACGGAGC TCGTCTCAA ACTGGTCTGG	7260
CTTTGCTGGT TTGATTTAAT GACCGGAAAC TGCCTTGACG ACTGGACGGA GAACCTGNAA	7320
CGGAAATCAG AAAAAGAGCT GGAGAAATGG ATCATTGAGC GCCAGAACCG GAACGCACCG	7380
CTGACGAATC TGATGGATCA GTACGTGCTC CTGGCATTCC GCACAACGGT TGACGATAGC	7440
CGCAACTGAT GTCTGCATGC TGCCSGCTGA AGCCATATTC ACGGGGCAGG GACGCCCTG	7500
CTTCCGCAAC AATCCGGGGT AATGGCGACG TACGCCTGCA GAGTGTGTTT ATCGTTGTCA	7560
CAGCCGGACA AGGTGAATAC CGTTGATGAT GCGGGGATGA ACCTGCTGGT CCACCGCGCT	7620
GTCATCAGA CGCGTCAGCG TGTATGGACG CCCCATCGA ATGGTTCTTC CGCCAGAGTG	7680
CACAGAAATG AGGCACGGAA CGTTACCTGA AGGGTGACCG GCACGGACTG CAACTTGTTG	7740
CCATTGATGG CGCACAAGTC ACATACAGCA GAATGTCGTG ACCGCACCTT ACCGGTGAAG	7800
CGAAACGGTG CTGCCCCACT CCACCACCAT CCCGGATAAC GCCATTACGC TGTCTGATAA	7860
GCGCTTTTAC AGCGCAAATC TGGTGCAGAA AAGCGTAAAG CTGACCTGCC GGAGCAGGAT	7920
GTGGGCATGT TGCGGGCTTA CAACCTGATA CGGCATGAGG CACTAAAAGC AGCATCAGAA	7980
ATCAGCCTGA GTTCGCGTTC CGGTTTATCC CGACAGAGAG GACAGTGCCG GGCAACACGG	8040
TGTCACCGGG GAGCATCCCC AAACGACCGG AGCATCTGCG GGATGCTCTG TAAGTGGTGT	8100

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TAAGGTGGGC	GGTTAAGGTA	TCAAAAAAAT	CGTTATCCTG	TGAAAGACAG	TGCGCTCTGC	8160
TGAAGTGAAC	GTCACCTGCCG	GGAAGCATCG	GGTTTCGCTA	CCGACAGTC	GCGGTAACGC	8220
GTTTACCGGC	ATCTGTCTGT	GTGGCAGGGA	TGGCTGATAT	TGTGGTTAT	ACCAGCGGCA	8280
GGTGCCTCT	GTTATCTGTA	AAATCAGGGC	GTGCGGTAC	ACAACGCCTC	GTTGATGCCG	8340
GTCACCTGAAC	GAATCATCCT	CTGACGAAAA	CAACCGTCGA	TACAACGCCG	GCGTAAAAAG	8400
AAAACCGGAA	ACCATCTTGT	GCACGACAGG	TACTCAGGGG	GGTATAACGC	CTGCGCACCA	8460
TCACATCCGG	GAACAGGGCT	GCTCCTCAGT	GTCTTCGTGT	GGCGAAGCAT	CTGCAACCGG	8520
ACGGTACTGC	CCTCAGAGCA	ATCTCCCTGC	TGCAGTGCAC	AGAGTAAGCC	GGAAAGCTGG	8580
TGAATGCCGC	CATGACACAC	TGCGACGTGG	AGAAACAAAC	GACACACTCC	GTCCGCAGTA	8640
ACACTGAAGG	TAGTCCCGCA	AACCTCAGAC	TTCTTCCTGC	ACGTTATCAG	CGGACTGAAC	8700
CCCGGTCAGC	CACTTAAACC	TGCTAATCGT	GTTGCTGCAT	ACCCGCCCGG	CCGGAAGGTG	8760
TTATGAAGCC	CGCCACCGGA	GCGCTTCTGC	AAATATCCGG	GGAGATAAAA	TTTTCGTGAC	8820
AGGATGACGG	TCGTGCTGCA	GACGTAAAGC	CGCAGGAGCG	GACACGACAG	ACAGTGTTCA	8880
CTGTGGCGTC	CTTTGCCGTC	GGTATCGTGC	TCACGCTGAG	GTCCCGGGGG	TACACCTGAC	8940
GACAAATACC	TGCGATTCCC	GGGACGGTCT	GTTCTCCGTA	AAATAAAGAA	AATGCGGGAT	9000
GCCTCCCGGA	CTGCAGAGAA	GAGGGATTGA	CAGACAGTGT	ATATTGCGTA	CGATTACAGG	9060
GGAAAAACAC	AGTAAATATG	GAGGTCAGGT	CCGAAAACAA	CCTACGAAAT	TTCTATGAAA	9120
AACGATTGAA	AAAATCATCA	AATTCAGTTC	GTTTTTCTAT	GGTAATTTTT	AAACACTCCC	9180
GATGATAACC	TGTTGTATGT	GCATGTGGGG	AACGCACCGA	AAACATCAGA	ATCATCTGAA	9240
AAAAACAACG	AACACACCAG	AAAAACAGGA	GCAACCATAA	CGAAGCAACA	TATTGATTTT	9300
AAACAGAATT	TAAGGTTAAC	AGACAAAAAA	CACTTTCAAC	TGAAGGAGAA	ATATACACTG	9360
GCGACAGTGC	AGGGTTTTTC	ATGCAAAAAA	AATGAGCTTT	TATCTCCGGC	GCATACTGAC	9420
CGGGATGCAG	CCATGACAGA	GCAAAAACCA	TTAAATATCA	GGAGGTAAA	CACACAAAAA	9480
GCTGACATGC	ATCAGGGAGC	AATCCCTCAC	AACAGAGGCT	GAGCGGCAAC	GCTTCCTCAC	9540
AGGACGGCAT	TCCTGAAAGG	ACAGGCAGCC	ACGGCTTTTT	ACTGCCCGTA	TCCGGTATAT	9600
TTATCTGCCG	TGACGTGCAG	AGGATTTTGT	GTTTCCGGAA	ATCAGGAAAA	CAGGAGAACC	9660
GCGGGAGATA	TGATGGAAAA	AGAACCGGAT	GATATCTGCG	CAGACTGTCC	GAATATTGAT	9720
GCAATAAAAC	GGCACAAACA	ACAGGCCGGA	GCCATCAGGG	AATACACTGA	GTGGTTAAAA	9780
AAACAACCGC	GTGCTTCTTA	CTTTTTTCTC	TTCCGGTTGT	ACGCATACCT	TCAGAATGAA	9840
GTGATATCCC	GAAAACAAAA	ACATTCGCTC	ACCAGCGATA	ACAGCCATCC	CCCGGAATCT	9900
GATGTCACCC	CTCCGGATTT	AACCCTTCCC	CGTCGCTACT	ACTGTGATTA	CGGTTACACG	9960 -
CCCTACCCCA	TGATGGGCGG	ACAGATGTCT	GTTTTTGCCA	CAACGTCAGA	AACCACCAGT	10020

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TCGACGAATG CAGTCCCCGG AAACGCAGTT ACCGGGAATG AGACTGAAAA GCATGAAAAC	10080
GCGGTACCGG CGACATTCCC CGTCAGCCGT TCTGCAATGC CCCCAGAAC TCTGCGGTTT	10140
GCCACGGGTT TTCCATCGCA ACCACTGCTT GCCGGTCCCC GGGAAAAGCC GATGCGCACC	10200
GTGCATCCTG ACATCCACAG CGAAATTATA TGGTTCTGCT CCACTTACCT GCTGAAATCC	10260
GGACCACAGA TTACGAAGAC GATTATCAAC TCAGTATTCT CTGAATGGGC CCGCATCAGC	10320
AATGATTACC CCTCCCCCTT TTCGTGGGTG GACAGCAGGG ACAGTGAACA GTGTGACTGG	10380
TTATGGAACG CCATGCAGCT CCGGTGTGTG GGAACCCCGC TGAATCCCCT TACCCCGGAG	10440
CAGAAATACT GGTTCGCTG CGCCACGTTT GATAACTGGG AGGGCTGGAA TGAGCAACAG	10500
ATACAGTTTT TACTGAAAAG TAATCCCAGA CGAAACAGAG CGAAGTTTAC GGTCACCTTC	10560
GGCCCTCCCT GGATTCAGCA TAAAGCCATT CTTCTTGATG AGCTGAAGAG TGCCCGGGAG	10620
CAACAAAAAA GGCAGCATGA ACGCGCTGAT GGTTCGCTCC CGCTGAAACT GTCCGGAAAA	10680
ATCCACAAAC ACCTTGAAAG TATTGCCCCG AGTCGTGGTA TCCCCCAAA AAAACTGCTG	10740
AATGAAATGA TTGAGCAGGC GTACCAGGAC TCAGTGGTGA ACAGCCGGAA TAAACCACTG	10800
ATTTAAATA ATTTAGACA GATATTATCT CCGTGAATCC CCCGCCACCT TTCCGGTGCG	10860
CGGGGTTTTG TCTTTTTTCA CCGGGAATAC ATGTATGAAT CCGTCTGATG CCATTGAGGC	10920
AATTGAAAAA CCGCTCTCCT CCCTGCCTTA CTCGCTTTCC CGTCACATCC TGGAACATCT	10980
GCGCAAACTC ACCCGTCACG AACCCGTGAT TGGCATTATG GGTAAAAGCG GGGCCGGTAA	11040
ATCCTCACTC TGTAATGCAC TGTTTCAGGG GGAGGTCACC CCGGTCAGTG ATGTTACGCG	11100
CGGCACCCGG GAAGTGCGGC GCTTCCGTCT GAGTGGCCAT GGTCACAACA TGGTTATCAC	11160
TGACCTGCCC GGGGTGGGCG AGAGCNGGGA CAGGGATGCA GAGTATGAAG CCCTGTACCG	11220
TGACATTCTG CCTGAACTGG ACCTGGTACT GTGGCTGATT AAAGCCGATG ACCGTGCCCT	11280
GTCTGTGGAT GAGTATTTCT GGCGACACAT CCTGCAACGC GGACATCAGC AGGTGCTGTT	11340
TGTGGTGACG CAGGCCGACA AAACGGAGCC CTGCCATGAA TGGGATATGG CCGGCATTCA	11400
GCCCTCTCCC GCACAGGCAC AGAACATTCG CGAAAAAAGC GAGGCGGTAT TCCGTCTGTT	11460
CCGGCCTGTA CATCCGGTTG TGGCCGTATC GGCCCGCACC GGCTGGGAAC TGGATACGCT	11520
GGTCAGTGCA CTCATGACAG CGCTTCCCGA CCATGCCGCC AGTCCCCTGA TGACCCGACT	11580
GCAGGACGAG CTGCGCACGG AGTCTGTCCG CGCTCAGGCC CGTGAACAGT TTACCGGTGC	11640
GGTGGACCGG ATATTTGACA CAGCGGAGAG CGTCTGTGTT GCCTCTGTTG TCCGTACGGC	11700
CCTGCGCGCT GTTCGTGACA CCGTGGTCTC TGTTGCCCGC GCGGTATGGA ACTGGATCTT	11760
CTTCTGAACC TGTTGTGGAT GATGTCCTCC CTGCCTCTGA GTCTGCTCAC AAAAGCGCTG	11820
TTTTCGTTAC TGTCTCTCTT GTCCGTGCAA TAGCTCAATA ATAGAATAAA GCGATCGATA	11880 -
ACTATTTTCA CGATCGTTTA TATCGATCGA TATGCTAATA ATAACCTTTA TTACCAACAT	11940

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GCGCAGATAC GCACAGACAG ACATTCAGGG GACGACAGAA CAACACTTCA GAAACTCCCG	12000
TCAGCCGGAC CTCCGGCACT GTAAACCCTTT ACCTGCCGCT ATCCACATCT GTGGATACCG	12060
GCTTTTTTAT TCACCCTCAC TCTGATTAAG GAAATGCTGA TGAAACGACA TCTGAATACC	12120
TGCTACAGGC TGGTATGGAA TCACATTACG GGCCTTTTCG TGGTTGCCTC CGAACTGGCC	12180
CGCGCACGGG GTAAACGTGG CGGTGTGGCG GTTGCACTGT CTCTTGCCGC GGTACGTCA	12240
CTCCCGGTGC TGGCTGCTGA CATCGTTGTG CACCCGGGTG AAACAGTGAA TGGCGGAACA	12300
CTGGTAAACC ATGACAACCA GTTTGTATCC GGAACAGCTG ATGGCGTGAC TGTCAGTACC	12360
GGGCTTGAGC TGGGGCCGGA CAGTGACGAA AACACCGGCG GSCAATGGAT AAAAGCGGGT	12420
GGCACAGGCA GAAACACCAC TGTCACCGCA AATGGTCGTC AGATTGTGCA GGCAGGAGGA	12480
ACTGCCAGTG ATACGGTTAT TCGTGATGGC GGAGGGCAGA GCCTTAACGG ACTGGCGGTG	12540
AACACCACGC TGGATAACAG AGGTGAGCAG TGGGTACACG GGGGAGGGAA AGCAGACGGT	12600
ACAATTATTA ACCAGGATGG TTACCAGACC ATAAACATG GCGGACTGGC AACCGGAACC	12660
ATCGTCAACA CCGGTGCAGA AGGTGGTCCG GAGTCTGAAA ATGTGTCCAG CGGTCAGATG	12720
GTCGGAGGGA CGGCTGAATC CACCACCATC AACAAAAATG GCCGGCAGGT TATCTGGTCT	12780
TCGGGGATGG CACGGGACAC CCTCATTTGC GCTGGTGGTG ACCAGACGGT ACACGGAGAG	12840
GCACATAACA CCCGACTGGA GGGAGGTAAC CAGTATGTAC ACAACGGTGG CACGGCAACA	12900
GAGACGCTGA TAAACCGTGA TGGCTGGCAG GTGATTAAGG AAGGAGGAAC TGCCGCGCAT	12960
ACCACCATCA ACCAGAAAGG AAAGCTGCAG GTGAATGCCG GCGGTAAAGC GTCTGATGTC	13020
ACCCAGAACA CGGGCGGAGC ACTGGTTACC AGCACTGCTG CAACCGTCAC CGGCACAAAC	13080
CGCCTGGGAG CATTCTCTGT TGTGGAGGGT AAAGCTGATA ATGTCGTACT GGAAATGGC	13140
GGCCGTCTGG ATGTGCTGAC CGGACACACA GCCACCAGAA CCCGTGTGGA TGATGGCGGA	13200
ACGCTGGATG TCCGCAACGG TGGCACCGCC ACCACCGTAT CCATGGGGGA TGGCGGTATA	13260
CTGCTGGCCG ATTCCGGTGC CGCTGTCAGT GGTACCCGGA GCGACGGAAC GGCATTCCGT	13320
ATCGGGGGCG GTCAGGCGGA TGCCCTGATG CTGGGAAAAG GCAGTTCATT CACGCTGAAC	13380
GCCGGTGATA CGGCCACGGA TACCACGGTA AATGGCGGAC TGTTACCGC CAGAGGGGGC	13440
ACGCTGGCGG GCACCACCAC ACTGAATAAC GGTGCCACGC TTACCCTTTC CGGGAAAACG	13500
GTGAATAACG ATACCCTGAC CATCCGTGAA GGTGATGCAC TCCTGCAGGG AGGCGCTCTT	13560
ACCGGTAACG GCAGGGTGGA AAAATCAGGA AGTGGCACAC TCACTGTCAG CAACACCACA	13620
CTCACCCAGA AAACCGTCAA CCTGAATGAA GGCACGCTGA CGCTGAACGA CAGTACCGTC	13680
ACCACGGATA TCATCGCTCA TCGCGGCACG GCCCTGAAGC TGACCGGCAG CACCGTGCTG	13740
AACGGTGCCA TTGACCCAC GAATGTCACC CTCGCCTCCG GTGCCATCTG GAATATCCCC	13800
GATAACGCCC CGGTTCACTC AGTAGTGGAT GACCTCAGCC ATGCCGGACA GATTCATTTC	13860

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ACCTCCGCCC GCACAGGGAA GTTCGTACCG GCAACTCTGC AGGTGAAAAA CCTGAACGGA	13920
CAGAATGGCA CCATCAGCCT GCGTGACGC CCGGATATGG CGCAGAACAA TGCTGACAGA	13980
CTGGTCATTG ACGGTGGCAG GGCAACCGGA AAAACCATCC TGAATCTGGT GAACGCCGGC	14040
AACAGTGCCT CGGGGCTGGC GACCACCGGT AAGGGGATTG AGGTGGTTGA AGCCATTAAC	14100
GGTGCCACCA CGGAGGAAGG GGCCTTTGTC CAGGSGAATA TCTGCAGGC CGGGGCCTTT	14160
AACTACACCC TCAACCGGA CAGTGATGAG AGCTGGTATC TCGCAGTGA AGAACGTTAT	14220
CGTGCTGAAG TCCCCCTGTA TGCCTCCATG CTGACACAGG CAATGGACTA TGACCGGATT	14280
CTGGCAGGCT CCCGCAGCCA TCAGACCGGT GTAAGCGGTG AAAATAACAG CGTCCGTCTC	14340
AGCATTCAGG GCGGTCATCT CGGGCACGAT AACAAACGGTG GTATTGCCCC TGGGGCCACG	14400
CCGGAAAGCA GCGGCAGCTA TGGCTTCGTC CGTCTGGAGG GTGACCTGCT CAGAACAGAG	14460
GTTGCCGGTA TGTCTGTGAC CGCGGGGGTA TATGGTGCTG CTGGCCATTC TTCCGTTGAT	14520
GTTAAGGATT ATGACGGTTC CCGCGCCGGC ACGGTCCGGG ATGATGCCGG CAGCCTGGGC	14580
GGATACCTGA ATCTGGTACA CACCTCCTCC GGCCTGTGGG CTGACATTGT GGCACAGGGA	14640
ACCCGCCACA GTATGAAAGC GTCATCGGAC AATAACGACT TCCGCGCACG GGGCCGGGGC	14700
TGGCTGGGCT CACTGGAAC CGGTCTGCCC TTCAGTATCA CTGACAATCT GATGCTGGAG	14760
CCACGACTGC AGTACACCTG GCAGGGGCTC TCCCTGGATG ACGGTAAGGA CAACGCCGGT	14820
TATGTGAAGT TCGGGCATGG CAGTGACAAA CATGTGCGTG CCGGTTTCCG TCTGGGCAGC	14880
CACAACGATA TGACCTTTGG TGAAGGCACC TCATCCCGTG ACACCCTGCG TGACAGTGCA	14940
AAACACAGTG TGCCTGAACT GCCGGTGAAC GGGTGGGTAC AGCCTTCTGT TATCCGCACC	15000
TTCAGCTCCC GGGGAGACAT GAGCATGGGT ACAGCCGCAG CCGGCAGTAA CATGACGTTT	15060
TCACCGTCCC GGAATGGCAC GTCAGTGGAG CTGCAGGCCG GACTGGAAGC CCGTGTCCGG	15120
GAAAATATCA CCCTGGGCGT TCAGGCCGGT TATGCCACA GCGTCAGCGG CAGCAGCGCT	15180
GAAGGTTATA ACGGCCAAGC CAACTGAAT GTGACCTTCT GATAATTCCG CATTGTCTCT	15240
CTGTGGTCCC GGTCATCATG ACCGGGACCC GGACAGGTGC AAACGCTTCA GTGCCACATT	15300
CACTGGCATT CACAATAACA TGATATTCAT CACGGAGTGA CTATGTTACA GATAGTCGGT	15360
GCGCTGATTC TGCTGATCGC AGGATTTGCC ATTCTTCGCC TTTTGTTTCCG AGCATTAAAC	15420
AGCACAGCGT CTGCGCTGGC AGGGTTCATA TTGCTGTGTC TGTTCCGGCC GGCTTTACTG	15480
GCTGGCTATA TCACTGAACG CATAACCCGG TTATTCCATA TTCGCTGGCT GGCAGGCGTA	15540
TTTCTGACGA TTGCCGGAAT GGTATCAGC TTCATGTGGG GACTTGATGG TAAACATATC	15600
GCACTGGAGG CTCATACCTT TGAATCTGTA AAATTTATTC TGACCACCGC TCTCGCCGCT	15660
GGTCTGCTGG CTCTTCCCGT GCAGATAAGA ACCATTACAG AGAACGGGCT CACACCAGAA	15720
GATATCAGCA AGGAAATTAA CGGGTATTAC TGCTGTTTTT ATACTGCTTT TTTCCTTATG	15780

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GCGTGTTCTG	CATACGCACC	ATTGATCGCA	TTGCAGTTGG	ATATTTACCC	CTCACTGATG	15840
TGGTGGGGCG	GGTTGTTGTA	CTGGCTGGGT	GCATTAGTGA	CGCTGCTATG	GGCGGCCAGC	15900
CAGATCCAGG	CGCTGAAAAA	ACTGACCACT	GCCATCAGCC	AGACACTGGA	AGAACAACCG	15960
GTGCTCAACA	GTAAATCGTG	GCTGACCACT	TTGCAAAACG	ATTACAGCCT	TCCTGACTCA	16020
CTGACGGAGC	GCATCTGGCT	CACGCTCATT	TCACAACGGA	TTTCCCGGGG	AGAACTGAGG	16080
GAATTTGAAC	TGGCAGACGG	AAACTGGCTA	CTGGACAATG	CCTGGTATGA	AAGAAACATG	16140
GCGGGTTTCA	ACGAAAAGCT	GAGAGAGAGC	CTGTCAATTA	CCCCTGATGA	ACTGAAAACC	16200
CTCTTCCGGA	ACCGCCTGAA	TTTATCACCG	GAAGCGAATG	ACGATTTTCT	CGATCGTTGC	16260
CTGGACGGCG	GTGACTGGTA	CCCCTTTTCA	GAAGGCCGCC	GTTTTGTATC	ATTCCACCAC	16320
GTGGATGAGC	TTCGTATCTG	TGCCTCCTGC	GGGCTGACAG	AAGTACATCA	TGCCCCGGAA	16380
AATCATAAGC	CGGATCCGGA	ATGGTACTGC	TCCTCTCTTT	GTCGCGAAAC	AGAAACACTG	16440
TGTCAGGACA	TTTATGAACG	TTCTTACACC	GGTTTTATTT	CCGATGCAAC	GGCGAATGGT	16500
CTGATTCTCA	TGAAACTGCC	GGAACCTGG	AGTACAAATG	AGAAAATGTT	TGCTTCCGGA	16560
GGGCAGGGAC	ATGGGTTTGC	CGCTGAACGG	GGAAACCATA	TTGTCGACAG	AGTCCGTCTG	16620
AAAAACGCAC	GGATCCTCGG	TGATAATAAT	GCCAAAAATG	GAGCAGACAG	ACTGGTCAGC	16680
GGAACAGAAA	TCCAGACGAA	ATATTGTTCA	ACTGCAGCCC	GTAGCGTCGG	TGCGGCATTC	16740
GACGGACAGA	ACGGACAGTA	TCGTTACATG	GGAAATCATG	GTCCCATGCA	ACTGGAAGTC	16800
CCCGTGATCA	GTATGCCGGC	GCTGTGGAAA	CCATGAAGAA	TAAGATCCGC	GAAGGTAAAG	16860
TACCCGGTGT	AACCGATCCC	GAAGAAGCGT	CCCGGCTGAT	TCGTCGGGGA	CATCTGACTT	16920
ATACCCAGGC	CCGTAATATC	ACCCGGTTGG	GGACCATCGA	ATCGGTCACT	TATGATATTG	16980
CCGAGGGGTC	GGTTGTCACT	CTGGCGGCCG	GAGGGATCAG	TTTTGCCCTG	ACGGCATCGG	17040
TCTTCTGGCT	CAGCACCGGC	GATCGCGATG	CTGCCCTGCA	GACAGCTGCT	GTCCAGGCAG	17100
GAAAAACCTT	CACCCGCACA	CTGGCTGTCT	ACGTCACAAC	CCAGCAACTT	CACCGGCTCA	17160
GTGTTGTTCA	GGGTATGCTG	AAGCATATTG	ATTTTTTCGAC	GGCCAGCCCG	ACTGTCCGGC	17220
AGGCGCTTCA	GAAGGGGACC	GGTGCAGGAA	ATATCAGTGC	CCTGAACAAA	GTGATGAAGG	17280
GGTCGCTGGT	GACATCTCTG	GCACTGGTAG	CTGTCACAAC	CGGCCCTGAC	ATGATCAAAA	17340
TGTTGCGGGG	ACGGATCTCC	GGTGCAGCAGT	TCATCAGGAA	TCTTGCCGTG	GCATCTTCCT	17400
GTGTGGCAGG	TGGTGCTGTC	GGGTCACTGG	CGGGCGGGAT	ATTGTTCACT	CCACTGGGAC	17460
CATTTGGTGC	ACTGACAGGG	CGTGTGGTTG	GCGGTGTTCT	GGGGGGAATG	ATTGCCTCCG	17520
CTGTATCAGG	AAAAATTGCC	GGAGCGCTGG	TTGAAGAAGA	TCGCGTCAAA	ATTCTGGCAA	17580
TGATTCAGGA	GCAGGTGACA	TGGCTTGCCG	GCAGTTTCCT	GCTGACCGGA	CATGAGATTG	17640
AAAATCTGAA	CGCGAATCTG	GCCCGTGTTA	TCGATCAGAA	TGCTNCTGGA	GATCATTTTC	17700

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GCCGCCGGTA

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(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

AATAACCAAT AGATGCTTAA GTTTACGATA TGCCTCAACC CGCGTCTGCT CTAAGCTGAT	60
AAGGCCAGTT TTGTAGAGAT CCGCTGCCAA GGTTCCTGC GTTGCACAT CCATGTAACC	120
GGCGGTGATT TCATTCATGG CATCGTTATC TTGACCAGTC AGCTTAGCAC GTCCTGTTC	180
AAGCTGCTTG GTTAGGGCGT CAACTCGGCT CTGTAATGAG ACTACGGCCG GTGCGGTTTC	240
CTTCATATAG CTSCGCAGTT GTTTTAGCTC CGCCTGTTGA CGCACCAGCT CTCCTTCAAT	300
CTGGCTGACC ACTCCCAAGC GTGCGCTGCT GGTAGATTCA GGGCTGAGAA GTTGGTGGCT	360
ATTCTGAAAT GCTAATACTT TAGCTTTTTT ATCCTGTAAG CGTTGATATG CTCTATTTAC	420
TTCTTTTTCA ACAAAGGCCA ATTGTTTCGAG CGCAACCTGA TGACCTAATT TGTTAATAAA	480
ACGCTCCGAT TCTTTGAGCA TTAACCAAC AACTCGCTGA CCGTATTGGG GATCAAATGT	540
CTGCAACTCA ACGGTAAGTA CTCCTGATAA TTCATCAAGG TGTAACGTCA AATGTTTGCG	600
GTAATAATCA AGAAAATCTT CCCTACTGAC TCCCTTATGC AACC GCGAGA AATAATCTGC	660
ACTATCACTC TGGAAATGTG CTTTAAGTGC AAGTTCTTTG TCCAACCTGG CCAGCATATC	720
CCATGACTTC ATATAATCCT GAACGAGTAA TATATCCTGA TGATTACTAC CACCTATCCC	780
TAACATTGAT AACGCATCAG GCAACATTTT AACTTGATCG GCTTGTTTAA TCATTAATTC	840
AGCCCGGSTC ACATAACGAT CGGAAGCAAT GAAGCCAAAA TAGAGCACTG CGATAGAAAA	900
GCAGATAACT ACCCAAAGAA AACTGCCTAG CTGTAACTT TTCTTCCACG AGCGGTGTAC	960
AATTTGATAT CCTCTCGAAT CAATCAAAAA TAGTTTTGGA TTATTGCTCA GTTTTCTTAA	1020
CTTTCGCGTA AGGCGAGATA TTGAGGATGA AGAATTCGGA GATGTCATAA TCAGTTGCTG	1080
CTCAAAGTGA CTGGTAAATT TTGATGGCAT CATCAATATT ATCAAAAACT TCTAATTTAC	1140
CATCACGTAA CAAGATGCCC ATATCGCATT GTTGTCGTAG ATTTTTCATA TCATGCGAAA	1200
CCATAATCAA ACTAGCTGTT TCTCGCTTTT TGTTAAATAC ATCAATACAT TTTTGTTTAA	1260
AACGTGCATC ACCTACTGAG GTAATTTTCA CGGTAAGATA TATATCAAAA TCAAAAGCCA	1320
TACTAACAGC AAAAGAAAAT TTTGATTTCA TGCCGCTAGA GTATGTTTTA ATAGGCAGCT	1380
CATAATGTTG TCCAATTTCA GAAAACTCTT TAACCCACTC TTCTACGGGG CTTGTATCGC	1440
GTACACCATG AATGCGGCAA ACAAATCGCG TGTTTTACG ACCAGTCATA CTACCTTGAA	1500

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ATCCCCCAGC TAGTGCTAGA GGCCAAGATA CTCGGCAGAG ACGAGTTACT TTCCCCCTGT	1560
TAGGCGTATC CATCCCTCCT AACAAACGTA ACAAAGTAGA TTTYCCKGCT CCATKGATAC	1620
CTAGAATACC TATATTACGG TCCCTTGGTA GCTCAATATT TACATTCCCTC AGGACATAAT	1680
TTCGTCCAAA TTTAGTTGGA TAATATTTTG ATACATTATC AAGAATAATC ATTTTTCTTA	1740
ACGCTAACTA GCAATCAATT GCGGATGCCG TAATCGGTAA CAACTCATAG CAAAAGTGAG	1800
CAA	1803

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGGACCCAAG GTAAAAACNG GTAAAAAATA CMATTGACCG ATTAAACTTT ATTTCTCTGC	60
CCGCATTAGT CTGGAGAGAG GATGGATGTC ATTTTAATTT NACTAAAGTC AGTAAAGAAG	120
CAAACAGATA TCTTATTTTT GATCTGGAGC AGCGAAATCC CCGTGTTCTC GAACAGTCTG	180
AGTTTGAGGC GTTATATCAG GGGCATATTA TTCTTATTGC TTCCCGTTCT TCTGTTACCG	240
GGAAACTGGC AAAATTTGAC TTTACCTGGT TTATTCTCTGC CATTATAAAA TACAGGAAAA	300
TATTTATTGA AACCTTGTT GTATCTGTTT TTTTACAATT ATTTGCATTA ATAACCCCCC	360
TTTTTTTTTCA GGTGGTTATG GACAAAGTAT TAGTACACAG GGGGTTTTCA ACCCTTAATG	420
TTATTACTGT CGCATTATCT GTTGTGGTGG TGTTTGAGAT TATACTCAGC GGTTTAAGAA	480
CTTACATTTT TGCACATAGT ACAAGTCGGA TTGATGTTGA GTTGGGTGCC AAACCTTCC	540
GGCATTCTACT GGCGCTACCG ATCTCTTATT TTGAGAGTCG TCGTGTTGGT GATACTGTTG	600
CCAGGGTAAG AGAATTAGAC CAGATCCGTA ATTTCTGAC AGGACAGGCA TTAACATCTG	660
TTCTGGACTT ATTATTTTCA TTCATATTTT TTGCGGTAAT GTGGTATTAC AGCCCAAAGC	720
TTACTCTGGT GATCTTATTT TCGCTGCCCT GTTATGCTGC ATGGTCTGTT TTTATTAGCC	780
CCATTTTGCG ACGTCGCCTT GATGATAAGT TTTACGGAA TGCGGATAAT CAATCTTTCC	840
TGGTGGAATC AGTCACGGCG ATTAACACTA TAAAAGCTAT GGCAGTCTCA CCTCAGATGA	900
CGAACATATG GGACAAACAA TTGGCAGGAT ATGTTGCTGC AGGCTTTAAA GTGACAGTAT	960
TAGCCACCAT TGGTCAACAA GGAATACAGT TAATACAAAA GACTGTTATG ATCATCAACC	1020
TGTGGGTTGG GGTGCACACC TGGTTATTTT CGGGGATTTA AGTATTGGTC AGTTAATTGC	1080
TTTTAATATG CTTGCAGGTC AGATTGTTGC ACCGGTTATT CGCCTTGAC AAATCTGGCA	1140 -
GGATTTCCAG CAGGTTGGTA TATCAGTTAC CCGCCTTGGT GATGTGCTTA ACTCTCCAAC	1200

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TGAARTTCAT CATGGGAAAC TGGSATTACC GGRAATTAAW GGTGATATCA CTTTTCGTAA 1260
TATCCGGTTT CGCTATAAGC CTG 1283

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TCAACCTGAC CAACCACTAG AATCAACTCA CGTCCGTCGT TAGGGGGCTC ATATTCTTGT 60
GTACTCCCCA CATTGTATTT ACTGACTCGT GATGATTGTA ATTGCGCTAA TAATGACTCT 120
GCGCGTGCTT CTTCTTTTCG ATCTAAAACG TACGTAGTGA GTAAGTGCTC AAGCTTACTC 180
GGACGGCGGC TATCAAATA GATTCCAACG GGGTCAATCG AGAGTGATGA AGGTCGACAT 240
AAATTAGACC CCAATCCGTT GGAGCGGATA AAACCATCTT CAATCCGGAT CACTGATTGC 300
AGTTCAGGAT AACGGTTTCC CCACACCAAC ACCTGTTCAT CATCTTTTAA CTGTGAGGGC 360
ACAGTACGAA CAAAACAAAG TTCATCTGCC AAATACGCAC AAAATGTGCG TATAAAAGCA 420
CGCTTCCACA GAGAAAAACC AACGAGATAA AGACGACGCC AAGGTTTGGG CTCTACCTGC 480
TGCTGAGCCA AAATCGCTAC AACATCTTCT ACCTCACAAC GTTTTCCCAA TATAGGATCT 540
AAATAACGCG GATAACGGAT CAACGCCGCC GCAACTAAGC GGGGCAATGA AATAGATGAA 600
ACGCCTTCGG CTGACATTGC TTCTTCACGG CGTATACAAC GTTTACTGTC ATGCGTTAAC 660
CCCCACCCAG CATAAAATGG CATAACGAAG CAATATACAG GTTTGCCCAA CAGCAACGCT 720
TCCAAAGCCA ACCTGCGATG AAACTGTGTA CACCGCATCC ACCATACGAA TTATTCTATG 780
CGGATGGCAA GTTCACTCAC CACCTCAACA TCAGCCAGTC GAGGATCACG CCCCCTAAA 840
CGTGCTAACA CGCCGCTTTT TTTGCTAAAG CGTGTATCTG GGTGTGTTTC CAACAATAGA 900
CGCGCATTAG GGTGATTACG GCGAGCCTCG ACCACCATAG AAACAAAATC AGCTTCGCAA 960
GCAAGAGCCC CAGAAATTGA CAAGTCTCCC GCTACTTGAT CCACAAGCAA AATACGCGGT 1020
CTTGATCAT CCAGTAAACG TGCTAAGTTT GAATGAGCCG TGAGGTGAAT AACTCAGGTT 1080
GTATATGTGT CGGTAAATCT AAAGAAGGCC CGTCAGTAGC ACGGGACAGA GCCATTAAAT 1140
GTATGCTCAG TGCTATTGGG TATAGCAGTT ATACTTGGTG ATTCTAAAC GCAAAATATC 1200
MGAGATCAGA TGCTCCAGCG CGCGCAAAGT AAAGCCGTAT CCAACAGGTT CCAATAATAA 1260
GCTGTTCTAA TTGACTCGTC TGATGTGCAT CATAATATAT CCCCAGAGGG TCAGCAATAA 1320
GAGAAACCGC CTTTCCTCCT TTTGCTGGGT GCCCGATATA GCCAATAAAA CCATCTTCAA 1380
GTTGCCAATA AGATATTCCT AACTCTTGAG CTTTCTGTTT AATCTGCTTA GTATTAGATT 1440

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TTTTTCCCCA	GCCAACTAAA	ACGTCATTTT	TAGAAAAAGC	CTCGTCTCCT	TTCATATAAA	1500
GCAATGGGTG	ACCAAGCATA	GGCTCAATAT	TATTTTYTCT	GGCAAGAATC	CCTTTTCGATC	1560
CCGTATATAA	ATACATGTTG	TCTCTGTGAA	CTGAAGATTC	TCTACAATGG	TGTATAAAGT	1620
GTGATTTAGA	TGAACAGCTC	TGCGCTCTCT	AATGACTTTG	CAATACTATC	TTTTGCTGAA	1680
GTGAGAATGT	CCGCCTTTAA	CTCGGGCCAC	CTAATACCAA	TTGTAGGATC	ATTCCATGCA	1740
ATGCCTCTAT	CACTGGCAGG	GGCATAATAA	TTAGTTGTTT	TATACAAAAA	TTCGGCCGAT	1800
TCAGTCAGTG	TTACAAAACC	ATGGSCAAAT	CCTTCCGGAA	TCCATAATGT	CGTTTGTTTT	1860
CCCCTGAAAG	ATGAACGCCA	ACCCATTGTC	CGRAGCTCGG	TGAGCTTTTG	CGAATATCTA	1920
CCGCAACATC	AAACACTTCA	CCGGCTACAC	AACGCACTAA	CTTGCCCTGG	GCATGGGGAG	1980
GTAAGTGATA	GTGCAAGCCA	CGCAGTACCC	CTTTAGAAGA	TTTGAGTGA	TTATCCTGCA	2040
CAAAGGTAAC	TGGATATCCT	ACAGCCTCTT	CAAACAACCT	GTGATTAAAA	CTCTCAAAGA	2100
AAAAACCACG	CTCATCTCCA	AATACTTTTG	GCTCAAAAAT	AAGCACACCA	GGAATTGCTG	2160
TCTTGATTAC	ATTCATCTAT	ATGCCACAT	TTAATTAAAT	ATTTTtaggg	GAAGCATATT	2220
CCCTCCCCCT	TCTCAATTAC	ATCACGCCTT	ATCAATCATT	TTAATAAAT	ATTGCCCATA	2280
GGCGTTTTTT	GCCAACGGAG	CAGCAAGYTC	ACGAACCTGG	TCGGCACTAA	TAACTTCTG	2340
GCGATAAGCA	ATCTCTTCCG	GACAAGCCAC	TTTCAATCCC	TGACGCGTCT	CGATGGTCTG	2400
AATAAAGTTA	CTCGCTTCAA	TTAGGCTTTC	GTGGGTACCG	GTATCAAGCC	AGGCATAACC	2460
ACGCCCCATC	ATTGCCACCG	ATAGATTGCC	TTGCTCCAGG	TAAATACGGT	TCACATCGGT	2520
GATTTCCAAC	TCACCACGCG	GCGATGGCTT	GAGACCCTTG	GCAACGTCCA	CAACGCTGTT	2580
GTCGTAGAAA	TAGAGGCCGG	TGACTGCGTA	STACTCTTAG	GCTCCAGTGG	TTTTTCTTCC	2640
AGTGAAATAG	CGGTACCTTG	ATTATCAAAT	TCGACCACTC	CATAACGTTT	CGGGTCGTGC	2700
ACATGATAGG	CAAATACAGT	AGCACCGGTC	TCTTTGGCCG	CGGCTGCCTC	CAACTGTTTC	2760
TGTAGGTCAT	GACCGTAGAA	GATGTTATCC	CCCAGCACCA	GTGCACACGG	GGCTGAACCA	2820
ATGAATTCTT	CACCTAGAAT	AAAAGCTTGT	GCCAACCCGT	CTGGGCTTGG	CTGAACCTCA	2880
TATTGTAAAT	TCAGTCCCCA	GTGGCTGCCA	TCACCCAGCA	ATCGCTGAAA	GGANGGAGTA	2940
TCTTGTGGAG	TGCTAATGAT	CAAAATATCG	CGAATTCCAG	CCAGCATCAG	GGTGCTCAGC	3000
GGCCGCAGTA	CTGGATCATC	GGCTTGTCAT	AGATGGGCAA	CAACTGCTTG	CTCACCGCCA	3060
TAGTAACCGG	ATAGAGACGT	GTACCAGATC	CACCGGCCAG	AATAATACCT	TTACGTTTAG	3120
TCATGATGCT	TGTTTCTTAT	TTTTAAATTA	CATAAGAATA	AAGTGGCTTG	AGCCGCGCCT	3180
TTCTGTTTTA	TCCTCACCTG	TGGTTTACTT	CCCCATGATC	TCAGTCAACA	TCCGCTCAAC	3240
ACCGACTGAC	CAGTCCGGCA	AAACCAGATC	AAATGTACGC	TGGAATTTTT	TAGTATCAAG	3300
TCGGGAATTA	TGAGGGCGTT	TCGCCGGGGT	CGGAAAGGCG	CCTGTCGGCA	CTGCATTAAG	3360

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CTGTGTGACT	GCCAGTTCAA	CTCCTGCGTC	TCTGGCTTTG	TCAAACACCA	ACCGGGCGTA	3420
GTCAAACCAA	GTGGTAGTAC	CGGAGGCAGC	CAAATGGTAC	AGCCCGGCAA	CGTCGGGTTT	3480
GCTCTGTGCA	ACTCGGATTG	CATGGGCGGT	ACAATCGGCC	AGCAACTCAG	CTCCAGTTGG	3540
AGCGCCAAAC	TGATCATTAA	TGACCGATAT	CTCGCGACGC	TCTTTGCCAA	GACGCAGCAT	3600
AGTTTTGGCG	AAGTTGGCAC	CGCGCGCAGC	ATAAACCCAA	CTGGTACGAA	AGATAAGGTG	3660
ACGTGAGCAG	AGTGCCGCAC	CGTGTTCCCC	TGCCAGCTTG	GTTTCGCCAT	AGACGTTGAG	3720
CGGGGAAATC	ACATCGGTTT	CCACCCAAGG	ACGTTACACCA	CTTCCATCGA	AAACATAGTC	3780
GGTGAATAA	TGTACTAGCC	ACGCACCTAA	TGCTTCAGCT	TCTTTGGCAA	TAACCGCCAC	3840
ACTAGTTGCA	TTGAGTAACT	CGGCAAATTC	CCGCTCACTC	TCCGCTTTGT	CGACTGCAGT	3900
ATGGGCCGCT	GCGTTAACAA	TCACATCCGG	CTTGACGAGA	CGTACCGTTT	CAGCCACCCC	3960
TGCAGAATTG	CTAAATCAC	CGCAATAGTC	GGTGGAGTCA	AAATCAACGG	CAGTGATGTG	4020
CCCCAGAGGC	GCCAATGCAC	GCTGCAGCCC	CCATCCACTT	TCTGGCCACA	CCAGACTCGC	4080
CAGCAAAAAA	GTGAGTGCTG	TCAATAACTC	AACCAGCGGA	TAACGCTTGC	TGATTTTCGC	4140
CTGACAGTCG	CGGCAGCGCC	CTTTGAGCAT	CAACCATGAG	AGCAGCGGAA	TATTGTCACG	4200
AACGCGGATG	GTCTGCTGGC	AATGCGGACA	GTGCGAACGC	GGTAGCGCAA	GGCTTATTTT	4260
TGACTGCGCA	CTCGGCATTT	CACCATGAAA	CTCCGCCATT	TGTTGGCGCA	GCATGATGGG	4320
GTAACGCCAA	ATCACCACAT	TCAAAAAACT	GCCGATGATC	AATCCTCCGA	CGGTTGCCAG	4380
TATGGGCATC	GCCGCGGGGT	ATTGCTGAAA	AACATCAAAA	AGCATGGTTA	AAGGTTATTT	4440
GTTGTAACTT	GCCGGATGCG	GGCCTGCGGG	TGTATGCCAT	ACGGCTTTCC	TTCAGGCCCC	4500
ATGCGCCTTA	TTTCATGCCG	GATGCGGCGC	GAGCGCCTTA	TCCGGCATAAC	AGGCTTACTC	4560
AGCTGACATC	TTATGCTCGG	TAACCTGATT	AATGGTTTCC	GGCCCTTGCT	GCGGTTTCGG	4620
CAGATTAAGC	GCCGCCAGTG	TCTCGTAAGC	CGACTGGCTC	ACACCGCCCT	CGAAGTTCAT	4680
CTCGCTCGCT	CCCGGCAACT	GGTAAGCATT	CGCGCCCGGA	TTCCATTTCT	TAAAGAACTC	4740
CGAAAGATCC	GTCTGGGCGA	CCCAGGATGC	ACACAGCATC	AGCTTGTCGG	CAGCGTTACC	4800
GTTGGATTCT	GCACAGTAAT	TTCTTTCGCC	AAACTTGGTT	TTGCCAACCT	CATCGCCGCG	4860
TGCTTTACGG	TGCATCAACT	GGAACAGGTT	CCAGCCTTTC	ATCCCTTCAC	GATCGCTGTA	4920
GAACTTAGGC	AGGTCACCTT	CTGGATACCA	CTGTTTGATA	TCAAAGTTTT	TCTCTGCCCC	4980
CTCTTTCAGC	TGTGCGTACA	TCAGCAGACG	GTCACCCGCA	CCGCCGCGCG	CCCATGCCTG	5040
ACCGTTGCTC	TCCTCCAGAT	ATTCCGGCGC	GACGGTAATG	TCGTCAGCGA	CACGGTTCAT	5100
CTTGCCGAGA	TAGCGATCCT	GCATSTACAG	CGCCAGCACG	TTGTTGCTA	CTTCAGTTGC	5160
GCCAGGAACA	GTCAGCGGCG	TTTCGGCGGC	GTTGTGACCA	ACTTCGTGCC	AGATCAGCCA	5220
GTCGTTGAGC	GGCGTCGTCG	GCAGCGTGGT	GCTGTTGCTC	GAGAAGCTGC	TGTTCAATTAC	5280

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CGGATAACCA GAGTGGCGAT CACCGATGGA GATCTGCACA TOSTTGGTGA AACGATGCTT	5340
GTGGCCCCGTC AAGTTTTTAT AGGTAAACAT CCGGTGCTTA CCGTCTTCAT CATTACGACC	5400
G TAGAAGTCA TTCATCGAGC TGGCAAAAGT ATCCAGATCT TTAGCGAATT CTGCTACGCC	5460
ACCAGTGAAA TTGCTGGCCT CAAGGTTCTT CTTCGSCGTG GTGTAGACGA AAGCGTCTGA	5520
CTCCAGCTCG CCCAACGGCG CAGGGGAATT CAGAGCGTTT TTCCATGCGC CATCTTTATA	5580
GAACGGCGCT TTCACCACAC CAGTAAAGGT GAATTCGGCT GACTCATTCT GTGGGCTGTT	5640
GCCCTTGATA TAAATCAGAC CACCGTAAGG AACCGTAAAC TTCACCTCAC CATTGGCTTT	5700
CAGCTCATAG GTTTTCGTCA CTTTTGGCGG ACGGTTCAGA GCGACTTCAT GCTTCTCACG	5760
TCCGGTAAGG TCGTCGGCCA GCGCCACGGT GACAGTCACA GGAAGTATG CAGAAGACTC	5820
AATGGTGACC TCTTTCTGAG CCGGAGCCCA CAGGCCAGTA GACTGCATGT TACCGCAAA	5880
CCATTTGGTC GGATTCGAGT ACAGGCTGAT GGTTTCAGTA ACCTTCTCAC CTTCTGCCGA	5940
TACCGCTCCC GGATACTTCT CGACATCAAC TTTGATGTTC AGATCCCACC AGGAACGACC	6000
CAGCATCAGG CGCGTCAGCG GTTTTTCCAT ATAGTTGAGC GGATAGCTCG GGTTTCATCAT	6060
GCCCGCTTTA TTAACGCTCT TCTCGCCGTA GATCATGTTG TTATCGACCA GCGATTTTTT	6120
CAGCTCATCA GAAACACTGC GTGCCGCCAG TATAGGCATC GTTGGCGTAG CAGTTCAGGA	6180
ACTCGGTGAA CGTTTTAAAG CCCAGCTCGT CATCCTTGTC GTTTTCATAG CGATATTCAA	6240
TTTTATTCCA CAGCCAGACC GACATGTTCT GTTACAGACG TTCCAGATCG ACGCTGCTCA	6300
GACGCTCACC TTTGCGACCA TTGGTCCGGA AGTAGAGCTC ATGCTGATAC AGACGCTGAA	6360
TGTTGGTGCC TAAATCCGCA GCCTGCACCA TCGCTTTTGC CGTGTGCGCG TTAAGGCTTA	6420
GTTGCGTATA CTGTGGAACA TACATCTTAC CAGTAACCGG AACCCCGGTG CCAGGACGAT	6480
ATTCCAGACA GTTGACCTCG TAGTGGAAG TTGGGTCCTT AACTCCTTT AATCCAGGAA	6540
ACTTCTCAA GATTTTTGCC TTCGCAGCCT TCAGAGAATC CTCTGTTTTA TGATCGGCCT	6600
CATCAATAAA GGCATAACGC GTTTCCTGTT TGCCATCTAC ATCTTCCAGC CAGCTGGCAA	6660
CTTCCAGCTT CGGTTTGTCA TCAGGTTTGT TTTCTACCTG ATATTTCCAC TTAATTCCC	6720
CTGTCTTACT ATCGATGGTG TACGGCAGCG CACCATCTAC GGCAGGATAA CGTTCATAGA	6780
CCCAAATGCC CGTTGCGCGC TGCTGACGAA CGCGGTTCCG ATACCCTTGC GGATCC	6836

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

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GGAAAAACNC GCCGTATATT AGCCCGCGCG GAAAAAGCCC CGTNACGGGC AAACGCAGCA	60
AGGTTTTTATC CCAGCGCAGG CGCATGGCAG GATTTTTTGAG TAGCCGTTGC CCCAGCACCA	120
GAAGCCCCAG CAATCCCGCC AGCCAGTAAA CGCCGCTGGT CTSTAACGTG TCGCTCATGG	180
CGATGAGCGT GCGGGTGGAG GCGGGCAGCG CGTGTCCGAG ATGATCAAAC TGTTCGATGA	240
TTTTTTGGCAC CACTGCCGTC AGCAAATAG TGACCACGCC CGTTGCCACC ACCAGCAGTA	300
CCAGCGGGTA GAGCATGGCC TGCAGCAGGC GTGAATTTCC AGNACCTGCC GCTGTTACGG	360
TGTAACCCGC CAGGCGATTG AGCACCACGT CGAGATGTCC GGATTTTTCT CCGGCAGCAA	420
CCATCGAACA AAACAGGGAA TCAAAGACGC GGGGATGTTC GCGCAGGCTG TCCGACAGGK	480
TGTAACYTTC CTGAATCCGC TGCGCAGCGC CATTCCGAGG CTTTTTACAT GCASTTTTTTC	540
ACTTTGCTCA CTGACCGCCT GTAAGCAGGT TTCCAGCGGC ATTGCTGCCT GTACCAGCGT	600
TGCCAGTTGG CGCGTGAACA GCGCAGATC TGCCGCCGCC ACGCGACGAT GTGCGTGCCG	660
CCGACGCTGC AACATCCCCC CTGCGAAGT ATTCATCCGG GCTTCAATAT GCACGGGGAT	720
AAGCTCTTTA CCGCGCAACA ACTGGCGGGC ATGACGCGCG GAATCCGCCT CAATCATACC	780
TTTGGTTTTG CGACCATTAC GCTCCAGCGC CTGATAGTAA AACAGTGCCA TTACGCCTCC	840
ATGGTTACCC GCAGAACTTC ATCGAGAGAG GTTTCTCCGG CGAGCACTTT CTCAATGCCG	900
TTGCTGCGGA TACCCGAGTA GTGTTGTCTG ACATAACGTT CCAGCTCCAG CTCCCCGGCC	960
TGACGGTGGA TCAAATCACG CAATGTGGCA TCCACCACGA TCAGCTCATG GATGGCAGTC	1020
CGTCCGCGAA AACCTTTGTG ATTACAGGCG GGACAGCCCT GTGGATGGTA CAGAGTGACG	1080
GTACGGGCGT CGGTAATTCC CAGCAGGCGT TTTTCTTCGT CGGTGGCAGG CGCGGCCTGA	1140
CGGCAGTCGG AGCACAGCGT GCGGACCACT CGCTGCGCCA TCACGCCCCT CAGACTGGAA	1200
GAGAGCAGGA AAGGCTCCAC GCCCATATCC TGCAAACGTG TGATCGCCCC CACCGCTGTG	1260
TTGGTATGCA GCGTGAAAG TACCAGGTGT CCGGTCAGTG AAGCCTGAAC AGCGATTTCT	1320
GCGGTTTCGG TA	1332

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCCAACGTTT ATCGTATTTT ATTAAAGTCC CTTGCCCGAT GCTATCTCGA GTTACATGAC	60
GAAATCGCTG ATTTGGATGT CATGATTGCG GCAATTGTCT ATGARCTGGC GCCTGAACTG	120
ATTAAACGTA ATGCTATTGG ATACGAAAGC STTCGCAGTT GCTGATCACG GCAGGAGACA	180

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ATCCCCAAGC ATTAAGATCA GAATCAGGTT TTGCGGCACT GTGTGGTGTC AGCCCTGTTC	240
CCGTATCTTC AGGAAAAACG AATCGTTATC GACTTAACCG GGSTGGAGAT CGTGCTGCAA	300
ATAGTGCACT TCACATCATT GCCATCGGAC GTTTGCGAAC TGACGATAAA ACGAAGGAAT	360
ATGTCGCCAG ACGAGTAGCG GAAGGGCATA CAAAAATGGA AGCAATACGC TGCCTGAAGC	420
GCTATATCTC ACGCGAAGTT TATACATTAC TGCCTAATCA AAACAGGCAG CTCAACAGCA	480
TCCCGATAAC GGCTTGACTC TTAGAAGGGC GTCCAGGGCA GCCACTATAC AAGCAGGCAG	540
TTCCGGCAGT TACTGTGGCG TTACCAGATC AAACAGAGTC TGAGTCGACG AGGAAATTGC	600
TGGGATAACA GCCCGATGGA GCGCTTCTTC AGGAGTCTGA AAAACGAGTG GATACCGGTG	660
ACGGGTTACA TGAAC TTCAG CGATGCTGCC CATGAAATAA CGGACTATAT CGTTGGGTAT	720
TACAACGCGC TCAGGCCGCA CGAATATAAC GGTGGSTTGC CACCAAATGA ATCGGAAAAC	780
CGATACTGGA AAAACTCTAA AGCGGTGGCC AGTTTTTGTG GACCACTACA TTTAGTGCGA	840
CACGGGAAGC GCGATATGAA CGATACGATA CATCAATGGT TTATTGCGGT GATAACCTGA	900
AGGGTGAGAT TGAGGCTATT TATAATAGTC TTGAGAGGCG TCAGGTTTAG AGCAGGAATG	960
CTGAGTAGCC ATCTTATCGA TTGTTTTCGA GCGTAAGATG GCTGAATGGA ATGGCTATTA	1020
TTGCACAGTC CTTAATTATA ACATTCATAC CGACATGATT ATCTTCTGTC CGGAAGAATC	1080
AGAGGCTGCG GTTTCAGACT GTCTGCCGGT ACATTCCTCT CTCCGTTAAA AACCATAACG	1140
GGTTCATTAT CTTCGTCTGT CAGCAGATTG AATGGCGGTA TATTTTCAGT ACGAATGCCG	1200
GTCAGCCACT GAAAAATACC TGCGAAATGA CGGGCACTGA TTTTCTGCT GACGGACTGA	1260
TGAGACGTGA TGTCCTGGC GGTAATAATC AGGGGAACGC TGTAGCCTCC CTGCACATGA	1320
CCATCATGAT GAACAGGATT AGCACTGTCG CTGACCGACA GACCATGGTC AGAAAAGTAA	1380
AGCATGGCAA AATGACGGGA ATGCCGGCGA AGGATACCAT CAAGCTGCCC GAGAAAGTTA	1440
TCCCAGTTTA CTGATGCTGG CGAGGTAACA GGCAATTTTT CGGGGATACT GCCCCAGGTA	1500
ATGATTCCGC CAGGAGTTAA GCCGGTCACA CGGGTTCGGA TGAGACCCCA TCATGTGCAG	1560
GAATATCACT TCGGAGAGGA TTTATCCGCC AGTGCACGTT CTGTTTCCTG TAACAACAAC	1620
ATGTCATCCG TTTTACGGGA AGCAAAGCTG CCTTTCTTGA GGAAAACGGT ATGCTCCGCA	1680
TCAGAAGCAA TAACAGAGAT GCGTGTATCA TGCTCCCCCA GCTTTCCCTG ATTGGATATC	1740
CACCATGTGC TGTATCCTGC TTTTGCTGCC AGCGCCACCA CGTTGTTGCC GGAGTCAGGG	1800
TTCTGCTCAT AGTCATAAAT CAGTGTCCGG CTCAGGGAAG GTACGGTACT GGCTGCTGCC	1860
GATGTATAGC CGTCAATAAA TAAACCGGGA GCAGTATTCA GCCACGGTGT GGTGGCAGC	1920
GGATAGCCAT ATACCGACAT ATAATCCCTG CGCACACTCT CACCAGTGAC GATAACAATC	1980
GTGTCATACA ACGGTACACC CGGCAGGATT TTCCAGTTGT CAGCCCCGTG CTGATTCACT	2040
TGTTTATAAC GCTGCATTTT ACGCAATGTG TCAGTTGTCC CCACAACAGT TCCTTTAACC	2100

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ATCCGCAACG GCCAGCTGTT TACTGAGCAT AATACGAACA GCAGCAGTGC CAGCCAGTTA	2160
CGGTGACCGC GGTGGTGTGT TCGCCAGAAA ATCACCATGA ATACCAGAAT CGCGGCACTG	2220
ACCAGAAAAT GATAAACAGG AATCATCCCG GTAAACTCCG CTGCCTCATC AGTTGTGGTC	2280
TGCAGCAACG CAACAATAAA ACTGTTGTTG ATTTTACCGT ACGTCATACC GGCAGGCGCA	2340
TACAGTGCAC AACAGAACAG AAATAACAGC GCTGTAATGG ATGTGAGGGT ATTTCTGTGT	2400
GCAAGAAGCA GAAGAAAGAA CAGCAGCAAC ACATTCCCGG TGGTATTCTT CTCAGTGTAT	2460
CCGCATGCAA TTGTGGTTAT GACAGAAACA ACAAAAAGA ATAAAAACAA TATAATCCTG	2520
AGAGTGTTCG CCGGACAAAA CAGTTTTCTG ATATTCATCG GAGTATATCG ACAACATTAT	2580
TATGAAGAGA ACAGGATAAT AAAAATCAGA AGTTATCTGT GAAACAGATA ACAGACANCC	2640
CTGCAGTATA ATATTACTGC AGGGTGTTC TTTTAATTA CAGAAATACG TAATTATCTT	2700
AATTGCAGAA ATATGCGCAA TTATCGTTCA GAAGCAGTGT CGTCAGAAGT TATAAGTCAC	2760
ACCAAGCAGG ATGTCATGAC TTTTAACATC AACCTCTGAT TTATATTTAT CCCCTTCTGT	2820
ATCCTTGTA TACAGGGAGG ATTTACCAGC ATCCAGATAG CGATAGCTGA GGTCAAGAGC	2880
GATATCCGGG GTTACGTCAT AGCGAACACC GGCCCCAATG CTCCATGCGA AGTTGTCAGC	2940
AGAGCCTGAG CGTGATATAG AATAACGCAC TCGCTCACC TAGCCATAAT CCCAACTACC	3000
GCTACCTGTT GATTCTTGAT GAATTCTGGC GTAACCAATT CCGGCAGACA CCCATGGCGT	3060
AAATGCACTG TCGTTTCTGA AATCATAGTA CGCATTGAGC ATCAGGCTGT TGAAGTACAC	3120
CTCATTCTTC AGGTCACTAT GTCCCGCGTG GTCCTTATAG AGGTTGTATG TTGTGTCAGC	3180
TTTTCCACGG GCGTAAACT CCAGTTCTGT ACGCACAGGA AACTGAACT GCGGATGCAA	3240
GTCATAACCA AACGCTATAC CTCCACTGAA TACCGTGTTA TGGCCATCCC CCCCCTATAC	3300
TTTGATGTTT CCTCTTTATT TTCGGACAGG AAACCTCTGGT CAGAAAGAGA TACTGCTGAA	3360
GTACCTGCTT TACCGGTCAG ATAAAAACCG CTTTTACCTT CCTCAGCACC CGCATTGCT	3420
GCAANCATAC AGGCAGCGGT AACTGCTGAA ACAGCAAAAA CTTTTTTCAT TTCAATTAAC	3480
TCCATTATTT CACTATTTTT GTAAATAGCA CTCCTAATAT TTTAAACCA GTCAAAAGAT	3540
AGTATCAAGC AAATTATTCA TGTCTAATGA ACAGATAAAA TCGACTATGT GTCGGCAAGA	3600
CTCTGCTCCA CCGATATTCC TCTTATTTCC GCCTCGATGA AATACCCCCG TTACCTTATT	3660
TGTACCCCTT ATAATGGGAT GTTGGCCAGC CAGACCCGGC ATGATTAGTT CTCCCTGTCTG	3720
ACTATGCTCC GGGAGGGATG TCACCGGGTC TGGTGAGGCG CGGATAACCG CTAATAGGGG	3780
AAGGTCAGGT ATTTTACACC GGGACCGTCA GGGCAAGATA ACGAAAGCCA GTCCTCCGCA	3840
TGAACTGACG CCAGATAGTT TCTGTCCATT GCTGCTTTTC TCATCTTACG TCTTAACCCT	3900
GCCTTGAATA CCTTATCTCT CGTCAAAATA TTAATAGCGA TATGCCGTAT CCCTGAAAT	3960
AATCCCGCTG CGTTTCCTCT TCTTACTTGC AGTCGTCTTC ATTCATTACC ACGTCCAGAC	4020

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GCCATGCAGC TTATTCTCCA CGTGCCAGTG ATTTCCGGATC GCTGTGACGA ACTTCTCTGC	4080
GGTTAAATCA GCAGAACTGA TATAATATCT GACCATTATT TCTGACTCTT GCTTTTGTTC	4140
TGCTATTATT GACCGAAAGG AGACTGCCAG GCATATTTTT TCAGCCCTTT CCATTCAAAC	4200
GTGAATTCAA TCAGCTCATC AGGGACNTCG CCAAACCATA TGAAGACGGG ATCCTNCTCT	4260
GCCGTGACTC TTGTCATAA TTGCGTAACA GTCATGCTCN GGGATAATTA AATCTTTCAG	4320
CGGAAATAAA AAGATTATCA GATATGGGGA TGACACCACA GCACCGCTGA GGCCAGTATG	4380
GATAAACCAT GTACCTTATT AACCAAA	4407

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TTTTTTGCAA GAGAATTTCC CTGAACCTGA AGCTCATCAT CGCCATCTCC GCCGTTTCAGG	60
TAATTATTAC CTGCTCCCCC AATTAACCTTA TCGTTGCCAT CACCGCCATA GAGCTGGTCA	120
TCTCCGTTTC CACCACTCAG TGTGTCATTA CCTTTATCAC CATATAAGCG GTCATTCCCCG	180
TCATTTCTTT CTATATGGTC ATCACCATCC GCGCCATGGA AGATATCAGC AAATTTACTG	240
CCAAAAAAGT TGTCGGCAGC CGTGGTCCCA ATAAGTTCTT CCACGGAATA TAAGTTATCA	300
GTCTCTGTTA AATTTTTTACC ATTGATATGA GTGAATTCAT AACTCCGATA TTGCGTTTTT	360
TCAGTTCTTT TTCCAACCTGA AACCTCCTGC TCCTTCACAA CTTCTGTAA AACCTTAACA	420
TCACCACCAA GTACACGTGT TACCGTGTA TTACCCGCTT CGGTTGCTTT TGTGCCATCA	480
ATGGTCAGAT AACCGGTGTC TGTTTTATCA TAATAACAA CATCATGTCC TTTACCTGCG	540
TAGATATTGG CTGAGCCGGC AGATAAAAAG ACCTTATCAT CCCCCTCTCC CAGGTGTGAC	600
TCAATACGAA TTTCCCGATA CTGGTTATTA CCGACTGATG CATGCTGAAT CAGGTTAGAG	660
TAATCATATA CAGACCCCTT GTCCTGNAAC CCCCTTCACC GTCCATTTAT CAACACCCTT	720
GACTAATAAC TCGGTAATAT ATTCATATTT TCCGGACTGC CTCCTTTCAC GAATTTCTC	780
ACCGGGAGTT TAACAATGGG CGTAACNAAT TTGCAATAAC GTGG	824

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GNGGCCGCAG TACTGSATCA TCACCGAAGT TTCGCGCGGA AAAGCGTTAG AGAAAGATCT	60
AATGCTTCAT GATGGTGATG GACTTTTCCT GATGGTGAAA TCCAGCGGGA AATGCTCTGG	120
CGTTTCCGTT ATCAACATTC GACAACAAAG CAGCGGACAA TGATGGGACT CGGTGTCTTT	180
TCCACACTTT CACTTGCTGA TACCCGAGGG CTAAGAGTGG ATTATATTTT CTTATTAGCC	240
AACAGAATCG ACCCGCAAAT TCAAGCTAAA GCCGTAGACG AAGAGCAATA TTTGAAAAGG	300
TGGGCACCTA CGTTACCAAT ACTGGCTTAA TGGCTACATA CGGCGGTCAG GGTGAGTTTA	360
CGCTTACAAA ATATAAAACA ATTTGATACA AAATATTCCT CTTATTCTAA ATAAAAGTAT	420
CTTGAAAACC TTCCAAGTGG AAGGTAGATT GAATTTATGC TAAACATAAA GAGGAATTGC	480
TTATGAATTA CGTTATCCGC ACTACCACCG TCGTCTTTAG TCTCATGCTG GGCAGGTTAC	540
GCAACTGCTG	550

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACTAAAGGC CCTGGATGTT TTTCGCTCAT TAGTAGACAT CTCGCTGATA ACGGCGCTCT	60
ACGCGCACTC ACTTAAAAAT TCATCCGCCG CTTCGGTGTC CATGCCACCA AATTCGGCAA	120
TCACTTCCAG AAGTGCCTGC TCAACGTCTT TCGCCATGCG ATTAGCGTCG CCGCAGACAT	180
AAATGTGGGC ACCATCATTG ATCCAGCGCC ACAGCTCCGC GCCCTGTTTCG CGCAGTTTGT	240
CTTGTACGTA AACTTTTTCT TTTTGATCGC GCGACCAGGC AAGATCGATA CGTGTGAGCA	300
CGCCATCTTT GACGTAGCGC TGCCAMTCCA MCTGGTACAG GAAGTCTTCC GTAAAGTGCG	360
GATTACCAAA GAACAGCCAG TT	382

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TAAATCAGCA GAACTGATAT AATATCTGAC CATTATTTCT GACTCTTGCT TTTGTTCTGC	60
TATTATTGAC CGAAAGGAGA CTGCCAGGCA TATTTTTTCA GCCCTTTCCA TTCAAACGTG	120

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AATTCAATCA	GCTCATCAGG	AACATCGCAA	ACAATATGAA	GAUGGATTTT	TTCTCTGCCG	180
TGACTCTTGT	CACTAATTGC	GTAACAGTCA	TGCTCTGGAT	TATTTAATTC	TTTCAGCGAA	240
AATAAAAGAT	TATCAGATAT	GGGATGACAC	ACAGCACCGC	TGAGCAAGTA	TGTATAACCA	300
TGTAATTATA	ACAAAAGGAG	ACGTAAAGAG	GGGAACGGGT	ATCAGAGGGC	CAATCAAAGC	360
AGGTATAATG	AACGCCAGTA	TAATTGTCCG	CAACCCAGAA	ATATATTATT	GAAGTGGTTA	420
TCTCCTGCGA	ATGCATATAC	TGCAACGGCC	GTTAAAATAG	CATTATATCC	ATAAAGCCCC	480
GCAGAGATTT	TATCAGGAGA	AAGCTCAGGA	ATACAGAATG	ATACCACCAC	ACTCAGAAAC	540
GAAGCGACAA	CCGTAATCAT	CAGTAGTTTC	CGSCTCCCTG	CAAGTAGTCC	CAGCATAACA	600
AGAATACCGC	CGACAGCATC	AGGAAACATA	AAAATCTCCA	TAAAGCTACC	AGACAATGCC	660
ACCGGATAGT	TTTTCAGCAA	AACAGAACCT	GCACTTCGCC	CGAAGGTACT	GACATATCAT	720
GAGGCATTAT	TCCGGAATGT	AATAACCACG	TAGCGATAAT	AAAGGGGGCG	GTCAATACGG	780
GTAACCCCTCT	GAGCACTGAC	GACAACAGGG	GAGTAAACAA	AACAATACCA	AGAGTTCCGA	840
CGATAAGTAC	AGCAATTCCG	GAGACTGACA	CAGGGACAAG	CATGCCACAG	GCTATGCCAT	900
ACAGAACAGC	ATTATATCCC	CATATACCTT	CATTAATCTC	CTCATCAGGA	TACCGCAAAC	960
ACCAGGCAAA	GAACGGAGAA	AGTGCTGCAC	TGATGGCTGA	GAAATACAGT	ATTTCGGGGT	1020
GCCCCATATT	AAAAGAGGCT	ATTCCAGTCG	CCAAAAA	GAACAAGCCA	GAAACAACAT	1080
TGTTCTGTAA	TAATACCTGT	GAATACCCCT	TACTAAAGGC	GGTTATCACC	TGTTTTACTC	1140
TCATGTAAAA	TGTCACACAC	ACCTCATACA	TAAACCATTC	TCCGCTTCTG	CGGGACAGTA	1200
CCGCCCCCTGA	CTCCACCTCA	CAGCGGATTG	TGTATTTTTA	AACAATCACA	GTCTTCTCAT	1260
ATACTTTCCA	TTCTGAAGCT	TATCTCTTCC	TCCGTGATAA	GCTTCCGTCG	CGGGATGTGT	1320
TATACGCCCT	GTAAGACAGT	TATAAAGGAC	ATCAATGCCA	TAGTTAATGA	YTACCGAATT	1380
CCGGTGGATA	GTCAGTACTG	GTTTGCCACA	AAACAGTGCA	GTCACACATG	ACAGGAGAAG	1440
ATATGAGCCG	GATACCGCTG	CTCTGAGACT	TAACGCTCAT	GTAAACTTTC	TGTTACAGAT	1500
TCTTCCAGGG	ACTAAGAAGA	TAAGTANTT	ACGTTCCGAT	TCCAGTSTTT	ATTTCTGCAG	1560
TGACAGCCAT	ACCCGAGCTT	AATGGAATGT	GCTTATTCCC	GGTTGACAAA	TCATTCTCTT	1620
CAACAGAAAC	AATGACATTA	AAAACGAGTC	CCAGTTTCTG	GTCTTCTATT	GCATCTAAAT	1680
TTATATTTTT	TACCTTACCC	ACCAGATAAC	CATATCGGGT	GTAAGGAAAA	GCCTCCACTT	1740
TAATGATGGC	ATTCTGCCCG	ACGTTAATAA	AACCAATATC	TTTATTTTGT	ACCAGAGCAG	1800
TAACCTCCAG	CGTGTCTCT	TCCGGAACGA	TGACCATCAG	TGTTTCCGCT	GTTGTAACAA	1860
CCCCACCTTC	AGTATGAACC	TTCAGTTGCT	GAACTTTTCC	CGAAACAGGG	GCCCTGATTA	1920
CTGAAGCCTG	TTGACGCTCT	TCATTTTTCT	CTAACTCCAG	AGTTAATAAC	TCAATGCTGT	1980
CTGTTGTTTG	TCTTAGCTTG	TCTAAAATTT	CATTTTTTAA	AAGCTGCGTG	ACAAGCTGAT	2040

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ATTCTTCTTT TGCAGACAAT ATCTCACTCT CAATTTGCTC CAGTTGCGAT TTATAAACCC	2100
GTAATTCATT TGCTGCCTCA ACATATTTAT TCTCCTGCTC AAGTACAGCA TGTTTTGCAA	2160
TTGCCTGTTT ATGCAACAGG CTCCTGAAAT CATCCAGACG GCTTTTTTCA ACCCTCGATA	2220
CATTTTCATA ACGGTTTATA CGGGCAAGTA TTGTTAAWCG CTCTGCTCTT TTCTTATCCA	2280
GATTCAGTTC TTTTGTATAC TTCTGATTTT GCCATGTGGA AAAGTGTCT TTTATCAAAG	2340
AAGTTAAACG CAGTACTTCC TCTTCAGATA CATTCTGAAA ATAAGGCTCA TCAGGAAGTT	2400
TCAGTTCAGG AAGTTTATTT AATTCAATTG ACCGGCTCAG AATTTGATAC CGAATTTGTT	2460
CCAGCCTGGC CTGTAACAGT GATGACTGCG TTTTAAACGT ATCAGCTTCA GCTCCCAGCG	2520
CTGTAAGCTT TAATAACACA TCCCCTTTCC GGAAGTACTC TCCTTCTTTT ACGAYAATTT	2580
CTTTAACTAT CGAGTTTTCA ATAGGTTTAA TTTCTTTNTA CGCCCACTGA GTGTTAATTT	2640
CCCATTTGCA GTGGCAACAA TTTCCACCTG GCCTAAAACA GATAAAATGA AAGCAATAAC	2700
CAGAAACCCC ATAATAAAAT AAGCAACCAG ACGCGGCCGT CTGGATACCG GCGTTTCAAT	2760
TAATTCCAGA TGAGCGGGTA AGAATTCATT TTCGTCCTTT TCACGTACCG GAGTATCTAA	2820
CTGCTTCCGG ATTTTCCATG TTTCACTCCA GACAAGTTTA TAGCGCAACA GGAAGTCGCT	2880
GAACCCCATT AACCATGTTT TCATATTCTT CTGTTCTTTC TGTTAGTCTG ACTGTAAGTG	2940
ATATAAGTAA CTGTATAAAC TTTCCGGTTC AGAAAGCAGC TCCTTATGTT TACCCTGTTC	3000
AACAATTTTC CCTTTTTCCA TGACAATAAT GCGGTCTGCA TTTTTTACTG TAGACAGACG	3060
ATGAGCAATG ATTATAACCG TTCTGCCCTT ACATATTTTG TGCATATTGC GCATGATGAC	3120
ATGCTCCGAC TCATAATCCA GAGCACTGGT TGCTTCATCA AAGATGAGTA TTTTAGGGTT	3180
GTTCAACGAG GCCCTTGCAA TTGCGATGCG TTGACGTTGA CCTCCGGATA ATCCTGCCCC	3240
CTGTTCCCCG ACAATGGTGT TATACCCCTC ACGCAATTCA GAAATAAAAT CATGAGCACC	3300
TGSTAATTTT GCTGCATAAA TAACTTTTTT GACGGACATG CCAGGATTAG CCAGTGAAT	3360
ATTATCAATA ATACTGCGAT TAAGCAGCAC ATTGTCCTGC AACACAACCC CCACCTGACG	3420
ACGTAACCAG TTAGGATCGG CCAACGCAAG ATCATGTCCA TCAATTAAGA CCTGGCCATT	3480
TTCAGGAATA TAAAAACGTT GAATTAATTT AGTTAATGTG CTTTTTCCTG AACCAGAACG	3540
TCCGACAATA CCAATAACCT CCCCCTGCTT AATACT	3576

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

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TCAGCCCCGT GAGCGGGTTT GACAATTCCG CACTCACCAT TGSGCTAAGG GTTATCAGGT	60
GSGGTTAAGG AAATGGCAAA ACCTACCCCC GTCCAACTC CAGTCGCTGC ACATTCACCA	120
TCCCTGGCTT CTCACCTGCG CTGACATCAA TTTGTGTAC CCGCAGCGCA TATTTTTCAT	180
CCAGTGCTTT TAACCAGTTC AGCAGGTCAT TAAACACCAC AGSTTCTATC CAGACCTGGA	240
TATTCTCCCC GCGCTCGGCA ATCCGTTTGA TGACCACCGA GTGCGCGGAA GCTGTCACTG	300
ATGACCCGCG ATACCTGTGC TGGCGTTGTC GTGCCGGATT TTCGCGCCGC AATAATATCC	360
GGCGCGGCGC TCTTCAGTCG CGCGTTCATC GCCACCAGCT GCTGCAACAT CGTCTCCTGT	420
TGCTCAATCC GTTCGCTCAA CGGCTGCCAG ATGAGAACGT AATATCCGGC GCTAAACAGG	480
AACACTACCG CTGCCAGTAA CATGCCTTTT TCACGCGGCG AACGCCCCGC CAGGTGTTGT	540
GTCAGCCAAT GTTCGCCACG GCTTAACTGG CGTTCACGCC ATTGCTGAAA ATAGTGAATA	600
AATTTATCGC GTAACATGTT ATTTCTCCG CAACGTTACG CCGCCGGAAA CCGCATCACC	660
CTCTTTCTGT AACGCGTCCT GTTGACAAC ATAATCTGCC GCCAGTGCGC TACGAGTTTA	720
TCGAAGCTGG CAAAGTTCGC AGCCCGTAGC TGGAGGTGAA GCGTCTGGCG TTTTGATCA	780
AAGGTGAAAC ACGCATTTTC ATGTCGGTAA GTGACGCTGA TTTCAGGGTA CTGGCGATCG	840
CTGACAATTC TCGGAGCAGC CGGGTATCGT CGGTCTGTGG GCGATATTTT TTCAGCGCCA	900
TCGTACCTG AGAGCGTAAA TTCACAATCC GCTTCTGCTC CGGGAATAGC GTTAAGAACT	960
GTTTCTCCGC CTGGGTGCGG CTTTGCGCCA CCTGTTGCT GACGCTCCAT AACGTCACGC	1020
CCCGTTCCAC TACCAGCGCA ACCAGAATCA ACAATATCGG CAGAATCATC ACCCGCCAGC	1080
GCGCCCACTG TTTTCGGTAG CTGACACGAG GCTGCCACGG CCCTGTTAGC AGGTTCCCTT	1140
CCGGTTCGCC ATAAGTGGTA ATGGCGGGCA GAGCGTAACG GTCAGCGTTC GGCGTCTGCA	1200
CCAGCCCATG CAGACAGTTC TTCCGGTGCA ATGCCGACCA CGGTTAGTGA AAGCGGTAAA	1260
TCCTGCTCAT TGAGCTGTGC TCGGAACATG ACCGGAGCCA GCGCCCGCCC GGCGCTCCAT	1320
CCCCGGCATT CATCGATGCG GMAGATAACC CGTTGCGCAT CGCCAGCCAT AAACCCACAA	1380
GGAATGGACA TCCAGTCCGG CGCGACGATA GCGCGGGTGA TGCCGTTTGC CTGCAACCAC	1440
TGCGCAATGT TGCGCATATG CTGCTGGTGA ATCACAGCTA CGGTTGCCAG TTGCTGGTCG	1500
ATTTTCAACG GGGCGAAATG CAGTTCATCG ATATCCTGGT TCAGCTCTTC TTCCAGCAAG	1560
GCGGGCAGAA TCGTCGGTAT CTGCTTGCGG GGCACATCAG GCAGTTCAAC CTGCCAGACG	1620
CTGATCCATT CGCCGGGAAT GTAGAGTCGA ATCGCATCAG TTTGCAGCCA TTGCTGGAGA	1680
CATTCATCAG CAACGTCAGG CCAGATGCCG CACTCCACGT CGGCGGTACG ACGCTGCCAA	1740
CGGATGGGAG CGGAAMGNCA AAGCGGGAAA AAAATCTCAA GCATGGAAC TACTCACTTT	1800
CTCCTGTCTG ATGCCAGAGA ACAGAAAAGT GTTGTGGGCC CATGCGGACA ATTAACGAAT	1860
TCATCGTCAG TTCAATCTCA TTCACGGTGA TATCTGAACG CAGCCAGAAG TAATTGCTGT	1920

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CCACGCTCAG GACGGTTTTT AGCTGTTTTT TAGTACGCTC ATCGACGTCA GCAAGTAACG	1980
GCTGTGCAAG AAACGTATCG ACATCTTCCC AGCCCTTCGC ATGACGTTGT TGTAATAACG	2040
CTCGCGCCTG AACAGGGCTT AACCACGGGT CAAACAGCGC CTCAAGAATC ACACTTTGCG	2100
TGACGTCTAA GGTATTGATG TTGATTTGCT GGCGGGTCAT CGGCAGCGCA CAGACCAGCG	2160
GTTTCAGTTT TTGATAAAGC CCGGCGTCCA TTCCCTGCAC CACGCGCATC TCGCTGATAT	2220
CAGCCAGCGG TTGATTAGCG GCGTAAACG GCACCGAACG GGCGAGATAC TCGCTGTCTT	2280
CACGGCCCAG ACGCGTCTGC ACGCTGCGGT CTTCGTCAAT AAACCTCCAC AGGCTTTTCGG	2340
CTATCAGTTC GGCCCGATAA GCAGGCACAT CCAGGCGCGT GATCAGGGCA ATCAGTTGTT	2400
GTACCGCGAG CGGACGCGAC GCCGTCGTCG GCTGAGCGAG GGCATTCAGG TTAAAGCAAG	2460
CCTGTGCGTC ACGCAGAGTG ACGGCGATTT GCCCTGCGGC AGTGGGAAAA AACGCGGGCC	2520
GGAAGCCCN ACGTGCGCCAG ATGCACGCGC TTTTCATTTT TCAGGCTCAG ACTGAGTGCG	2580
CTCAACGCCA GGCTTTCCGC ACTGGCGCTG TACCACAGCG CCTGCTGGTA CTCCTGCTGG	2640
TGCGCGTTTCG CCCAAGTTGT TTCTGCATCC GCCCGGAAAG CGTGATGGTC ACCAGCATCA	2700
TAACCGCCAG CAATACCAGC ACCACGACCA GTGCCATTCC GCGTTTTGGT GGTGAGGTGA	2760
TCATGATAAT TGCGGCCCGC GTAACAACCA GATGCGTTCA ATTTGCGCCC ATTGTGGCGA	2820
ATGCAGGGTT ATGCGTACTG CCACGGGGAT CGCCTGCACT GATGACCAGC TCTCCTGCCA	2880
GCGCGTGCCG TCGTAGAACT GCAAACGGAG CGAATCCGCC GGGATTAATT TTTGCGTTGT	2940
TGGCTTCACG CTGCCTGCCG CATCGGTCAG TGGCCAGGCT AACCCTTCGA GATAACCACC	3000
ATGAATGCGG TAACCGACGG TGAGCAGATT ACTGCGCGGC AGACGCATCA ACGGATTAAC	3060
CACGCCGCCA CGTACAAAAC GCATCCCTTC ACTCTCAGAC GCCAGCACGC CAGCGCCCGC	3120
CAGTAACGCT RGTTCACGCT GGCCCTGATC GCCTCTTACC GGACGCGGCA TCATTTGTGT	3180
CAGATCGTGG GTCAGAAAAC TCATCGTTTG CTGCATGAGG TTTAGTTTTT GATCGTGTCC	3240
GGCGACGGCG CTATTCACGC GTGTAACCCG TTTGTACCT GCTGCGCCAT CATTGCCAGT	3300
GAGGCAAAAA TGCTATTGC CACCAGCATT TCCAGTAACG TGAAACCAGC GCGAGTCCTT	3360
CTCACTGTTG GTCTCCACG GCGCTAAACC ANGCGCGTCG TGAAGTGAATC ACTGACGAAA	3420
AGTCNTCATG AAGACTGACT TCAATATCCA CNGCATGGAG CAGCGCATTA NCGGTATTCA	3480
GTGGTGTTGG TTCGCCAGAA CCAAGCGGCT TTCCTGCCAT AATCGCTCTC GGCCCTGGGT	3540
G	3541

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTACTGGACA TCTTTGATGA ACAAGCTCCT CAGTGTAAT TGTACGTCTC TGATCGTAAT	60
CTTCCTGAGG GCGTTGAACA TCTATCCGCT GAATTTATAC CCTATACTCC TGAGTCGGCA	120
GATTTTCTGA TTCAACGTTT TTTCTCTGAA ACTATCCATA TTGAAAGTGC AATTGTTGTT	180
ACAGCACTTA AAATTGCCAA TCAGATTGCT CTATCTCAAA ATGAGACCAA GAATGTGTAT	240
CTGCTTGGAT TTGATTTTAC GATAAAGGGG GGGTTCAC TA GCAAGATCCC CTGCGCAGCC	300
TTGCATGCCG AACCAGAATA TCAAGAGCGA ATTATCAGTA GTCAAGAACA GCTATTGCAG	360
ATGCTCCTTG CAGAAAAAAC ACGCCTGAAT ATCAATATCA ATCATGTTGG TAATAAGCCT	420
TACAGCGTAT ATTCTGTTGA TGCATTTAAT CAAGTGTTCC CTGCCCCGCA TCGTGGAGTC	480
GTGCTGCCCC CACATGCCCC GATTTCCACT ACATCATCAC AAAATGGGGT GAAGGTGATC	540
GCAGAGATTA CTAATAATCA CTTTGGTGAT ATGGACCGAT TGAAGTCAAT GATTGTAGCG	600
GCCAAGCAGG CAGGGGCTGA CTATATCAAA CTGCAGAAGC GTGATGTTGA AAGTTTCTAT	660
AGCAGGGAGA AGCTGGAGTC ACCGTACAAC TCTCCTTTTG GCACCACCTT TAGGGACTAT	720
CGGCATGGCA TTGAAC TCA TGAAGAGCAA TTTTCCTTTG TCGACTCTTT CTGTAAAGAG	780
ATTGGTATCG GCTGGTTTGC TTCTATTTTA GATATGCCCT CGTATGAGTT CATTTCGGCA	840
TTTGAACCAG ATATGATCAA GCTACCATCA ACTATATCTG AACATAAAGA TTATTTGGCT	900
GCTGTTGCTT CTGATTTTAC TAAAGATGTA GTAATTTCAA CTGGTTATAC TGATGAGGCC	960
TATGAGCGTT TTAYCCTKGA TAACTTTACC AAGGTTAGAA ATATTTATCT GCTGCAATGC	1020
ACCTCGGCTT ATCCCACACC GAATGAAGAT ACCCAGCTAG GTGTGATAAG ACATTATTAT	1080
AATTTGGCGA AAAAGGATCC ACGTATTATT CCTGGTTTTT CCAGCCATGA TATTGGTAGC	1140
CTTTGTTCCA TGATGNTGTC GCAGCCGGTG CAAAATGAT TGAAAAGCAT GTTAAATTTG	1200
GCAATGTGGC TTGGTCTCAC TTTGATGAAG TTGC	1234

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ATGGGACCTT TCTTCAATGA TGTTGCCGAG TGGTTAGAGT CATTAGGTCG TAACGCTGTG	50
AATGTTGTAT TCAATGGAGG AGATCGTTTT TACTGCCGTC ATCGACACTA TCTGGCTTAT	120
TACCAAACGC CGAAAGAATT TCCTGTTTGG TTACGAGATA TCCACCGGCA ATTTGACTTT	180

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GATACCATTCTCTGTTTTGGT	240
TGACTGCCCGTCCATTGCACA	
AAGAAGCAAAACGTTGGGCG	
AAGTCTAAAGGGATCCGCTT	300
TCTGGCATTGAAGAAGGAT	
ATTACGTCCGCAATTTATT	
ACTGTTGAAGAGGACGGTGT	360
AAACGCGTATTCATCGCTGC	
CGCGCGATCCTGACTTTTAT	
CGTAAATTACAGATATGCC	420
TGCACCACATGTTGAGAACT	
TAAAACCCTCGACGATGAAA	
CGTATTGGTCATGCAATGTG	480
GTATTACCTGATGGGATGGC	
ATTACCGACATGAATTCACT	
CGCTACCGTCATCACAAATC	540
ATTTTCTCCTTGGTATGAGG	
CTCGTTGCTGGGGCGTGCG	
TACTGGCGTA	600
ACTATTTTACAAAATAATGC	
AACGTAATGTATTGGCTCGG	
TTAGTGAATGATCTGGACCA	660
ACGTTACTATCTTGTTATTT	
TACAAGTTTATAATGATAGC	
CAAATTCGTATCACAGTAA	720
TTATAATGATGTGCGTGATT	
ATATTAACGAAGTTGTATAT	
TCATTTTCGCGATAAGGCACC	780
GAAAGAGAGTTATTTGGTGA	
TCAAACACCATCCGATGGAT	
CGCGGTCCACAGACTCTATCG	840
ACCATTAATTAGCGGTTGA	
GTAAGGAATATGGCTTAGGC	
GAGCGAGTCA	900
TATACGTACACGATCTCCCA	
ATGCCGGAATTATTACGCCA	
TGCAAAAGCGTTGTGACAA	960
TTAACAGTACAGTGGGGATC	
TCTGCACTGATTCATAACAA	
ACCACTCAAA	1020
GTGATGGGTAATGCTCTGTA	
CGACATCAAGGGGTTGACGT	
ATCAAGGGCATTTGCACCAA	
TTCTGGCAGG	1080
CCGATTTTAAACCAGATATG	
AAACTGTTTAAAGAGTTTCG	
TGAATATTTATGATGAAGA	1140
CGCAAATTAATGCTGTTTAT	
TATGGTGTAAATCAAAAAG	
CAATAGAAGTCCGCATTCC	
TAAACGGTAGCAGATGATGG	1200
TTTTCATGGGCGTTTCAGGT	
TACTCAATCAGCCAACAACC	
GCAGCGAAAA	1260
CCCTGCTTTCGACCAGTT	
CAGGCCGGTTTACCTCCAA	
TGCTTTCCGT	1320
CAGAACTGAGATTTTCAGCCA	
GTTGCCGGATAGGTGTGTCG	
ATTTGCAGCAGTATACTTTT	1380
TCGTACAGCCAGAATGTGGC	
AGACTGAGGTGGAATAGATA	
ACGTCCGTATGCCCCGTCAC	1440
CACCTCCGGCGGGAGTGTG	
TGGTATCTGACATCATCATT	
TTTCTTTCTGTTTATAAAT	
GAAAACGCCAGCCGTGTTCA	1500
GGCTGACGTCAGGGAAGTGA	
AATCGGGTGA	1560
GTGATCTTCATGTTCTGG	
TGCAAAAGTTACTGTTGGCG	
CAGGGTACGGATACCCTCCC	
TGGCCTGTTC	1620
GATACAGGGCAACAGTGCTG	
CCGAATCTGTTTATCCTCA	
TCGTTGTGCAAGATAATTCC	1680
CGATTCGCAGTCGATATTGT	
CCTGCAGCCA	1740
CGTAATCAGATATCCAGCG	
CTGTTTCCGTGGTTAATGAT	
TTCATGTTGTGAATTTCCGG	
ATTACCAGTCAAGAGTGGGT	
AAACCTGGCA	1800
GACATCTGGC	
ACTGGCATCCAGATGAATGA	
GACTGACACCATAACGCCGG	
ATGAGTGTGA	1860
CGACCAGACGACGGAACGTA	
ACAGATAACGGTACCGGTA	
AAATGAATCCATTCTGATTC	1920
ACCAAAGTCACTGGTCTGGT	
GTAACAGCGAGTACAGCCAG	
GCGTTGTCCTTTCCGTGAT	
ATGTGCGGTA	1980
CTGCAGCGTATGCCGGAAAG	
AGTCGTAAACGGTTGTGGAG	
TGCAGGTTGATCTGTTGGTCA	2040
GATTCATCCA	
CCACGCGGAGTGAATAACCG	
TTTTCAGCGACCTTGTTAAT	
CAGTTCAGCG	2100
AGATTAATACCATCGACGTC	
AACGACAATGCGCCCATAT	
TCAGTGCCTG	

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TACGTTAACG CTGTCGGCTT CCGGCGTCAG GGAAAGTTTC ATTGTTTCAC CTCGCGGTGC	2160
TTACCCAGGA TAATATTATT TACCGCTCTG TAATTGTCGC GGGTCATCAG GCCGCTCGCC	2220
CTGCGAGGDC GGAGGATATC GATGCTGTTT ATTAAGTGAAG AGCGGGTACA GGCGGTGAAT	2280
CCCGGCTGCT CGGTACGCAC CAGCGCGTAT TTTTCCACGA GAAAGTTTCAC CGCATCACAC	2340
AGTGAAATGC CTGCCTCAAT ATGCTGCTCG ATCACACGTT CATCGGCAAA CGGTGTGTCA	2400
TTCAGTGTGA GGCCGTAGTG CTGGTCCAGC AGTCGGGACA GAAGTATCTG CCAGATTTCA	2460
ACAGGAGACG GGCGAGAAGT GGCCGCTGC CCGGGTAATA CAGGTAATGT TTTCACTAGT	2520
AAGATTTTCC TGATATGCAG ATATAAAAAAT GGGAAAGTGG CGTGGTGAAA ACACCAGGCC	2580
GTAGCAGAAG GCTATTCTGG AGAGTTAATT TTTCAATTCG GCGCTCGGAT AAACAGCCAG	2640
ATAAACGTAA CCACAAGTGC TGAGGGTATC GGCTTTGCAG GTCAGCCCTT TTGCATACAG	2700
CGTGACGGTA TGCTGATGGC GGGGATTCAG TTCACCGCTG GTGAGCATGA GTTCCAGTTG	2760
TTTCATCAGC AGCGGAAAGG CCTGGTCCAG GTGGTACGCA TCTGCATTGC TGTATAGGCC	2820
TCTGATACCG GCGCGGTCCG CAAGGTAATG CAACCGGTTA CCCTCCTGCA CCAGACGTGC	2880
CCCGAAACAG GGCGTCACGG TGCAGGGCAG CCCCCACCAG GGGCGGTCTG GATTGTCTGC	2940
GGGAAGTGTT GTCCCGGGGA GTGTGTCTGA CACGATAAAA TCCCTACAGA AAATCGGCTA	3000
AGAATGCTCC GGTATTGGCG ATAATTCTGC TCATCAGAAT TCCCACTCAG TTCAGGGTGA	3060
CGCTCATCAG CCGGACATAC GGGCCAAAAC TGTCCTTACG GCGTTCAGCA AACACGGCCA	3120
GCACACCGGG AATATCCTGT ACTTCACGAC CGGTATACGC CTCAGCACTG CCGTGCCAGC	3180
GGTACTTACC GGTGCAGAAC GGAAATAGAC GGGATGCAGG ATGCTGTTGG TGAATACGCA	3240
TGGCTTCACC ACGGGTGATG ATTTTCATAA TGGGATACCT CTGAAGACAG AAGATAAAAG	3300
TGAAAACAGG TGTGATGTGG TTGTGACGGT GACGGGTAA AGCAGACCGT GTTCCGCAAA	3360
GGAGAAAACC TGACTGCCAC CAACTATCAG ATGGTCCGGT ACCCGGATAT CCACCAGGGC	3420
CAGTGCTGT ACCAGACGTT CCGTGATAAG GCGGTCTGCC TTAAGGGGG TGAATTCACC	3480
GGACGGGTGA TTGTGTGCCA GTACCACGGC GGCGGCATTG TGGTACAGGG CGCGTTTAAT	3540
CACTTCCCGG GGATGGACTT CCGTGCGGTT GATGGTGCCG GTGAAGAGGG TTTCACCGGC	3600
AATCAGCTGA TTCTGGTTGT TCAGATACAG TACCGGAAC TCTTCACGCT CCAGTCCCGC	3660
CATCTTCAGA ATCAGCCATT CCCGTGCCGC ACGGGTGGAG GTGAAGGCCA CGCCGGGTTC	3720
ATGAAGATGG CGGTCCAGGG TTTTCAGGGC CCGCAGAATG AGACTGCGCT CGCCGGGCGT	3780
CATCTCTCCG GGCAGAAAGG AAAGTTGTTG CATTGTGCTT CTCTCCATTC AGTCGATGAT	3840
GCGCATAATG GCGCTGCATT CCGGATGCTG CAGGGCGTAA TCCCGCAACC GGTAATAATG	3900
GATCGTCATG GCATAAAGT CCGTACGACA GGCATGATGA CTGTACGTCA TCAGACAGGC	3960 -
GGCAATGCCG GCGGCTTCCG GGCTCATTTT AGCGCGGTAA CCGTTCATGG CATTGAACAG	4020

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TACCCAGTTT TCGTCATCAT CGTCATCCGG TTCGGGTGCC ATAAATGCCC CGCCGTTGTT	4080
CAGGGTGTAC AGATTCCAGA TACACCCGCA GTAGTCTTCG CACAGACGGT CCATCCAGCC	4140
GAAGACACGG GGCTCCAGGG TCACCCACTG TGGGAATGAGG CCAAAGTGCT GCGGCCAGAA	4200
GCTGATGCGC TGTTTCATCAG GGACTATGGT GGCAACCAGC TGAGGCTGGT CATTCCCTGA	4260
TGCAGCGGTT ACGGAAACAG AAGSAGTGGT GGAATTATGC AAGACGGTTG TCATGAGATT	4320
ATTCTTATA AAAAGTAAAT GAATGGAAGA AACCCCGGGG GAAGGGACAG ACGTGAGTCA	4380
GAAGTGCCTT TTCAGGGAAA CGGCATCAGC GCATACTCTC CAGCAGCGTT TCAGCCATCA	4440
CCCACAATGC GCGGTTGAGC TTAATGTCGG TGTCGATGCT GTGAATGGCA CGGGTATGGA	4500
TACGTTTTCC TCTGGCACTG CGACCGGAAA TTCCGCCTTT CAGCATATTC TCCTGAATGG	4560
TCTGATAAGC ACTCCACAGG TCCTTACCGT AATCCTCCCG GCGTCGTGGT GTCAGAATGT	4620
CGGCGGTGGT GACGGGCTGA TGTTGCTCAC CATAACGGTA AGTCAGTGCC GCCTGTGCCA	4680
GCGCCTGGCG TGCCGGTGGC GGCAGAATCA GCGACTGCAT GGCATCACGC TTTTCCTCAA	4740
TCCGGTCAAA AACCCCCACC ACCTCGTAAG CCCCTTCAAT AACTTTCTCC ACCACATTC	4800
CCCGGTGCGG AACACGCACT TCCCCAGAG ACTGACCACA GACGCATCCG TTCTGGCAGA	4860
CGAACCTGAA GTAACCCGGC AGCATCTGGT AGCTGGAGGT ACCGTCATGA GAGTTGAGCA	4920
GAATAATTC AGGGACATGT TCTCCGTTTA TCTCTCCGGC CCGCCGCAGA CGCAGCATGT	4980
GTTTGGTGTA TTCCCGGCGG TCCGGGTCAC GTACGCGGGT CTGGCAGGCG AAGAATGGCT	5040
GAAAGCCTTC CCGCTGCAGG CTTTCCAGTA CCGTGATGGT GGGGATGTAC GTATAGCGTT	5100
CACTGCGGGA GGTATGCCGG TCTTCACCGA AAATACCCGG TACATGGTGC ATCAGTTCTT	5160
CGTGTGTCAG CGGACGGTCA CGGCGTATCT GGTTGCATA ACCAAAACGA CTGGCTAGTC	5220
GCATAATTTG CTCCTTATCG GTGGTTAAGA TTTACTGGTG TAATAAATGA AAAAGCCACG	5280
TCTCCCGGAG AAGACGCGGC CTGACAGATG AAATGAATGA CGTTTATTGT CTGAGAAGCC	5340
CTTAAGTGGC GAGCTGAGTA TTAAGCTGTG TTCCGGCATC ACCAGCGCAA CTGACCTTCA	5400
GCATTACGGA TAACCAGCCG GGAATATGTT CCCTGGTCAT CTTCAGTAAA CACATTGCGG	5460
TAAGCTGTTA TGACAGCAAC CGCCTGCCCC TATGAGAAAG ATCCTTCAGC CAGGACATAC	5520
TCTGTGTGTA ACCCGGCATA TCTGGTTTCT CCTGATAAAT AGCCTCTGCC ATACGTTGTG	5580
GCAGAGGCTG AAGCATGAAA CTGACTTCAG GGATCAGTTA ACATTTTTTC CGGAAACGGT	5640
AATCAGCAGT GGATGGTAGT CCTGGGGATC GAAAACCGAT AACGGCAGAC TGACACGATG	5700
GCCGTTACTT TCTTCAGTTG CTTTAATGAT TTCGGTTGTG GCGACATTTT CCACGCACTC	5760
CGTTTCCAGA AATGCGTCTG TGTTTCGCGT GGCATTACTG TCACCAAAGG CTTCCGTTTC	5820
CATTTTTCTG GTCACCAGCG TCTGACCATA TTTGTCTTTG AGTTGCAGAG TGATGGTGAG	5880
GGGGCCAAAT CCTTCATCGT TTCCGCCATT ATCCAGCCGG AACTGGTAAG CACAAATATT	5940

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TCCCGGGAGC CATATCGTAT CTGTATTGCG TATACTGATG TAACGTTGAT CCTGTGCCCCG	6000
GAGTGGGGCA GACCACGTTA ACCCCAGAAT GAAGGCGGTA ATCATGCAGG TTTTGAACAG	6060
GTGAATCATG GTATTTACCT CTCTGAGTCA TGACGATTAC ACTGACAAAT CAGGTGATAA	6120
AACGTAAAAG GCGCAGAATA GCCGTTATGC CGGTAACTCC GGGGGTAATG TTTCTTCCAG	6180
TCGGTTAACC ATATTGCCGA GATGGGATGC ATCATATTCC ATGACGGGGC GTTGCCTGAT	6240
GATACTGACC ACCAGTGGTT TGATTAACAT GTTGGTCGCG GCCCSTTGTT GTATACCGGC	6300
GGCGAAAATG ATC	6313

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGTTGGCCGC TTGCGCAGAT AAAAGCGCGG ATATTTCAGAC GCCAGCACCG GCTGCAAATA	60
CGTCTATTTC AGCAACACAA CAACCAGCTA TCCAGCAACC GAATGTCTCC GGTACCGTCT	120
GGATCCGTCA GAAAGTCGCA CTGCCGCCTG ATGCTGTGCT GACCGTGACA CTTTCTGACG	180
CGTCGTTAGC CGATGCACCG TCAAAAGTGT GGCGCAGAAA GCGGTGCGTA CTGAAGGTAA	240
ACAGTCACCA TTCAGCTTTG TTCTGTCATT TAACCCGGCA GATGTTTCAGC CGAACGCGCG	300
TATTCTGTTG AGTGCGGCGA TTACCGTGAA TGACAAACTG GTATTTATCA CCGATACCGT	360
TCAGCCGGTG ATCAACCAGG GCGGAATAA AGCCGACCTG ACATTGGTGC CGGTACAGCA	420
AACCGCCGTG CC	432

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GGGCTGATTA CGATTTTATC AATCTGTCTA TAGAACATGA ACTGAATGAA GGAATAGCTG	60
GCAGAGAGAG GTTATGCCGG ACTGGCGGAT AACCGGAACC GGTGGCAGA GGTGGTTACC	120
CGTAAATTGC AGGACAGCTT TTATATGAAC TTTCTGGGA TGCGCTGAAC ACGGCATACA	180
GTGAACACCC AGAGTGGTTT TCCGGGCTTG TCTCCGGGGA TGAGAATTAA AAAGTGGATT	240
ATGCTGCTAT AGCGCGGCGT GATTTCCTGC AGGGATTTC ATTTATAAGA ATACGCCGCT	300

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TCGGGGAATC TCCGGTTCTC CTGAGAGTTA CGATTGTTTT TTTACTCAA TCCACAACAC	360
CTGAACTGGA ACTTGTTGTTG CATCCCTGAT TGTTACTCTG CAGGAAACAT CTTTTTTACC	420
ATCAAAGGAT GACTGTTTTT CTTTCTCCCC TCCGTAAAAC ACAACTTCGA TCACATTTCT	480
GACATTTTTT CCAGATTTTA CATAACAGGA TTGTTTCTGT ATGTTTTTTA TCTGGTGTA	540
ATTTACAGCAC TGACATTCCG CTTACGTAA TTTACACTGA ATACCCACG AGGAGAATAT	600
GCAGCACCGG CAGGATAACT TACTGGCGAG CAGAACGTCG TTGCCTGGTA TGGTTTCCGG	660
TCAGTGCGCA TTAAAGCTCC GCACTTTCTC TCCGGTGGCA CGCTATTTTT CCCTCCTCCC	720
CTGCCTTTGT ATTCTTTCGT TTTCTCTCC GGCAGCCATG CTGTCTCCGG GTGACCGCAG	780
TGCAATTCAG CAGCAACAGC AACAGTTGCT GGATGAAAAC CAGCGCCAGC GTGATGCGCT	840
GAAGCGCAGT GCGCCGCTGA CTGTCATACC GTCTCCGGAA ATGTCTGCCG GTACTGAAGG	900
TCCCTGCTTT ACGGTGTCAC GCATTGTTGT CCGTGGGGCC ACCCGACTGA CGTCTGCAGA	960
AACCGACAGA CTGGTGGCAC CGTGGGTGAA TCAGTGTCTG AATATCACGG GGCTGACCGC	1020
GGTCACGGAT GCCGTGACGG ACAGCTATAT ACGCCGGGGA TATATACCA GCCGGGCCTT	1080
TCTGACAGAG CAGGACCTTT CAGGGGGCGT ACTGCACATA ACGGTCATGG AAGGCAGGCT	1140
GCAGCAAATC CGGGCGGAAG GCGCTGACCT TCCTGCCCCG ACCCTGAAGA TGGTTTTCCC	1200
GGGAATGGAG GGAAGGTTT TGAACCTGCG GGATATTGAG CAGGGGATGG AGCAGATTAA	1260
TCGTCTGCGT ACGGAGCCGG TACAGATTGA AATATCGCCC GGTGACCGTG AGGGATGGTC	1320
GGTGGTGACA CTGACGGCAT TGCCGGAATG GCCTGTCACA GGGAGTGTGG GCATCGACAA	1380
CAGCGGGCAG AAGAATACCG GTACGGGGCA GTTAAATGGT GTCCTTTCCT TTAATAATCC	1440
TCTGGGGCTG GCTGACAACT GGTTTGTCAG CGGGGGACGG AGCAGTGAAT TTTCCGTGTC	1500
ACATGATGCG AGGAATTTTG CCGCCGGTGT CAGTCTGCCG TATGGCTATA CCCTGGTGGA	1560
TTACACGTAT TCATGGAGTG ACTATCTCAG CACCATTGAT AACCAGGGCT GGCAGTGGCG	1620
TTCCACGGGA GACCTGCAGA CTCACCGGCT GGGACTGTCG CATGTCCTGT TCCGTAACGG	1680
GGACATGAAG ACAGCACTGA CCGGAGCTGC AGCACCGCAT TATTCACAAT TATCTGGATG	1740
ATGTTCTGCT TCAGGGCAGC AGCCGTAAAC TCACTTCATT TTCTGTCGGG CTGAATCACA	1800
CACACAAGTT TCTGGGGGGT GTCGGAACAC TGAATCCGGT ATTCACACGG GGGATGCCCT	1860
GGTTCGGCGC AGAAAGCGAC CACGGGAAAA GGGGAGACCT GCCCGTAAAT CAGTTCCGGA	1920
AATGGTCGGT GAGTGCCAGT TTTACGCGC CCGTCACGGA CAGGGTGTGG TGGCTGACCA	1980
GCGCTTATGC CCAGTGGTCA CCGGACCGTC TTCATGGTGT GGAACAACCTG AGCCTCGGGG	2040
GCGAGAGTTC AGTGCGTGGC TTTAAGGAGC AGTATATCTC CGGTAATAAC GGTGGTTATC	2100
TGCGAAATGA GCTGTCCTGG TCTCTGTTCT CCCTGCCATA TGTGGGAACT GTCCGTGCAG	2160
TGACTGCACT GGACGGTGGC TGGCTGCACT CTGACAGAGA TGACCCGTAC TCGTCCGGCA	2220

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CGCTGTGGGG TGCTGCTGCC GGGCTCAGCA CCACCAGTGG CCATGTTTCC GGTTCTTTCA	2280
CTGCCGGACT GCCTCTTGTT TACCCGGACT GGCTTGCCCC TSACCATCTC ACGGTTTACT	2340
GGCGCGTTGC CGTCGCGTTT TAAGGGATTA TTACCATGCA TCAGCCTCCC GTTCGCTTCA	2400
CTTACCGCCT GCTGAGTTAC CTTATCAGTA CGATTATCGC CGGGCAGCCG TTGTTACCGG	2460
CTGTGGGGGC CGTCATCACC CCACAAAACG GGGCCGGAAT GGATAAAGCG GCAAATGGTG	2520
TGCCGGTCGT GAACATTGCC ACGCCGAACG GGGCCGGGAT TTCGCATAAC CGGTTTACGG	2580
ATTACAACGT CGGGAAGGAA GGGCTGATTC TCAATAATGC CACCGGTAAG CTTAATCCGA	2640
CGCAGCTTGG TGGACTGATA CAGAATAACC CGAACCTGAA AGCGGGCGGG GAAGCGAAGG	2700
GTATCATCAA CGAAGTGACC GGCGGTAACC GTTCACTGCT GCAGGGCTAT ACGGAAGTGG	2760
CCGGCAAAGC GGCGAATGTG ATGGTTGCCA ACCCGTATGG TATCACCTGT GACGGCTGTG	2820
GTTTTATCAA CACGCCGCAC GCGACGCTCA CCACAGGCAG ACCTGTGATG AATGCCGACG	2880
GCAGCCTGCA GGCGCTGGAG GTGACTGAAG GCAGTATCAC CATCAATGGC GCGGGCCTGG	2940
ACGGCACCCG GAGCGATGCC GTATCCATTA TTGCCCGTGC AACGGAAGTG AATGCCGCGC	3000
TTCATGCGAA GGATTAACT GTCAGTGCAG GCGCTAACCG GATAACTGCA GATGGTCGCG	3060
TCAGTGCCCT GAAGGGCGAA GGTGATGTGC CGAAAGTTGC CGTTGATACC GGCGCGCTCG	3120
GTGGAATGTA CGCCAGGCGT ATTCATCTGA CCTCCACTGA AAGTGGTGTC GGGGTTAATC	3180
TTGGTAACCT TTATGCCCGC GATGGCGATA TCACCCTGGA TGCCAGCGGC AACTGACTG	3240
TCAACAACAG TCTCGCCACG GGGGCCGTCA CTGCAAAAGG TCAGGGCGTC ACCTTAACCG	3300
GCGACCATAA AGCGGGAGGT AACCTGAGCG TCACAGCCGG AGCGATATCG TTCTCAGCAA	3360
TGGAACGCTT AACAGCGACA AGGACCTCAG CCTNGACCGC CGGCGGCAGA AATTCACTCA	3420
ACAGAATGAA AAAGTACTG CCGGCCGGGA TGTAACGCTT GCCGCGAAAA AACATCACAC	3480
AGGGTTACCG GCCA	3494

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GNCCCAAGCT TAGGTTTCGG GCCGCACTAC TGGATCTATT GCCAGCTTCA CCGCCAGACT	60
GTCAGTCAGT ACATCACCGT ATTTCTGCTG GCAGGTTGCC GGGCGGCTGC ACAGTCACTG	120
ATCAGTTGCT TCTGCTGTGC CGTACTCAAC TCTTCGTACT TTTTGATAAT ACCGCCGCAG	180
TCACCGCCTT TCGCCTGACA GGAATTCATT TCAGCAGAGC AGGCATCTAT CTGCTTATTG	240

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CTCAGGTAGT TATTCTCAAC AACAAACCACA GGGGATTAGA AGCCTTTTAG CCTGAAATAT	300
TTTGCGAGAG CACATCCAAT ACCAATAAAT GAGCCAATCA CACATCCGAT AAACAAAACA	360
TGCCGAATCT CTTTCAAACCT AATATTTAAA TTACCTGTTA TCAACCACTC CACCAAAGAA	420
AAAAACACAT CAATACATAG GAATGACACC ACTATAGAAA GAAATGCGAT TATAAAAATA	480
ATAACAATT CTGATAAGTG CTGAGAATTG CCGCTCATTT TTTCACCTCC GGAATGTAAG	540
ACTCAATCTT TTTACCTTCA TACTCAGAAG CAAAAGAAGC CGACACATCC CCAGCTATAC	600
CAGGAATCCT ACTGGGTGTC ATTTCTTTTG ATAGCCCCAA TTCTCCTTTA ATATCGGTAT	660
ATTTTTGAAG TGTTGGATTA AATTTCTGGGT CCCAGCCGTC TTTTAACCAG TTAGCACCAC	720
TATTAATGCC CCATGAAAGG CCTTTACCAA TGCCATATCC AATAGCAGAA CCAGCACCAT	780
TGATCAACGC ACCAGATGTT GGGGCTTTTC CTTCGAGCCA GTTTCCTAAT GCTCCTCCAG	840
TTGCATTCCA GCCAACTGTG CCTACAACCTC CATTCCCTGC ACTAATCACA TTAACCCAAC	900
CACCGATAAT CGCTGTTGTA GGATCTATAG TTCCATCCGT CAGATAGCTA ACACCTGCAT	960
TAGCTCCTGC CCCTAATCCC CACATGGCCT GAGCACCGCC AGTAAGAGAG CTACACTACC	1020
AGTGGCCAAC GCTCCGGCAT ACGCTTTATT GACTGCTTCT CCTCGCTTAC AGGCTTCACC	1080
GCCTGGGGCA TCGTTACAGG AAAGTACATC TGCGCCATGC GTCTGAGCAG CTTTGCTCTG	1140
CTCGGACTCT GTGCCACCAA CCAGGTTATT CTCAGCAATG TTCTTCCCGA CACCAGCCCC	1200
AGCAGCCGCG CCAGCCACAT CGCCACTGGC AATGCCGCCA GCCATACCCG CTGACAGCGT	1260
TGCCAGCGTG CTTACGGTTT GCTTCTGATC TTCTGTCACT TTCGACGGAT CTACGTCCGG	1320
ATAGAGGCTT TTCGCAATGG CTGACGAGAT CACTTCACCA GTACCCGCAC CAATTGCGCC	1380
TGCTGCCGCA CTGTTGCCCT GAAGGGCTGC TGTCACACCA CCGAGAATGG CATGGGCAAT	1440
GGCTTTTGCC GCTGTATTGT CATCAATACC CGCGTGATGA CCGATGATGT TCGCCAGCTC	1500
CGGCGCCGAA GCTCCGGCCA GAGCACCTGC TAAATTACCC CCCGCCAGCC CCTGAAGTGC	1560
AGCCGTTGCA GCCTGGATAC CGCGCTGCAT ATCGCTGCCG GTACCATACT TTTCTGTTC	1620
CTTTTTGTAT TCCGGCGTAT CACGCAGTTT TGCCAGATAT GCCTGCCGCT GTTCTTCCGT	1680
CGCATCCGCC GGAACAGGCC CATATTTATC CTGCGCAGCT TCAACGCATT CAGTTCCCCC	1740
TGCGTCCGCG CAATATCCGC CACCTGACTG CCTATGTCAC TGATAAGCCC CACTGTCTGC	1800
AGACGCCTCT GCTCCTTCTC CTTGTCAAAT ATCGGGCTGA TACTGTCATT AGCGTGCGCA	1860
GGGTCACGGC TCAGGTTCTG CAGATTCTGC TTCTGATTGC CCCTGTCCCG GATGGTGATA	1920
GTGCCTTCTG CCACTGCGGC CTGAGTCGTT CCTTCCGCAT GTCCGCTGTG ACCTCCGGCG	1980
GATATCATGC CACCCGGCAT GTTACCCTGA AATTTATCCC CGAAGCTGCC ACCACCGCTC	2040
AGACTGATTC CACTGTGACT GACTTTATAA TCCGCTTCGT TGTGAAGGTC ACTGAACCCC	2100
AGCGTTCCGG TATCCAGGTG GTTTTTATCC GGTGTGGCAG TGGAGGCAAT CACCGCACCA	2160

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TCCAGTTGGG	TATGTTTACC	CACTGTGATG	TCGAAGCCGC	CGTCACCGGC	AAACATTCCG	2220
GTTTGTTCAG	CAACGGAGTC	AAAGCGGCTC	TTCATCTTAT	CCCGGGAGGC	AGCGATGTAA	2280
CCTGAGCCGG	TCATGGAGCC	AAAGGTAAAA	CTSCCGCCGG	CASCCACGCT	GGTCTGTTTA	2340
CTGTCTGACT	TACTGGTGTC	CTGCTGGCTG	CTTATCAGCA	GGTCTGGGCC	CACATCGGCG	2400
ATAATCCTGT	TGCCGTTGAC	CTGAGCACCG	TTCAGTACCG	TATCCCGACC	ACTGTTGATG	2460
GTGACGGTTT	TACCGCTGTC	TGTTGTGGTT	TCAGTCCACT	CAGTACCGTT	ACCTTTCTCG	2520
CTGCCTTTTG	CCGCATTAAC	GCTGSCAAAG	ACACTGATAC	CGGCACCTTT	ACCTGCACCG	2580
ATACTGACAC	CCACGCCACC	GCCACTGCTG	CTGTTCTGTC	CCGTTGTTTT	TTGTGTGTTT	2640
GCCGCGCCAC	TCAACAGAAC	ATCATTCGCA	GCATCCAGGT	TTGTGTTACC	ACCGGCCTTA	2700
AGCTGGCTTC	CGGCAATCAC	AATATCTCCG	CGGTTATCGC	CCCTGTTTTT	ACCGGTTGCG	2760
ACAACAGACA	GATTATTCCC	GGCATTACAG	GTA CTGCCGG	ATACTGTGTC	ACTTTTCAGAA	2820
TGTTGTTGTG	ATTTTCGATTT	CTGGGTGGTG	AGCGACAGGC	TGACTCCCGT	CGCATTCCGG	2880
TCACCGGTTG	CGGAGGCCAT	TGCCGCAGCC	TGTCCGGCCT	GCACACCAGA	CAGCGCTGTC	2940
TTTGTAGCCT	GCAGGGTTTT	CAGACGGCTG	TCACTGCTCT	CCTTCGTCTC	CTGTGCACTG	3000
GTGACCGCAT	TATTGATGGC	ACTGCCCACT	GTGCCGGAAA	GGGCAACCGT	CAGCCCGCTT	3060
TTCTTCTGCT	CAAATTTTTC	GTCCACAGTA	CGACGGTCAT	GCCCCGGGTC	AACCACCACA	3120
CTGTCACCGG	TAATGCTGAT	ATCCCGGTTT	GCAATCACAT	CCGAACCGCT	GATATGAGCC	3180
TGTTTGCCCC	CGGTAATACT	GACATTACCG	GCAGTGGAGC	CGATGGTACT	GGCACTCTGA	3240
CTCTGCGTTG	TCCCGGCCTC	GCGGCGGTCG	TGCGTTGTCT	TACTGCTGCC	AATGGTGAAG	3300
CCAATACCGC	CGGTACCCAT	CAGACCGGAT	TTCTTCGTTT	CCTTAAAGCG	CCAGGACGTA	3360
TCTGTACTGG	TGGCAGCAAG	AACATCAACA	TGGTTACCCG	CCGCCAGTGA	CACATCCCGG	3420
TCAGCCACCA	CATCCGAACC	CTCTACCGTC	AGGTTATCAC	CGGCGTTAAC	GGTCACGCGG	3480
TTCCCCGACA	GCAGGGAACC	TGYTTCACGG	GAGGCACTGT	CCTCACTGAT	GGTGTGGGTG	3540
GTTTTCTTAC	TGAGAAAACC	TCCGCTTTTT	TTCTTCGTTT	CCAGATAGTG	ATAGTCACTT	3600
TCTGTGCGCG	TGGTCAGGGC	AACATCACGA	CCGGCATTCA	CGCTGATATT	GCCGGTTGCG	3660
GTAACGGATG	ACGCAACAGC	GGTGATATCC	CGTCTGCGG	TGACGGTGGT	GTCACCACCK	3720
CTGGCGATTT	CCGTTCCCTG	CTGACGGACT	GTCTCGTTAA	TCTCTTTCTT	TTTCTTCGAC	3780
GTATAGCTGT	CGCCTGCGCC	GGCAGACTCT	GCCACCAGGT	TCACATCACG	TCCGCCCCGG	3840
ATGACCACGT	TATTTTCCGC	AGCCATAACG	GCAGCCTGAC	TGGCAATATC	ACGACCGGCA	3900
ACAAGGAGGA	GGTTATCGCC	CGCCGTCACC	GTGGACACAG	CTGCGTGGCT	TTCATGACTT	3960
TCTGACCTGC	CGTTGCGACT	GTTTTTGCTT	TCCCTGACTG	CATTCAGACT	CAGGTCGTTA	4020 -
CCTGCAGAAA	GCAGGGCGCT	GTGCCCCGCA	GAAACAGAGG	ATGCTGTGAC	ATCCAGATTA	4080

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TGGCCTGCAG CCATCGCCAG GTTACCGCCG GCGCTGATGC TGCTGCCCTG TGAGGTGGTG	4140
GATGATGAAC TGTTGTCAATC AGTGTGCCAG AAACCGGACT GACTTTTGCT CCCGCTTATC	4200
AGGTTTACGG CAATGTTGAT GTCATTACCC GCAGACATTC CAAGGTCTCC ACCGGACGAG	4260
ACCGTTGCCC CGGTAATATC AATGTTTTTC CCTGCATCCA GTGAAAGTGA ATCAGTGCCT	4320
TTAATGGTCG CAACCGGACC GGTGTCCGTA CCGCTGAGAT GCACACCACC ATATCGGCTG	4380
TCACTGCCCC CATTCCATTG CTGACGCCGG GTGATATTGC TGATGTTGCC ACTCACGCTT	4440
TCCAGTTGTA CGGTTTTACC GCTGATGACT GAGCTGATAT TGCTGATATC CCCGATGGCG	4500
CTCAGGTCCA GGCTACCGCC CGCGCTTATC AGCCCTGCAT TCAGGTTGTC GATATAGCCG	4560
GTACTGTGCA GCGAAAGGTC GTTCTGTGCG TTGATGCTGC CGCCGCTGTT GGTGATATTG	4620
CCGTCCGCAA GCTGCACGTT GTTCCCCTG ATAACGCTGC CGTTATGCAG GGTGATATCT	4680
TCCGGCGACA GATACAGTTT CGGGACCATG ACTGTCTGTC CGTTGATGGT GACTGACTCC	4740
CACCACAGCA TGCTGCCGTC AAGCTGAGCA ATCTGTTTCA CTGTCAGCGC CACACCAAAC	4800
TCTAATCCCA GTCCTTTCTG TTGTCTGGCC GCGTTATCCA TCAGATACCG CATCTGTTCC	4860
GTGTCTGAAC CCAGTCCGTT GAGATAACGT GAACCCGTCC GGCTCAGCAC CGCGTTACTG	4920
ACATACCGGG TATCAAAGAC CGCATCCCC AGGAAACGAT AATCTTTTTT CGGTTTCAGC	4980
CCGAGGCGGT CAAGAAAATA CGATGAGCCC AGAAACTGTT TTTCATCGGT ATACGACGGA	5040
GCCGTTTCAC GTGGCGCCTG ACCCGGTTTC GCTCCAAGAA GCTCATAACAG TCCGGCAAAC	5100
AAATGGCTGT CCACCTGTCC GAGACCATCC AGTTTCGGGT TCACCGTAAT CAGATACGGA	5160
CTGTCCGGGT CCGTGGACGG AACCAGGTAT CCATTGTTGC CGGAAGGCAG TGGCCAGTCA	5220
TCACTGATAC CGGTCTGACC GGTCAGTGGC GAACCTCCGG CAATATTTTT CAGGGCACCT	5280
GCCAGTTCAT CGTGCCATTG CGGAGAGCCA ACCACCACCG GCTCATACTG CTGCAGCGCT	5340
GTCTGTGTCA GACTGTCTCC GCCGGTCTGC TGACTTAACG TATTCAGTAC AGGTGCAGAG	5400
ACCACCGGAC TGACACTACC TGCATGTGCA GTGGTTGTTT CGTTATTGAT ACTGCTGGTA	5460
AAACGGGTCT TAACATCCCC GCGCGCTGA ATAACGGAAT AATACGTCTT ACCGGGCGTG	5520
TAATCTTTTT CCCGGCCATC CAGTGAAAAT CTGATGGTAT TGTTTTCAA TTCCGGTGAC	5580
AGCAGGGGCA GTTTATCCAG AGAGCCTGTT GCATAGCTAC CGTAAACGT TTTCCGGTCTG	5640
TAGCGGTATA CCAGATATTC ATTCTCTGTC CCCGTCTGCC AGCTCTGATT GCTTAACTCT	5700
CTGCCCCGAGA GTGCGATATC CCCATTGCC AGGATAAATG ACGCCCGGTT TTCCAGTCGT	5760
TCAGCCTCAG CAGAAAGATT ACGCCCTGAC GCAATGCGGC CTGCCGGATT ATCAGCACCG	5820
GTTACTGTTG TGATGTTCTG GCTGCTGAGA AAGCGCTGTG TGGCACTGTC AGCAAACGGA	5880
GCGTAATAAT AAAGCGTATC CATTGTGATA TTGCATGCCC CGTGCCCGTT GCAGGGCGTA	5940
CCGTGCTGAT TTTCAACTTC ACGGGTGAAA TAGCCATAGC TGCCGTCAGG AAGAAGGGAA	6000

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AGGGGAATAT CAACCAGAGC ATTTCCDATT CCCTGAATGG ATGAGGGGTT AGTCCGGGTT	6060
GTTGTTGTGG CAGAAAATCC CTCCCGGTGG TTCAGAAGAT GCGCGGTTCT TACAACAATA	6120
TCGCCCTGAT GCGTCTCAAT ATTCOCBGAA GTATTGATAA TCTCTGTGTT TGCACCGCCG	6180
GAAGCATCCT TCTGTACCCA CAGACTGTTG CCGGCCAGGA TATCACCATG CTGGTTATGC	6240
AGACGGTCTG TAAACAGCTT CAGGTTATTC CCGCATAAA TCAGCGCACT GTTCAGCAGG	6300
GTACCGGCCA CATTCATTGT CAGACTGCCT GCCGTGCCGG TAAAACCACT GATGGTGATA	6360
TCACTCCGSC TGTTCAGACT CACATCGCCA CCGGCTGAA GTGAACCCGG TGCCTTAAGG	6420
AAAAGACGCT GTGCGCTGAA AACACTGTTG CCTTTACCGG CAGTCAGCGT TCCATTGTTG	6480
GTGAATGCCT CTCCGGCACC GAGCACCATG GCATCACCTT GCATGACACC GCCGTTGGTG	6540
ATGGCATT TT GCGACGTGAC GGAAAGGGTT TTCCCTGCGG CCAGGGTACC GTAATTCGTG	6600
AGGGCAGCAA TCAGTTTCAG TGTGACATCA CCGGTGGCCA CCACCTGCCC CTGACCACTG	6660
AAGTCCTGAG CGTCAAGCAG CAGGTTGCCT GCACTGTACA GCGGCCCTGT ACCATTTTGC	6720
AGCAGTGAAC TGCCCTTGAC GCCAAGCCCG GAGGTTCCCA GCAGGGTACC GCTGTTGCTG	6780
AATGTGTGGT AATTCACCAG CAGGTCCGCA CCCTGAAGCG TACCGGTATT ATTCAGCGTG	6840
GTTCCTTTAA CGTCGGCACT GCCGGTGGCA AGTACGCGTC CGCCGTTGAC AGTATTCACC	6900
ACATCCAGCA GCAGGGTGGC AGCCTGTACC AGTCCGCTGC CGGTGTTTCGC CAGCACCTGC	6960
GCCGTCAGCG TGAGGTTACT GCCGGAGAGG ATTTTGCCGT CGTTCTGCAG ACGGTCAGTG	7020
GCGTTCAGGG AAACCCCGCC ACCACCCTGT ATCGTGCCCT GGTTACTCAG GGTCGCAGTA	7080
CTGACATTCA GTGCATTCCG GCTCATCAGA ACACCACCGG AACGGTTGTT CACGCCACCG	7140
GAGGCGGCCA GCGTCAGCGT TTCGCCCTGC AGATGCCCCG CGTTTGTGAG TTGTCCTGCC	7200
GTGATGGTGG TGGCATTTC CTGTAATTGC CCGTCGTTT TGACACTGTC TGCCTTCAGC	7260
GTCAGCACAC CTGCACTGAG CAGTTTTCCG CTCGCGTGAT TGTGCAGCGT CTGATTCACC	7320
GTGAGCGTGA GAGCATCCAC ACCGGTGATG TCACCCGCAC TGGTCAGTGA GTTCGCCTTC	7380
AGGGTCAGAT TTTTGTCAAT CCATTGTCCG CTGTTGCTTA AATTCAGTGC ACTGAGCGCC	7440
ATTTACCGT TCGAGGTGAC TTTGCTGCCT GCTGTGCTGA CGAGCTCACC CGTCAGACGT	7500
GCAGTCAGGC TGTCAGCCGC CTGGATCGCC CCGCTGTTT CCAGACTGTC TGCGGTGATC	7560
AGCACCCGTT TGCCCTGCCA GTGTCCGGAA CTGGTAATAC TGCCTGCGGT GATTGTCAGA	7620
TCGCCGCTGG TCAGCAATGA ACCTCCGTTA TTCATCAGCG CAGGTTGAGG GGATGCCATA	7680
CGGGCGGCAA GCGTCAGCGC GGCTATCCCG GTGAGCGTGC CACTGTTGGT GACACTGTTT	7740
TGGCGAATCG TGACATGGTT ACCCTGGACA GTGCCGCTGT TATCCAGTGA GTTTCCATCA	7800
AGGGAGAGCG TGCCGGCCGA AAGCAGACTG CCGCGTTGT CCATGGTGGC TGCTTTCAGC	7860
GTGGTGTAC CCTGGCTCAT GATATCGCCG GTACTGGTCA ACTGACCGGT TGCCGAAGCA	7920

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GTAAGGTTAC CGSTTGCCAG CACGGAACCA CTGTTGCCCC AGTTGTCCCG CYTGACGGT	7980
GAGATTCTGT CCCTGCGTGG TCCTGCGGTA TGCAGTGTTC TACCCCGGAG GGTGAGGTCG	8040
CCCGCCGTCA GCCAGCGCCC GTTACTACCC TGTGAGAGGG TGTCGCCAGC AAGCGCCAGT	8100
GCACCGGCGC CCTGCAACAG GCCGTCACCA TCCAGCGTGG TCGCCCTGAC GCTCAGCGTG	8160
TCAGCGATGA TTTTCCCGG ATTGCTGAGG GAGACAGCAT TTAACATTAA ACCATTATCA	8220
CCGGTGATAA GCCCGCTGTT GCGGATGTCC GGTATATCCA GCGTCAGGTC TGCAGCACTG	8280
TACAGCGTGC CGTTCTGCTG ATTATCAAGC CTCTGTGTGT TAACGGTAAG TGAGGCCTCC	8340
CCCTGCAACA GACCGCTGTT GGTCAGGGTC TGTGACTGTG TATTCAGGGC GGAACCAACA	8400
AGTACGCCGC TGCTGGTCAG TTCCGGCGCA CTGAGGCTGA GCGACGGGGC ACTGCTTTTC	8460
CCGCTGTGGG TGAGCTTTTC ACTGGCGTTC ACCACCATGG TCTGTTGTGC TGCCTGCGTA	8520
CCTGCAAGAC GTGCATCTCT GGCCTTGATG CTGAGATTTT TACCGCTCTG AAGCTGTGCG	8580
CCCGCTGCGG TACTCAGTTT GTCTGCCTGA ACCCGGAGGG TGTCACCGGC ACTGTTTTCC	8640
CCGTCCAGCG CCACTGTTGT CACATTCAGC GTCATCGCAG CATCGCTGTG GGTGACCGAT	8700
TTTTTACCGG AGCTCAGCGC CTGCGCACTG ACCGTCAGCC CTTTGCCGCC GGACAGCACA	8760
CCGTTCTGTG TCACATCCTG CGCCTTCAGC ACCAGTACAT CATCGCTCAC CAGCGAACCT	8820
GTACTGGTCA GTTTCCCACT GGCCGTGATA TCCACTTTGC CCTTCGCGCC AGTGCGGCCG	8880
CTCTGGGTAA AGTCGCGGGT ATTCACGGTC AGGGGACCGC CACTGAGCAG GGAGCCACTG	8940
TTGCTGAGCG TTGTACTGCC GAGCGTCAGG GAAGCCCCCT GAACAGCACC ACTGTTATTC	9000
AGCGTGCCGG CATCGAGTCC CGCATGACCT TTCGCCAGCA ATATTCCGTC CTGTGTCAGC	9060
GTGGTGGCGC TGGCCGTGAG ATTCTGCCCC GCGTTATCT GTCCCTGTGT TGTCAGCGTG	9120
TCACTGGCGA CAGTCACGAT ATCGCGGGCC GCGTTAATCT GGCTGGCGGT ATCCTGTGTG	9180
ATGTTTTTTCG CGGCAAGCGT TACATCCCGG CCGGCAGTCA GTTTTTCATT CTGTTGAGTG	9240
ATTCTGCCGC CGGCGGTCAG GCTGAGGTCC TTGTCGCTGT TAAGCGTTCC ATTGCTGAGA	9300
ACGATAATCG CTCCGGGCT	9319

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 551 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ATGAGGCGAT TAAAGCAACA TTGGGCAGTG ATAATGCCCC CACCCAGCCA CCTAACGCAG	60
CGAAGAGTAA TACATCGCCC ATGCCTAATG CTTCTTTACG CAGAACTATT CCGGCTATCC	120

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AGCGSAGGGA GTAAAAAGTG ATAAATCCCA CCAGTACGCC GGTAACTGCG TCTTGTAGCG	180
TTAACGGACT CTGTTGCGCC CATGCTGCAA TCAGCCCGGT CCACAATACG CCTGAGTAA	240
AAACATCGGG CAGCCATTGG TTGTCGAGST CAATGACGCT CGCGGCAATC AGCCAGGCGG	300
ATAATATCAT CACCGCCAGC CCCCATCCAC TTTCTGGCCA CACCAGACTC GCCAGCAAAA	360
AAGTGAGTGC TGTCAATAAC TCAACCAGCG GATAACGTTG CTGATTTTCG CCTGACAGTC	420
GCGGCAGCCC TTTGAGCATC AACCATGAGA GCAGCGGAAT ATTGTACGA ACGCGGATGG	480
TCTGCTGGCA ATGCGGGACA GTTGCGAACC GGGTTAGCCA AGGGCTTTAT TTTTGGACT	540
GCGGCACTCG G	551

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CATTTACCAA ACCCCGTTTC AATATCTTAT CTATTGCCCA TCTCATATTA AATATAACCG	60
ATAATTTGGT GGATACTAAT AGTAATTACC TTGTTATTGA AAATATAATT ATTGTTATTT	120
TTAGCCTCAT TAATTAAATT GAAAAATCCT CTCTAATTTT TGTCAGATTA GGGCTGTAGA	180
AAGGATCGAG TTCAAGATGT TTACCCATT TGCTTTTCAT AAAGTCCACT TCCCTGGCAA	240
ATCTGGCTAG TTTCTCCGGT GAATCTTCGG CTCCTCGACT AATCGATTCA TAGTGGTAAA	300
GCTCGGCATA AGGTGTCCAG AGATTACGAT ACCCCGCTTC GNGTACTTTC AGACAGAAGT	360
CCACATCATT AAAAGCAACA TGCAGATTCT CTTTCATCAA CCGGCAACT TCCTCATAAA	420
TATCTTTGCG AATAAGCAGG CAAGCCGCCG TGACGGCCGA GAGAGTTTGT GTCAACAACA	480
AACGGCTGAA ATAGCCCGGA TGGTGGCGAG GATAATGTTT ATGGGAGTGT CCAGCTACAC	540
CACCAATACC GAGAATCACT CCGCCATGTT GTAAAAGTAT CATTACTGTN ATAGG	595

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TGGCAGTTGA ACAGATTTTC ACATCAGCAA CAGATTAGCG AACGGGACTT GGCATTAGCC	60 -
GAGCGTTTTA GTGAANGTTT AGCTCTAACA CGTCTATTAG AAGAGCGCAC GCAGNATTAT	120

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CACTGAACTA GAGATTGAAA AACAAATTGCT TACCACCAAG TTGTCTGGCG TAGAGCAGCA 180
 GTTAAGGGCT GAGCAAGAGT CGCTTCAGCA GGCCCACTCT GCATTGCTCT CAGCAGCAAA 240
 AGAAAAGCAA CATCAACTTG ATGAGTTGGA ATCGGTGCTC AATGAGCGGT ACAGTGAGAT 300
 TGCAACCTTA ACCCGTTGGC TGGAAGAACG TGATCAGGCA CTCCTTAGTG CAGCAAGTGA 360
 ACAACAACAG ACCAATGANA CCATATAGAG CTCAGCCAG 399

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1013 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ATACTCTGCT TGTTGAGCAG CCATTACGTC GCTTTGTGAC GCAATATTAG ACTCGTGCAC 60
 TGCTATTAGT TGAGTCAGTT CATCACATTG TTTAGAAGCC GCAGCCAAAG CAAGAGTTTG 120
 CTCATCTATG CTTTGCTGCA ATGTTTGTTG CACAAGTTGC CCTTCTTCCA GCTGTTGCTG 180
 TAGATTTGCA CTTACCTTTT TCAGTGCATC ATATTCCAAG CCTAACGTAT CGTGCTGTGC 240
 TTCCAGTAAT CCATAAGCAT GCTGCAACTG GTTTTTAGTT TGCTGCTCAC CGTCAAGCTG 300
 TTGCTGCAAT GCATTAGCCT GCTGTTGCAA CAAGTTCACC ATATTGTCTC GCTCGGCCAG 360
 TGTACGAACC TGTGTATCCT GGATATGTAG CGCTTGTTCC AACTGAAGCT GTAATTCGGT 420
 AATTTGCCGC GAATGTTTCG TCAATGCTCT GTTGCTCTTG CTGAGCGCGA GAGTAAGGTG 480
 AGATGCACGC TGTGTTTCTT CACTCAATTG TAACGTCAGG GTATTGACCT GTTGCTCCAG 540
 TTGATGGCGA GCTTGCTCCT GGCTCGTGAT GCGACTCTGT TGCTGCTCTA GTTGATGCAG 600
 AGCTGTATGC AACTCATCGT TGGCTTGAT TCGCTCCTGC GACCATACAC TCAAGTTTGT 660
 TTGGGCCTCA TTGAGCTGTT CTTGCAATAA TGCCACCTCA GATGTCAGCG AATTGATATG 720
 TTGCTGGGCA AAAGATAGCT CATCAGATTG CACTTGAGCA TGTGCAAGCT GCTTTTCCAT 780
 TTCTAATATG CTGTTATGTT GTGCAGTAAT GCGCTCGGCA AGACGCCCCC TTTCCAATGC 840
 CTGCTGTTCT ACCAATAGCT GCCGTTGAGC CTGAATGTCA TCTTGTTGTG TAGACAAGTG 900
 ACGTTTTAAC TGGGAATTCT CCCAACTCTC GCTACAAGAT TTNCCCAAAC GACAAAAGAT 960
 GTCTTGGAAT TGTNTGGGTT ACACGAGCAT TTTCTGAGGA TTTTATACCA ATN 1013

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 689 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GATATCCACA TCGAGACGTT TGAAAAGAGT CTGGTGATCC GTTTTCGTGT TGACGGCACA	60
TTACATGAAA TGCTGCGTCC GGGGCGCAAA CTGGCCTCGC TGCTGGTGTC GCGTATCAAG	120
GTGATGGCGC GGCTGGACAT TSCCGAAAAG CGCGTGCCGC AGSATGGACG TATTGCGCTG	180
TTGCTGGGCG GCCGGGCGAT TGACGTGCGT GTATCAACCA TGCCTTCCGC CTGGGGGGAA	240
CGGGTGGTGC TGCGACTGCT GGACAAAAC CAGGCTCGCC TGACGCTGGA GCGTCTGGGT	300
TTAAGTCTCG AACTGACTGC GCASTTGCGC CACTGTTACA CAAACCGCAC GGCATTTTTC	360
TGGTGACGGG GCCGACCGGT TCCGGCAAAA GCACCACGCT GTACGCTGGA TTGCAGGAGC	420
TGAACAACCA CTCGCGTAAC ATTCTCACGG TTGAAGACCC TATCGAATAC ATGATTGAAG	480
GGATCGGTCA GACGCAGGTT AACACCCGCG TCGGCATGAC ATTGCCCCGT GGCCTGCGCG	540
CAATTTTGCG TCAGGACCCG GATGTGGTGA TGGTCSGTGA AATCCGCGAT ACCGAAACCG	600
CAGAAATCGC TGTTCAGGCT TCAACTGGAC CGGACACCTG GGNACTTCN ACGCTGGNAT	660
ACCAAAAAAA AGGGGTGGGG GGATTATAC	689

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCAGCAGAA CCGAGATCTT CCATCAGCTG GCGGGCCTCG GAAGANTCCC GCTGCCAGAC	60
CGCATTCAGC CGCTGTTCAA ATTCGGCCTC GTCGATTGTC CTCAGCGTAA AGGGCGCGTT	120
CAGCCCCCGT TGCAGCTCCT GCAAAACAGA GAGCGACAAC GGATGCACAT GGAGGATCTC	180
CAGCGACGCT TCGCACCATG CCACCAGGCT AAACCGACGG CTGAAACTAT AGGGCAGACG	240
CACGGTGTTA GCGGTGGTTT CCTGTGCTAC AGGCACCATT AACGCGTTCT CCCGGCATT	300
AGGAACGCAC GAACTTCTGG CGGTAAGGCC TGATTTTGCG CAGGCAATAT CGCTGCGCAG	360
TGTGCGGCAT CAGGCTTAAG CCCTGCTCAT CGCGGTAGAT TTGCTCGGCG CGCATGTAGT	420
TATATTTGCG CTGCGACACA CCGTCTGCCG CCATACCGTC ACGCAGAATG GTCGGGCGGA	480
TAAACACCAT CAGGTTACGT TTTTCTTTTT TATCCGCCGT CGATTTAAAC AGGTTACCAA	540
TCAACGGGAT ATCGCCCAGC AGCGGCACTT CTCGCCACGC TTTCTCCCGC CTGGTCGTCC	600
ATCAGACCGC CAAGCACAAT TAGCTCACCA TCGTTAGCCA ACACGGTGGT TTTCASTTTG	660
CGCTCACCAA ACACCACGTC GAGGCTGGTC TGTCCTTCCA CCTTCGACAC TTCCTGCTCA	720

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ATCACCATCT GTACCGCGTT TCCTTCGTTA ATCTGCGGCG TGACTTTCAG CATGATGCCG	780
ACTTTTTTTC TCTCTACCGT GTTGAAAGGA TTGCTGTTAT TGGAGCCAAC GGTAGATCCA	840
GTTAATACCG GAACGTCTCTG GCCCACCATG AAGAAGGCTT CCTGGTTGTC CAGCGTGGTG	900
ATGCTCGGCG TGGAGAGCAC GTTCGAGCTG GAGTCGTTTT TGACCGCCTG TACCAGCGCC	960
ATCCAGTCGG CTTTCAMCAC GCCAACC GCC GTACCGCTAA AGCCAGAAAG AAGCTGAGCA	1020
AGCGTGGAGA GATCGCCGTT AGTATCCGGA TTTATGGTGG TAGCGCCGTT TTCACTGATC	1080
ACCGTGGAGC CTTTCTGCGG TTTTGCTGA GAAATCGTGC GCCCAGCGTA CCAATAGGGA	1140
TCTGCGTACC GTTAGCAAAC TGCATTAATC CGGCATCTTT CGACGCCAC TGCACGCCGA	1200
AATTGATAAT TCACCTTCGG CAACTTCCAC GATCAACGCC TCGACATGTA CCTGAGCACG	1260
GCGAATATCC AGTTGTTCAA T	1281

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CAATATTAGC GCACGGCACC AAAGGTGATG AATGAGCAGG CTGRAATATT ATTTTCCCGC	60
GGTGCAGAAA TCCTTGTTCT TGGTTGTACA GAAATCCGG TTATTCTGGC GCAACGTAA	120
AGAGCAGCCT TCCCGCTATA TTGACTCAG GCGTCACTCG TTCGTGCCGG AATAAAATGG	180
TACGAAAATC GTGTCGGTAA ACATTATCTT TTAACCCAAT AATCATTTAA ATCGCAGCCA	240
GAAAGTTATT CGCTTTTAAC TGAATTATAT TTATAACGGA GAACATTATG GTTTGGCTGG	300
AAATTATCGT AGTACTTGGT GCAATAKTTT TTGGTATTCG CCAGGGGGGA ATCGGTATTG	360
GTTTATGTGG CGGGCTTGGG CTTGCCATTC TGACTCTGGG ACTTGGTCTG CCTATGGGGG	420
G	421

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GTTACAATG GCGTAACAAA TTTCAATAAC GTAGAAGATT TGCTGTCAGA AAGGTCAATA	60
TTTCCTTTCA ATGGGTCAAA GACTTGCTTC TGGAATTCAT CCGGTTTTTT CTCCAGACGT	120

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TTTCCTTCTT CATAATAGTC AATATAACTT TTACCACTGA GTGTTTTGKC YCCATTTCTG      180
GTGACACCAG CTAAGTCACC TATCAGCGTA TCCCMATCTT GCTGGGTAAT GAGGACTGAT      240
CTTTCAACAG AATACTCTTT ATTATACTGA GATAATATTT TAAAGTTATC TTCTAAAAAT      300
GCAGCATGGG GGGCATCATA TCCCATTTTC AAAGTAATTT TTGCCGTGTT TTTTCTCCCA      360
TTCAGCAATA ACATCGGCCA TTTTACTGGC GACATGTTCA AACATTGCCT GTTTTGAAGC      420
CTCAAGGATG CCGTGAATTA TCCCCGTAAC AGCCCCCTACC AGCGCGCTTA CCGGTGCACC      480
AACCAGAGAT GTCGTTGCAG CAGCACTAAT ACCTGAAGAT ACTGAAGCCA GAACAGTGCT      540
TATCGTTGTT AACGATGCAT CAATAGCTCC TGTTTCTTTG TGGAAAGCAG CAAGTAACT      600
GTCACCATCG TATCCAAGTT TTTTGAATCG TTGTGAATAC TCCTCTATTT TATTGGCAGC      660
TTTAACTTA TCGSCAATGG ACAGGAATGA GAGGGGACTA ATTGCCAGTG TCACAACAGA      720
AGCAATTAAA CCGGCAGCAG CAGCAGATGT AGATAACCCC TGTGCTGCAC GCTGTGCGAY      780
NAATATATTG AGAAATACCT TTTCCAACAT TACCCAGTAC TTTCGTTGTT AATTCAACAC      840
CTGCTGCAGC TTTAGTTCCG GTATCTGCAT CTGCATTGCT CAGAATGAAA CTTGCTGAAA      900
TCGCAGATAA AATACCCGAT ACAGTATCTA ACCCTGCACC GATATTATCA AGGTTAGGTA      960
AATTCTGTAA CTTATTACCA ACACCGTTTCN GGNCTGTTGG TATTGGGATA ATACACTT     1018

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(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

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GGCAATGTTC AAATCGATAT TGTGCAGCAC CTGGGTTGGG CCAAAGTGCT TGGAGACGTT      60
TTTAAATTCA ATCACAGGAT TTTTCATCCTT CTTTCCAGAC GACGCAGAAT AAAGCTCAGC      120
ACCAGGGTAA TAATCAGATA GAACACCGCC ACGGCGCTCC AGATCTCAAG GGCGCGGAAG      180
TTACCGGCAA TAATTTCTTG CCCCTGACGG GTCAGTTCCG CCACGCCGAT CACAATAAAC      240
AGCGAGGTGT CTTTAATGCT GATGATCCAC TGGTTACCCA GCGGCGGCAG CATACGACGC      300
GTGCCAGCGG TAAAATGACG TAGCGAATGG TTTCCCMACG TGAAAGACCG AGCGCCAGTC      360
CTGCTTCACG AAAACCTTTG TGGATAGACA GCACCGCACC      400

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(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1857 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CGTGTTCCCC TGGCCNGCTT GGTTTCGCCA TAGACGTTGA GCGGGGAAAT CACATCGGTT	60
TCCACCCAAG GACGTTACAC ACTTCCATCG AAAACATAGT CGGTGGAATA ATGTACTAGC	120
CACGCACCTA ATGCTTCAGC TTCTTTGGCA ATAACCGCCA CACTAGTTGC ATTGAGTAAC	180
TCGGCAAATT CCCGCTCACT CTCCGCTTTG TCGACTGCAG TATGGGCCGC TCGGTTAACA	240
ATCACATCCG GCTTGACGAG ACGTACCGTT TCAGCCACCC CTGCAGAATT GCTAAAATCA	300
CCGCAATAGT CGGTGGAGTC AAAATCAACG GCAGTGATGT GCCCCAGAGG CGCCAATGCA	360
CGCTGCAGCT CCCATCCTAC CTGACCATTT TTGCCAAACA ACAGAATATG CATCAGGTAC	420
GCTCCCTATA GTTTTGTTC AATCCAGGATT GGTAGGCACC ACTCTTGACG TTGTTAATCC	480
ATTGTTGATT ATCCAGATAC CACTGCACGG TCTTGCGAAT ACCAGACTCA AAAGTCTCCT	540
CTGGCTGCCA ATCCAACGCA GCGCTCATCT TGCAAGCATC AATCGCATAT CGGCGATCGT	600
GTCCGGGGCG ATCCGCCACA TAAGTAATTT GATCGCGATA AGAGCCAGCT TTCGGTACCA	660
TCTCGTCAAG CAGATCACAA ATAGTATGTA CTACATCCAG GTTCTGCTTC TCGTTGTGAC	720
CGCCTATGTT ATAAGTCTCC CCGACCAAGC CAGTGGTCAC TACCTTGTAG AGTGCTCGTG	780
CATGATCTTC CACATACAAC CAGTCACGAA TTTGGTCACC TTTACCATAA ACCGGCAGCG	840
GCTTGCCATC CAGCGCATTG AGGATCACTA GCGGGATCAG CTTCTCGGGA AAGTGGTAAG	900
GGCCATAGTT GTTGGAGCAG TTAGTGACAA TGTTTGGCAG GCCGTACGTA CGGTACCAAG	960
CACGCACCAG ATGATCGCTG GAAGCCTTGG AGGCAGAATA GGGACTGCTA GGAGCGTAGG	1020
AGGTAGTTTC GGTAAAGAGC GGCAATGCCT CACCGGAGGC TACTTCATCC GGATGGGGCA	1080
GATCGCCATA TACTTCATCG GTAGAAATAT GGTGGAAGCG AAAGGCCGCC TTGCTCAACT	1140
CGCCCAGACT GCTCCAATAG GCGCGAGCCG CTTCCAGCAA TGTATAGGTG CCTACGATAT	1200
TGGTTTCGAT AAAGTCGGCT GGCCCTGTGA TAGAACGATC AACATGGCTT TCAGCAGCCA	1260
GATGCATCAC GGCATCTGGC TGGTGCAGAG CAAACACCCG ATCCAACTCA GCACGATTAC	1320
AGATATCAAC TTGTTCAAAC GAATAACGCT CACTTGACGA TACTTGGCC AAAGATTCCA	1380
AATTGCCAGC ATAGGTGAGT TTATCCAGAT TGATAACGGA GTCTCCAGTA TCACTAATGA	1440
TATGACGCAC CACGGCAGAG CCGANAAAAC CAGCACCGCC AGTAACGAGA ATCTTCATAT	1500
ATTCGCTCT CTTATTTTAC AATTAATAGC TATTAAAAAT AAAGTTGTTG ACTCCGATAT	1560
ATTAGAAATA TCGGGATACC GAACTAAATA TTTTATATG CTTTGGCCAA GCAGACTCTA	1620
TATCCACCCT GTATCACTAT GCTTCTGGC ATACAATATC CCATCATTGA CACAATGATA	1680
AACATATAAA TAAAGAAAAT TTAAATCAT ATAACCAAAT TACTTTCATT TATTATCAAT	1740 -
AAGTATTTTG ATAAGAATAC CTATACCACA GGGAGCCCCC TGAAACATAA TATTAGCGAA	1800

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GAATGATAAC TGATAGTTAC CATCTTAGAG ATAAAACTT ATTTGTGTGG CGGGATG

1857

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGCTCTTTTCG TGTAAAATAA AATACAGCAT ATCCTATATA GCTTACAATC ATTAAATGAA	60
GTCGCCAATA TTTATATGTT TTATCAATAT CAGCTTGACT CATTGTTATT TCTTTGTCAG	120
GAGACTCTGA AAATATGGAC ATATATAACC TCTTTTATTA TGAAATATTT TCAATAATAA	180
TAATCCGTTA GTAATCCTAT CATAGGGTAA TGTCTCATCA TGTTAAAATG ATCACATTTA	240
TAATCATGTC AAAAAGAACA ACAGAAAAAA TCATATAAAA TCAATTAAAT ATAATTGCCA	300
CATATTGTTG TTATTWAAAC ATTGGTGGTG AATTTAAAGC GAGAACAGTT TGTAACAGTG	360
ACTCCTTGCA GACTAAGTTA GAGTCTCCTT CTAAAATTAG ACGGWKTTCT ATTGATGGAT	420
AATAGTAAGC GCACCGTGAA KGACGTGGGG TAAAAATTAG TTTACAGATT GAGTGACATT	480
CCAGGGCAAC AACTCTTTCA CGCGGTTGGC AGGCCAGGTG TTGATTACAC TGATCACGTG	540
GCGTACATTA CCGGACTCGA TTCCGTTAAG TTTGCAGCTA CCGATCAGGC TGTACATCAC	600
TGCCGCACTC TCGCCTCCAC CATCAGAGCC GAAGAACATG TAGTTACGCC GCCCCAGTGC	660
AATACCCGGA GCGGTTTTCA CACAGGTTAT TGTCGATCTC CACCCAGCCA TTGCGGCAGT	720
ATTCGTTTAC AGCGTCCCAT TGCTTCAGCA GATAGGTGAA CGCTTTTCGCT GTATCCGAGT	780
GGCGCGACAG TGCTCATCTG CCCCTGGAGC CACTCATACA ACGACTGCAT TAGCGGTACC	840
GTTCTGGCTT TTCTGACCGC CAGTCGCTCT TCTGCCGGAC TGCCGCGGAT CTCAGCCTCG	900
ATAGCGTACA GTTCACCGAT ACGCTGCAGG GCTTCCGTGG TGATGTCAGG TGGCGCTCTT	960
GCATGCACAT CGTGGATTTT TCTCCGGGCA TGGGCCATAC AAGCCGCTTC GGTTACCTGA	1020
CCGCTTTCGT AAAGAGCATT GTAACCCGCA TATGCATCGG CCTGCAGGAT ACCTCTGTAG	1080
TCCGCCAGAT GTTGCTGTGG GTGGATGCCT TTGCGGTCGG GAGAGTAT	1128

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

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GTTTGCTTAC GAACCGTGAA ATATGACGGT CCCATATAAC TGCTGATAC TTGTATATCA	60
TATACTTGTG CATGCATGTC ATCATTAATA AGTACTTTGT CACCGTCTTT AAGTTGAAGA	120
CGTGTAATAAT CTTTATACGG CAAGTAGACG GAAAACGGGC GCTTCCCTG TCGCCAATCA	180
CACCGACATG ACTGACTTTT GCGAGAGGAA GTGCATAATT CACCAATTCA GAGCCTAATG	240
CATTGCGCTG GGTAAGCTCA AATCGGAATG GGTTCGAAC CTTCCCGCA ACATTGATCA	300
TTGGACCTTG TTGCTCAACT GAAATCACA TCTTGATCTT TTAATGCCAG CTTCGGGAGT	360
TTCCCATACC GTATGAAATC ATAAAGATCA ATTTGCKGTG NTTACTGCTA TTTTGTGCGT	420
GAACACCTTA ATTTTTCGG	439

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TATTCGTAAT TAGTTATAAA CAGATGATGT AAACACCACT TGACTAGAGT CAATCTTATA	60
CTGGCAACAT CTATGATTAA TTTGTGTGGT TATAATTTTA AATATCTTAT ATTTATGGGC	120
TATTATTGAT ATCTGTCAGA GTATCAATAA TAGAAGGTAA TTGTTTTACA TACTATCAAC	180
TTTTGGATAA CGTTTTTAAA TGCACCTTGC ACATCGTATT TTATTATTTT CACTAATCTT	240
TTTTATAACG GCCTGCGCAC ATGATCCAAA ACAAGTTGAA GCCTCTCGTC CATTGGTAAC	300
AGCGATTAAT TCTTCTTATT CTCTTATTCC TGAAGATTG CAGGCACCAT TAAATAACCA	360
AGATCAAGGC ACGACATTCA ACAAAAATGG CGTAATTTAT ACTATTGAGG AAAGGTATAT	420
ATCGGCTTTA GGTTCTCAAT GCATAAAGTT AAGTTATGCG ATGAATAAAA ATTATTCAAA	480
GCGAAGTGTT GTATGTAAAG AGAATAACAA GTGGTATCAA GTACCTCAGT TGGAACAAAC	540
ATCAGTTAGC ACTTTGCTTA TTGAAGAATA AAGTTGAAGG TAGACGGTTA GAAAATAATG	600
AAAATTTTCG AACTTAGCAC TCTTCTCTTT CTTATTTCTG CATCAGCATT CGCCGCAATA	660
GAGCAAAATC AATCTAATGG TTCACATTTA GATTATGATC TTGCTGCCTC GACAGGAGAG	720
TCTCGGAAAA TGCTAGCAGA CATCACTGGA CAGCCTAATA CAACCTCCAC AACAGGAAGC	780
TTCACACAAC AGAATCGTAA TGGGATGTTG CTTCCAGGAG AGTCAGATGT ACGAAAATTA	840
CTGCCGCAAT CTGAAGCAGG CTTACCTCCT CCGTATGGTG CTAATTTATT TGCCGGAGGC	900
TATGAA	906

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGGCCTGAT ATATGCCGTT ATTACAAAAA GAGGATCAAC CACACTGCCT TTTGGACCGT	60
GTTTAAGTCT GGGCGGTATA GCAACACTTT ATCTACAGGC ATTGTTTTAA TGATAACCAC	120
GTCATTATCA AAGTGACATT TTAACCTTTA TTAATAACCT TAGAGATTAT TTACCATGTC	180
GATAAAACAA ATGCCAGGGA GGGTATTAAT ATCGCTATTG TTGAGCGTTA CAGGATTATT	240
AAGTGGCTGT GCCAGCCATA ATGAAAATGC CAGTTTACTG GCGAAAAAAC AGGCGCAAAA	300
TATCAGCCAA AACCTGCCGA TTAAATCTGC GGGATATACC TTAGTGCTGG CGCAAAGTAG	360
TGGCACGACG GTAAAAATGA CCATTATCAG CGAATCGGGT ACTCAGACCA CGCAGACACC	420
TGACGCCTTT TTAACCAGCT ATCAACGACA AATGTGCGCT GACCCAACGG TGAAATTAAT	480
GATCACCGAG GGAATTAATT ACAGCATAAC GATTAATGAT ACACGTACAG GTAACCAGTA	540
TCAGCGGAAA CTGGATCGTA CCACCTGTGG AATAGTCAAA GCATAACGTC GGGTAGATAT	600
AAATTGGCGC GGGTTGTTTT TCGTGACGCA CGAATTTATC TCATTCAATG GCTGACAAAA	660
ATTCGTCACA CTCTTAACCA GAGACAATCT CTTAATACAG ACAAAGAGCA TCTGCGCAAA	720
ATTGCACGCG GGATGTTCTG GCTGATGCTG CTTATTATTT CTGCAAAAGT GGCGCATTCA	780
CTCTGGCGCT ATTTCTCCTT TTCTGCGGAA TATACGGCGG TTTCCCATC GGCGAATAAA	840
CCGCTCCGTG CGRATGCAAA AGCGTTCGAT AAAAATGACG TGCAATTAAT CAGCCAGCAA	900
AACTGGTTTTG GCAAATATCA GCCCGTCGCC ACGCCGGTAA AACAACCCGA ACCTGCACCT	960
GTGGCCGAAA CGCGTCTTRR TGTGGTGTG CGTGGGATCG CCTTTGGTGC CAGACCCGGC	1020
GCGGTTATTG AAGAAGGTGG TAAACAGCAG GTCTATTTGC AGGGTGAACG CTTGGCTCGC	1080
ACAACGCAGT GATTGAGGAA ATCAACCGCG ACCATGTGAT NTGCGCTATC AGGGAAAAAT	1140
AGAGCGCCTG AGCCTGGCTG AAGAGGAGCG TTCCACCGTT GCGCGACCA AAAAAAAGC	1200
TGTCAGTGAC GAAGCAAAGC AAGCTGTTGC TGAACCTGCT GTCAGTGCGC CAGTTGAGAT	1260
CCCNGCTGCC GTGCGTCAGG CACTGGCGAA AGATCCGCAG AAAATTTTTA ACTATATCCA	1320
GCTTACGCCT GTGCGTAAGG AAGGGATTGT CGGTTATGCA GTGAAACCGG GGGCAGATCG	1380
TTCTCTGTTC GATGC	1395

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACTTGAATA AA	ACTGACAC CG	TTTACCTC CA	TAAATAGTG AG	CATAGCCG CC	ATTGCGGC	60
CTGATCGGCG AA	CCGGAAAT CG	CAACCTGC GA	ACGACAAC CG	AACCGGCA AG	CGTGCGGG	120
AAGGACGGAT ACC	GGACTCT TTC	GCCACTT CAG	CAATCAC CG	GAGCGTG G	AAAAAACAA	180
TAAACCCAGT ACC	GGCCATA AT	GGTCATAG ACC	AGGTGAT AAT	CGGCGCG ATT	TATGTTGA	240
TATATTTTCGG GT	TACGCCGC AT	AAAAATTAC CAG	CGACGGT ACC	GATAAT CC	ATTCCCCT	300
GCGGCCTGTA AG	GCTGAGGC CG	CCACAACA ACG	GTCATAA TA	ATCAGGAT C	ACGTCGACT	360
GGCGGCGACC CC	ATAGGCAG					380

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTTTACGGTT TA	ATAGGGGA AN	GCCGACTG GA	TGNAAAAA TG	GAAATCTGG AG	CCCAGAAT	60
AAATCTGAAT TT	AATGTGGA CT	GGATATGC TC	CAATAACC CC	GGCAGGGA GT	CATCTGTG	120
CGAAGATATT TG	CGTTATGC TG	TAATATAA TA	ATTCAATG TA	TTTCAGGA AC	AGTAATAT	180
ACTACAGTTT CT	ACTTTCTT GT	ATTTAATA AA	TGTGTTCCG CA	TGCTAAA AG	CAGGTCTT	240
TCAGAAGCCA CA	AGAATTCT GT	GGTCCCAG TA	TATTTTAGT TA	TCCTATTT TT	TATATCTAA	300
CTTGTAATAC TT	ACAGCATT TT	CATTCATC CT	AATGGAAG GT	GTAATAA TC	TTTGAGCT	360
TAGAAACATC AAA	AATTATGC AT	CTCATTA TTT	TGTCAGT CAC	ACGACCT CT	GGTAAAAA	420
TAAAACCCCC AG	AAATATGC CA	TTTTCTAGG G	GGGGCGTAA GA	ATCAATAT AT	TTTAGTGT	480
TGTTACATTT AG	CTCTTAGC TC	TCTAGCTCT TAG	CTCTTAGCTC TT	AGCGTTTG		540
TAGTTTCATC GCA	ATGAGTA AA	AGGACAAC AAG	AATAAGT GATA	ACGTTA AG	AGAAGAGC	600
ATAGAAACCA TT	CCAGTGGT AT	ATTTCTAT TAT	TTTAGAC AAT	GGATAGC CAG	CCGCGGA	660
CGCACCAAGA TA	TGCGAATA AA	CTAACAAA ACC	AGTAGAA GC	ACCAGATG CA	TATTTATG	720
TGAGTTTTCA GC	AGTGCCA TT	GCGATCAG AA	ATTGTGGC CCA	AAGATAA AG	AAGCCAGT	780
GATGAAAAAT AAT	AACGAAA AA	CATATTTT ACT	TATCAATA GAA	ACCAACC AT	AGACATGC	840
AGAAGCAATG AT	TATACCAA TT	GTATAAAT AAC	ATTCATT TG	AGAGCGAT TG	CCCTTAAA	900 -
CAGAATATCT GA	TCCCCATC CA	GCTACGAT AG	CACAAAAA AAG	CCTCCAA CCT	CAAACAT	960

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CATTACTGTT GCATTTGCTG TTAGCAAGTC ATATT

995

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TAAAAGCGAC TCCATGTGAA ATTTCTGTTT GTCGTTTTTT CCCC GTTGTA GCGGCTCTGC	60
TCCTGGCTTC COTGATAGTC AGCCCGCAGG CGCCAGGGCC CCAGATTCCC CCCCACAGTC	120
CCGTTATAAC TGAAGTATG AGAGTCTCCT CCCTGATAAT TACGGGAAAC CGTCCCGTTG	180
AGGTTATAAT CCAGCATCAG TCCGGGAATG CCGTCGTCCC AGCGTGAGGG AGGCAGCCAG	240
GTGGCATCAG AATACTCAAG CCAGGCCTGC GGCATATTGA TGCCTAATAC GCCCGCTCCG	300
GTATCAGGAC GAATATCCAC TCCCGGCAAC CCATGAAAAT CCGCACACTG ACCATCATGC	360
CAGTAAACAA CTTTATCCAG AGATTCTGCT GTTAACCCCA TCAGTCTGAC CATATCTGAT	420
GTCAGACAGC TCGGGCAATT TTTTCTCTGC CTTATCTCCT GACAACGCAG GTTCAACAAA	480
TGAMATCTGT AACGATGCGG GAGAAATACT TTGCCCCGTTA ACAATCACAT CCAGAAGATA	540
TTGCCCCGGC AGAACATAGC CGGCTTCTGA AAAACGGGTG AAGTCAATAT TTTTCTTGTC	600
CGCTGCGTCA AGTACATCTG TATTAACTC AACGGCACTG GCTGCGTTAC AAAACAGAGA	660
CAACAATATC ACACAGGTAA TATTGTTGAC TGCAAAAGGT ATTCTGTCTT TCATTCCACG	720
CATCACCAGA TTCACAAAAA AGATAAATAA CCGGACATCT CACCGGAGTG ACTCACTCAT	780
AATCGACCCG GAATCCCAGC ACAGCAAAT AATTTCC	817

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTTTGTCAG AGCGTTCCT CTCTGGCTGG ATGATTTCCG CTCGGGAAAT GCAGGCTTAA	60
TGTGGGGACT GTCGGGGATG TTTGAAAGGG TAAAAATAAG TCATGAGTTT TTTCATTATG	120
TCCTGAAAAA CGGGTGTGCA ATGCCACTTC TCCGTGCTGT GGCAGACACT GTTGCTGTGTC	180
ACAACAGAGG CGTGATACTC GAAGGTGTTG AAAATGAAGC GTTGTTCCGT ATTGCCAGAG	240
ACATGAATGT CCAGGGCTGT CAGGGATGGC TCTACAGGCG TGTGGGGGTT GATGAATTAT	300

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CCGCGCTTAT TCAGCAGTAT GAATAATCCT TTTTCACAGA CTGGTCAGCT GTCAACATTT	360
ATGTTTTTTT ATCTGCGGGA ATTTATCCGT CTGCCTGTCG GGACTACTCT GTCATACAGA	420
AATCAGGCCA GAATAAATTG TTGTGGAAAG GTGAGATTTA CCGGATGACT GATGTGCTCT	480
TGTGCACAGG TATACAGGCA GTGTGTTTCC AGTATATGGA AAATGATTAA ATGAATAACA	540
CAGACTTATT AGAAAAAATC ATCAGGCATC AACAAAACAA AGATCCTGCA TATCCTTTCC	600
GGGAACATCT TTTGATGCAA CTCTGTATCC GTGTAAACAA AAAAATACAG AACAGTACAT	660
CTGAGTTTTT TGGTGCATAT GGTATAATC ACTCAGTATA TATGGTTCT	709

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TCATCAAGGG ACGGGGCATA TCTGGATGCG ACAGGGCAAA CCAACCACTG AGAATCCAAC	60
CTGCCAAAGC CTGACCAGGA AGTCCGACGT TAAAGAAACC AGCTCGACTG GCAACGGCAA	120
AACCAAGACC AATCAAGACC AGAGGACCCA TAGCACGGAA GATTTCTCCA ATCCCACGCA	180
GACTGCCAAA GGCTGTATAG AACAATTCTT CGTAGCCCCA AATAGCATCA TAACCGAAGA	240
TCCACATGAC AATGGCTCCG AGTAAAATTC CTAGGAATAC AGAAATCAAG GGAACCGAAA	300
TTTGTTGTAA TTTTITAGAC ATCACTCTTC TCCTTTCCCA AGTTYCCACC AGCCATCAAG	360
ACACCAAGTT CTTGTTTATT GGTTGTTTCT GGTGATACAA TACCTTGAAT CTTACCATCG	420
TGGATAACGG CAATACGGTC TGAGACGTTT AAAATCTCAT CCAATTCAAA GCTGACNACA	480
AGGAC	485

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

AGCAGAATAG GCAACATCAC CACGCCGACA AACAGCGAGA AGAGAATGAC GCCAGCCGCC	60
AGGAACACCA GTCATAGCG CGCCGGGAAG ACGTTACCAT CCGGCAAGAG CAGCGGGATA	120
GAGAGCACAC CGGCCAGAGT GATCGCCCCA CGCACCCCGG CGAAAGACGC GATCAGGATT	180
TCTCGTGTGG TCCACGAACC AACTCCATC GGCTTCTTCT TCAGGAAGCG GTTGCTGAAC	240

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TTTTTCATCG TCCACAGCCA GCGGAAACGG ACCAGCATCA GCGCCGCATA TATCAGAATA	300
ATATTGGTAA ACAGCATCCA GATTTGACG TTAGGGTCGA TTTCTTGCTG GCCATCAGCG	360
GACGTCTTCC AGRATTACCC GGCAGCTGCA GACCTTAACA GCAGGGAACA CCATGGCCGT	420
TTTAAGGACA ATTCNAGEA TCGGCCANG TGCTGTTT	459

(2) INFORMATION FOR SEQ ID NO: 106:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTAATAGCAC TAATACTGTC CTGCTCTATT CCGCTGACAT TTTCAGTCAG CTGCTGTATG	60
GGATGGGTTA CCCAAAACCA GACCAGCATA CCTGACAAGA GACCGCATAT CACTACCAGA	120
AACAGCGACC AGTACAGTGC ATTCCATAGT GCCTTTGTCC AGGCTGTATC AGTAAGAGCA	180
TTAAGTTCCT CTCCTGTAA AATAATATAC AGATATCCTT TCGGTTTCATC ACTCTGGTAA	240
AGCGGTGCGG TACTGAAAAC TTTTGTCTTA TTTACACTTC GGGGATCATC ACCATATACG	300
GGCCAGACAC TGCCGGAGAG AAATTTTTTC AACGGTGCAA TATTGATATA CCGGCGTTTG	360
AGATGACCCG GAGGGCGGCC TCCACAAGCA GTCGCCCTTC CGGTGAAACC ATATACAGCT	420
CCCACTGGG ATTAAGCGTC ATCAGACGCT CAAACAGACT CGTTAATGTC CCGTGTTACC	480
AGACAAAACA AGCATCGCAA GACGCCACAA ACGGTGCGCT TACTTAAATA AGCCGGTTAC	540
AGGTGAAAAA TCACGTCTTG ATATTCAAAT GTTTTTTCAG GTCATATTTT AGCAGGACAC	600
TACCAGCACC TAACAGCAGC ACATCTTTTA TAACAAAAC TCAACTTTC CCCAGTTGTG	660
GTAACAGGCT GAGCGTGGTT ATTCCTGTAA CAATAACGAT AATATCTCCC AGTACACCAG	720
CAGCAGGCCT GAAGAAACCG ATAATCAATG CCAGAAATGT GATAGTTTCC ACTATGCCGA	780
GGAAATAGCT CCCTCCATGA ATACCAAATA TAATATACAG GATATTCAGC CAGGTGGGAT	840
ATATCAGGGG CTTGAGAGCC ATAACCTCAA AATCAAACCA TTTATAAGTC CCAAAAAGCA	900
TAAATATT	908

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

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CGGGCTAACC CAATATGCTT TATTAACCCG GGATAATTAC CCTGTTGCAT ATTGTAGTTG	60
GGCTAATTTA AGTTTAGAAA ATGAAATNAA ATATCTTAAT GATGTTACTT CATTAGTCGC	120
AGAAGACTGG ACTTCTGGTG ATCGTAAATG GTTCATTGAC TGGATTGCTC CTTTCGGGGA	180
TAACGGTGCC CTGTACAAAT ATATGCGAAA AAAATTCCTT GATGAACTAT TCAGAGCCAT	240
CAGGGTGGAT CCCAAACTC ATGTTGGTAA AGTATCAGAA TTTCACGGAG GTAAATTGA	300
TAAACAGTTA GCGAATAAAA TTTTAAACA ATATCACCAC GAGTTAATAA CTGAAGTAAA	360
AAACAAGTCA GATTTCAATT TTTCATTAAC AGGTTAAGAG GTAATTAAAT GCCAACAATA	420
ACCGCTGCAC AAATTAATAAG CACACTGCAG TCTGCAAAGC AATCCGCTGC AAATAAATTG	480
CACTCAGCAG GACAAAGCAC GAAAGATGCA TTAATAAAG CAGCAGAGCA AACCCGCAAT	540
GCGGAAAACA GACTCATTTT ACTTATCCCT AAAGATTATA AAGGGCAGGG TTCAAGCCTT	600
AATGACCTTG TCAGGACGGC AGATGAACTG GGAATTGAAG TCCAGTATGA TGAAAAGAAT	660
GGCACGGCAA TTAATAACA GGTATTCGGC ACAGCAGAGA AACTCATTGG CCTCACCAGAA	720
CGGGGAGTGA CTATCTTTGC ACCACAATTA GACAAATTAC TGCAAAAGTA TCAAAAAGCG	780
GGTAATAAAT TAGGCGGCAG TGCTGAAAAT ATAGGTGATA ACTTAGGAAA GGCAGGCAGT	840
GTACTGTCAA CGTTTCAAAA TTTTCTGGGT ACTGCACTTT CCTCAATGAA AATAGACGAA	900
CTGATAAGA AACAAAAATC TGGTGGCAAT GTCAGTTCTT CTGAACTGGG CAAAAGCGAG	960
TATTGAGCTA ATCAACCAAC TCGTGGGACA CAGCTGGCCA GCCTTTAATA ATAATGTTNA	1020
ACTCATTTTC TCAACAACCTC AATAAGCTGG GGAAGTG	1057

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TACCGGGCCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT TCCTGCAGCC	60
CGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAGC TTTTGTTC	120
TTTAGTGAGG GTTAATTTTC AGCTTGGCCT AATCATGGTC ATAGCTGTTT CCTGTGTGAA	180
ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCT	240
GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC	300
AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG	360
GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC	420
GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG	480

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GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCACCA AAAGGCCAGG AACCGTAAAA	540
AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCTCT GACGAGCATC ACAAAAATCG	600
ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC	660
TGGAAGCTCC CTCGTGCGCT CTCTGTTTC CGACCCTGCC GCTTTACCGG ATANCTGTNC	720
GGCTTTCTCC CTTCGGGAAG CGTGGCGCTT TC	752

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTTGGGTAAT NGACCTCATA TCCCTCCGCC AAAAAAGSAT CTACATGCGA TTTTGCGAAG	60
CCAGCGTTGA TTGTAGGCGA GAGAATGGTT CTGTTGTTTT GGTACATTTC AGTTGTCATG	120
GATTTACAAA ATGTAGCATG ACCTTTCACC TGTCCAAGAG ACTGCAACAC CATCTGTCCA	180
AAACAATAAA TAGGAATCAA ACAGGCTACC AACATCAACA AGTATCCCAA TAAGGCTCGT	240
AGTTTAGTCC TTGACATGAC GCCCTCCAA TTGCTTTTCT AGTCCTTTGA CAATCCGTCG	300
ATTACGATAC ACGCGATACA GCAAGAGAAG GATGACCGCC ATCGCTCCTA GTAATAACCA	360
CAACCAGAAT TGCCCACGCT CTCTCACC GC TCGATTCCGC TCTGCAATTG GTGCCGTATA	420
CGGAATCCGC TTCCCACGTA CCAACAGACG ATGACTGTTA ATCCTATACG GTGTACNAGT	480
CAACCA	486

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTACGCNTTC AACCAGGTCT TCTGGTTTAC CAACGCCCAT CAGGTAACGC GGTGTGTCTG	60
CCGGAATTTG CGGGCATACA TGCTCCAGAA TGCGGTGCAT ATCTGCTTTC GGCTCACCCA	120
CAGCCAGACC GCGGACAGCG TACCATCAAA ACCGATATCT ACCAGACCTT TAACAGAAAT	180
ATCACGTAAA TCTTCGTAAA CGCTGCCCTG GATGATACCA AACAGCGCAT TTTTGTCTTC	240
GAGACTGTCA AAACGCTCAC GGCTACGTCG CCCAACGCAG AGACATCTCC ATGGAGCGTT	300
TTGCGTAATC CCA	313

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(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (E) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

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CGGAAATCCC AGTAATTCCA TCCTCANATA TTCCACTCAN CCTCACTGTA ACAAAGTTTC      60
TTCGAATAAT AAAAATCATG CTTTCTGTTA TCAACGGAAA GGTATTTTAA TTCTCTGTGT      120
TTGCTTTATT TGTGAAATTT AGTGAATTTG CTTTTTGTTG GCTTTATNTG ATGTGTGTCA      180
CATTTTGTGT GTTATTTTTC TGTGAAAAGA AAGTCCGTAA AAATGCATTT AGACGATCTT      240
TTATGCTGTA AATTCAATTC ACCATGATGT TTTTATCTGA GTGCATTCTT TTTGTTGGTG      300
TTTTATTCTA GTTTGATTTT GTTTTGTTGG TTAAGATC GTTTAAATCA ATATTTACAA      360
CATAAAAMMC TAAATTTAAC TTATTGCGTG AAGAGTATTT CCGGGCCGGA AGCATATATC      420
CAGGGGCCCG ACAGAAGGGG GAAACATGGC GCATCATGAA GTCATCAGTC GGTCAGGAAA      480
TGCGTTTTTG CTGAATATAC GCGAGAGCGT ACTGTTGCCC GGCTCTATGT CTGAAATGCA      540
TTTTTTTTTA CTGATAGGTA TTTCTTCTAT TCACAGTGAC AGGGTCATTC TGGCTATGAA      600
GGACTATCTG GTAGGTGGGC ATCCCGTAAG GAGGTCTGCG AGAAATACCA GATGAATAAT      660
GGGTATTTCA GTACAACACT GGGGAGACTT ATACGGCTGA ATGCTCTTGC AGCAAGGCTT      720
GCACCTTATT ATACAGATGA GTCGTCGGCA TTTGACTAAA TTATGGCATT CCGGAGTTTC      780
TGGAAGATAA AAAAAGAAGC CCTTATCAGA AAGCAGACAG GTTATATCAG TATTCTGTCTG      840
ATAAATAACC TGCCCTGAAA ATACGAGAAT ATTATTTGTA TTGATCTGGT TATTAAAGGT      900
AATCGGGTCA TTTTAAATTG CCAGATATCT CTGGTGTGTT CAGTAATGAA AAAGAGGTTG      960
TTATTTATGA TTAAGTCGGT TATTGCCGGT GCGGTRCTAT GGCAGTGGTG TCTTTTGGTG      1020
TAAATGCTGC TCCAATATT CCACAGGGGC AGGGTAAAGT AACTTTTAAAC GGAAGTGTG      1080
TTGATGCTCC ATGCAGCATT TCTCAGAAAT CAGCTGATCA GTCTATTGAT TTTGGACAGC      1140
TTTCAAAAAG CTTCTTGAG GCAGGAGGTG TATCCAAACC AATGGACTTA GATATTGAAT      1200
TGGTTAATTG TGATATTACT GCCTTTAAAG GTGGTAATGG CGCCAAAAAA GGGACTGTTA      1260
AGCTGGCTTT TACTGGCCCG ATAGTTAATG GACATTCTGA TGAGCTAGAT ACAAATGGTG      1320
GTACGGGCAC AGCTATCGTA GTTCAGGGGG CAGGTAAAAA CGTTGTCTTC GATGGCTCCG      1380
AAGTGATGCT AATACCCTGA AAGATGGTGA AAACGTGCTG CATTATACTG CTGTTGTAA      1440
GAAGTCGTCA GCCGTTGGTG CCGCTGTTAC TGAAGGTGCC TTCTCAGCAG TTGCGAATTT      1500
CAACCTGACT TATCAGTAAT ACTGATAATC CGGTCGGTAA ACAGCGGAAA TATTCCGCTG      1560

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TTTATTTCTC AGGGTATTTA TCATGAGACT GCGATTCTCT GTTCCACTTT TCT

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(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

NTAGTCCATG GCCCCATGGA GCGAANTCCA AAGTGTGGAT ATTGTCGTTT TAATTCATCC	60
CAAAAGCTGA AATACGCCAA AACCCACGTT CCCTAACATT GGTATCATGC ATAATGACCA	120
CAGCCNTTCA GAAAGCTTTG GCAACCAGCT TTCAAATCA TGGGTACCGC TTCAAACGTA	180
TGCAAACCAT CAATATGAAG CAGATCAATG CTACCTTG TG AAAAATGCTC TAACGCTTGG	240
TCAAATGTAC TGCGAATGAG AGTAGAAAAA CCTGAATAGT GCTGTTGATT ATATTCTGAT	300
ACTTGCCTGT AAACCTCTTC GCCATACAGC CCCGCATGTT CATCTCCCCC CCAGGTATCA	360
ACGGCAAAGC AGCATGTTTC TAAATCTAGT TTAGAGACTG CTTGGCAAAA TGAGAAATAA	420
GAACTTCCAT AATGAGTTCC CAGCTCAACA ATATTTCTTG GCCGCAGTGT GTCAACTAAC	480
CAGAAAGCAA AAGGAATGTG TTCTAGCCAA GCAGATTGTG CAAGGTATGT AGGACACCAN	540
AAAAGAGATG GTTTGAAAAT GAAATTCAAT TCCCTGCCAA TATCAGTGAT GGGATATAAC	600
TCACGATTCT CTACTAACTG ACTAATTTTT TGACTATCCA TTGAGGAAAA CTCACATGTA	660
TTTATAGAAT TAAATCAAGA AACCTGAAAA TACCTATAGT GCGGTAACCT ATTAATAAC	720
ATTTAAATAT TAACAATACA CTTGGAAATA TTAGTTAAAA ATAAATCATT ATGATTTCTC	780
ATCAATCCTG GTGCTCAGC AAAGTTGCCA GCCCCATAAT AATAAGACCA TAGAACAAGC	840
AAAGTAATAC ACCCACAGTC GCAAGATTAT AGAATCGCCG TGGATATTCG GCATCTTCCG	900
CTAAAGTTGG TTGGGTAATA ACCAATAGAT	930

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ACGATATCCC CCCTCTGCTT TTGAGAGGCA ATCTGCTTTA ATACATGATT CATCACAACA	60
CCTCTTGCTG CGCTTTGATC TTAATTTTAT ATTTTGGGT AGGGAAAAGT AATTGCCCCCT	120
GATACGGCTC ACCATTTACC AACGTTTCAC AGCTATGTTT CAGAGCTAAA TTAAGACCTG	180

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GTAGAAATATC CCAGCAATTC ACCCCTTTGA CATTTTCAAA GCTGTCATAA GCACCGGNNNA	240
AGGGGGGGGCC AACATGTTAT ACATGGAGCA GCCAATGATA CGATATTCAA AGCCCTCTTC	300
CAGTTGCATC AGATCCTGCT TGGTAASGGA GGAAGAGAGG CCACGAATAC GAGAGCGATG	360
ATGTGTAATC GGCATACCTG TGATATGAAG ATCATTCAAT TCAGGTAAGA AGATGCAGGA	420
CTCTTGATGT TCCCCCTCGG TGTAATGCT GATACCAATG CCCCCTCTT TGAGCCCAGA	480
GACAAAGTTT TCTGTGCCAT CAATTGGATC TAGAACAATG TAAGAACCTT TGGGATTCCA	540
CTCAATATCT CCTAAAGGGG CTAATTCCTC TGAAATTAGC ACATGCCCTG GTAGATGCTT	600
TCTACAGAGT TCGAAACTA TATCTTGAAC TTTTAGATCC AGTACTGCGG CCGCGATCC	659

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCGGATATA CATCAGGAGA AATTGGAGCA GCAATTGGAT GCGCCATTAA TGCCTGGTTA	60
GGGATCCCCG CATGTGGGCA CGCAAATGGC TCAGAATATG ATCGACCTTC ACCAGATAAA	120
CCAAATCTGA GCGAACCATT TATCCCAAGA CCCACGTATG ACGCTTCACT TCATTCTCGG	180
CATGGCGGAT ACTGAGTAAA TCATCCTGAA TCATTATGTT CAACATCATC AATTCTCCGG	240
ACTTGTTGTC AGATGTCCGG AGAATATTAA CCTTTTCTTC AGAAACAGAW TGATCAAGAA	300
TCACACTCCT TCTTTAAGAG GATTTTATCC AGAAACTGA CTTTCTTCTA TCAAATMAC	360
AGTATCCTGT TTTATCAGGA ATAATCTTTA CCTCCGGTAT CATTCCCATA ATCAGATATC	420
AGAAAAATGT GCCAGTAATT TTTTACTGAT GACTTCAAAC ATTTACATT CATCACACGT	480
CAGATTACTC CAAAGTTCTT TCAGATATGT GTTCTGCGCC AGAGTGAGTC TCTGAATAAA	540
AAACATACCT TCAGAC	556

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TACCTGTTTG TGGAATTTGA CCCAGAAGTG ATTCATACCA CGACTATCAA CGCGACCCGN	60
GTGTNCAGCC ACTTCGTGCG CTTTGCGGTN CGCAGCGATA GTCCCATCGG CGGTTATTCA	120

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TCAGCTATCG GTATATAAAC CGAAAGACAT TGTGATTCC GGCAACCCCT TATCCGGGTG	180
ATAAGGTGAT TATTACCGAA GCGCGTTCTGA AGGCTTTTCAG GCCATTTTCA CCGAACCCGA	240
TGGTGAGGCT CGCTCCATGC TATTGCTTAA TCTTATTAAT AAAGAGATTA AGCACAGTGT	300
GAAGAATACC GAGTTCCGCA AACTCTAAAA CGCAATCCCA AACAGTGTTT TGACATTAGC	360
ATCCGTGGTG GCAGCCAGCC ATGCGGCATC TTCTCCACGC CAGTGCGCAA TACGTTGCAA	420
AATATGGGGC AGATGGGCTG GCTCGTTGCG CCGGGATGAN GGCTTTGGCG TGAGATCGCG	480
AGGGAGCAGA TACGGNGCAT CAG	503

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTTAACATCA AAATTACCTG CAGCTGAAAT GATTTTGCTG ATTTTCATTAA TTAATGGATT	60
AAGATTACCC TGACTTCCAT AGGCTAATGC ATCATTCCCA TACACATAAC TTGCCTTATT	120
ATTACTCTGT TGATACTNAA GTGCCTTTTT AAGGGAATCT GGTGTGATTA CCCTGCCGTC	180
TTTATCAAAA ATCTGCTCTA TCTGGTGATT AGAGATATCA CCTGACTCTT TTTCAAACCA	240
TTTTTTAAAT GTAATACCAT TTTTGTGGCC AATGGAAAGA ACATTACCTT CAGCTTTATA	300
CATGATGAGG TCATTACCTT CTCGCCTGAA GGCCACATCC CGGAAATCAA TATCAGCCAA	360
ACTGAGTTTA TCGTCTTTC CCCCATCATC GTCAATAATA TGATGGCCAT ATCCTGAAAG	420
ATAACGATAA ATA	433

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCTCTGTT CCCGTTCCCTG TTCATCACCA TCGCCTGTGG TCGGTATCT GGCTTCCACG	60
CGTGATCTC TTCCGGTACG ACGCCAAAAC TGCTGGCTAA TGAAACCGAC GCGCGTTTCA	120
TCGGCTACGG CGCAATGCTG ATGGAGTCCT TCGTGGCGAT TATGGCGCTG GTTGCTGCGT	180
CCATCATCGA ACCGGGTCTT TACTTCGCGA TGAACACCCC GCCTGCTGGC CTTGGCATCA	240
CCATGCCTAA CCTGCATGAA ATGGGGTGGC GAGAACGCGN CGGATTCATC ATGGCGCANT	300

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GA

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(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTAATAAG CCAAATACTA CATCACGTAA TACTTGCAAA GAAGTGCCTG GAGTTTGACT	60
AATAATGGGT TTGTCCATTA ATACTTACCC AAATAATCGG CTCATTATAG CAACGAGCCT	120
CCGATTAAAA TTTAAATAC TCAATCATTT AATAGCAACG TTAGCAGCTA CAGCGATTTG	180
ATAAATAATT TGTGTGATAT CTTTAAATGA TTGCATGGTT TTGCTATCAA CCTGAGGTAG	240
AACCAATATC TGATCCCCCG GTTGTACTTT ACCTTGCCCT TTAAATTCTA CAAGACCATT	300
TGCATGTACA ATAGCAATTC GCTTGTCGTT AGCTCGCTCA GTAAAACCTC CGGCCCATGC	360
AACATAATCA TCCAAATTAG CATCGGCATT ATATACTACT GCTTGTGGCA TCAACACTTC	420
ACCCCCCACT TGAATAAGAT CAGTCTTATT TGAATAACT ATTTGATCGC CTTGTTCTAA	480
TTGGATAWTG GCAATAACAC CTTTATCTGC AACTACTACT TTACCAAGCG GTKGAACTTT	540
ACGAGCCTTT YCAACAACT GCATCACTAA CTCTGCTTCT TTAGCACGTA TATTCGCCTC	600
ACCATCAGAT CGCGCGGGTG TGGTAAANTT CATACGTTCC AAGCGGTTTA GAGATT	656

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATATGTTATC TGGATCCAGA TAAAGAGCGT TCTTGACCCG CTATATCCAG ACAGGTCAGT	60
TACACCCTGT CCGGAAAAAC TGATCGGAAT AACAACAGTA TATTTTCTAA TAACTGGCA	120
AATGGTGCCG GCGGTGTGGG GATTGAGCTT CTGGATAGCG CTGGTAATGC GGTGCTGCT	180
GGACAGAAGA AATATCTGGG ACAGGTAGGA CCATCAACAT CTCTCAATAT TGGATTAAGG	240
GCATCTTATG CACTGACCAA TGGACAGACT CCACCTACTC CCGGACGAGT TCAGGCGTTA	300
GTTGATGTTA CCTTCGAGTA TAATTAGGAA TGTCGGGGAT GGGCTATCCC CGATATTATT	360
GCAGGATTAG TCTGTGATAC AGATATACAG CCCATATGAA CAACTGTTTG CATATATAAA	420
AATGATGATA ATTTTA	436

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(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AATAATTAAA TTTGGAGGGA TCAGTTTTCT GATAATGTTT TGTTATTAAA ACATTATCCC	60
ATGGGGCGTA GTTATATCAA TTAGCAGGAT CTTATGAGTT AACTAACATC AGTTTTGAAT	120
TTTTAATGGG GGTAATTTAT CTTTACTAA AAATATTTTA ACTATTAATA TAGCATCATG	180
GTTGTTACGG TTTGTTTTAA TTCTATTTTA TAATGTGCTA TATATTGTAT TTTTGTGCTT	240
AGATAAATAT GTTTTTTCAT TACTTTAGTG ATGTTAATAT TTTGCGTGTA GTAAAAATCA	300
TTGTTATAAC AAATGTCACT GTTGCTATAC TTTGCTGAAC TGTTTATCGG TCATTTTGAT	360
TCAATCACTG GTTCTATATT TTTTAATAAC CGTTCGTAG CGATTAATAT ATTGCTCTCC	420
AGAGGATACA CTATATGAAA TATATTAAAA GTCATTAATT TTNATTCAAT GTTGTTTAGA	480
GTTATGTTCA GTGTTTGGNA ATAGGATGTG TTTCTAAACC GTCTTGGGTT CTATAATAAA	540
TTCTATTCTT ANAGGTTTT	559

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CATGTCCCTT CCTGAATACT GGGGAGAAGA GCACGTATGG TGGGACGGCA GGGCTGCTTT	60
TCATGGTGAG GTTGTCAGAC CTGCCTGTAC TCTGGCGATG GAAGACGCCT GGCAGATTAT	120
TGATATGGGG GAAACCCCGG TACGGATTTA CAGAATGGTT TCTCCGGACC TGAAAGAAAA	180
TTCAGCCTCC GGCTCAGGAA TTGTGAATTT AACAGTCAGG GTGGGAACCT TTTCTCTGAT	240
TCCCGGATAA GGGTGACTTT CGATGGCGTC CGGGGTGAAA CGCCGGATAA GTTTAATTTA	300
TCCGGTCAGG CAAAAGGCAT TAATCTGCAG ATAGCTGATG TCAGGGGAAA TATTGCCCGG	360
GCAGGAAAAG TAATGCCTGC AATACCATTG ACGGGTAATG AAGAAGCGCT GGATTACACC	420
CTCAGAATTG TGAGAACGGA AAAAACTTG AAGCCGAAA TTATTTTGCT GTCTGGGATT	480
A	481 -

(2) INFORMATION FOR SEQ ID NO: 122:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

CCATATAGTG ACTTCATTGA AAAAAATGTA AATGGAATCT TGCTGGAGAA TGACCCACAT      60
ATATGGATAA AAGCTCTTTC ATTACTTGTT AGTGCAGATC ATAAACGTAG CGAGTTGGCG      120
TTCAATGCTA AAAAATATGC TTGTAAAATT GTAGGTGTCG AGTAAAAAGA TATTTTTATT      180
TAATTGGTGC TATTGAATGT TAAAAATCG AACTGATTGG TGTTTTAATA TTAATCATAG      240
GTTATGATGC AAAAATATAT TAGGCATTGC CTGCTTCAAT TAAGTTGAGA GTGTAAGTTG      300
AATTGAAATA TGGTTATATG ATAAAGCAAT ATATGTTAAT ACATATGTCA ACCGAAAATG      360
CCATTATGTG TTTTTACTT TATCTGTAAC GACACAATAT ATAAAATAAG GCTAATAATC      420
AAAACGCTTT TTAATTTGAT TGTTTTGAAT CAAGTACTA AGAAATTCTC TTGCTGCAAA      480
TAACTCCCTT AGTGATTTTT TTTGAGTCTA TTTTATTCTC TGGGCATGGT CATGC          535
  
```

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

CCGGCCCCAT AATGATGGTT TTATTAAGGT TAGCGCCGAC GGTTCGATG AACGATTTCA      60
GGTCGGTATC TTAAAATTA GCGGTGAAAG TGGCTTCTTC CGCCAGACC GGTGAACTGC      120
ATAATGCCGC TGCCAGCACC AGCGGCAGTA AACGCTTTTT TGTTTTGAGG CCAGTTGTCT      180
TCTTACGCCA GACCGACAAC GTCATATCAC GCCAAAACAC GATGAATGAT TCTCCTGGAT      240
TAAATGCGGT TAGCGCAGCG CGATGGAAAT GTCGTGGCGC GCACCCTTGC GTAAAACCGT      300
AAGTTGAATG GAATCCATTG AAGGTAAGTG CCGCATCAGA GCAATCATTG CTCGTGGATC      360
AGTGAAATCC TGCTGATTTA GCGCAAATGC GATATCGCCT TCCTTAAAC CG              412
  
```

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TAGCCTGTTT	AGCGTATATT	TGGGATGAGA	AGCCAAAGTG	GCTTTGGTGG	TGTCCAGCC	60
CAGGTTTTTA	TTACTGCTGG	TTATTTACCT	TTCATGTTTT	TCAATAAAGT	TGTGACTCAG	120
TTGAAATCTG	CTGTCAATGC	TAATATGGGA	CTTTTTTGTT	ATAGACAAGT	GACTCCTTTT	180
GCAACTTTTA	TAGCACGTTT	TATGCTAGAA	ACAATGGTGG	GCATGATTGT	CGGTATAATC	240
CTAGTACTAG	GATTATTGTG	GTTTGGCTTT	GATGCAATAC	CTGCGGATCC	ATTGCAAGTG	300
ATCCTTGGTT	ATTCTCTTCT	GATGCTGTTT	TCTTTTTCTC	TGGTATTGT	ATTTTGTGTT	360
ATTTGTAATT	KRGCARAGA	GGCAGATAAA	TTTCTTAGCT	TGTTAATGAT	GCCTTTGATG	420
TTTATCTCTT	GTGTTATGTT	TCCTCTTGCT	ACTATTCCCC	CTCAATATCA	GCATTGGGTT	480
TTTATGGAAT	CCACTTGTGC	ATGCTGTAGA	ACTAATCCGA	AGGGCATGGG	ATATCTGGGT	540
TATCGTAGTC	CTGATGTAAG	TTGGGCGTAT	CTGTGC			576

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

TTACCAAGCA	GGATCTGATG	CAACTGGAAG	AAGGCTTTGA	ATATCGTATC	ATTGGCTGCT	60
CCATGTATAA	CATGTTGCC	GCCGTACGCG	GTGCCTATGA	CAGCTTTGAA	AATGTCAAAG	120
GGGTGAATTG	CT					132

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GATTAGGGGT	CACTCAGGAT	TATAAAAAAG	CGGCAGAATA	CTATAAAAAA	GGTGATAAAA	60
ATAATGATAT	TACAGCACAA	TACCGTCTGG	CAAACTTTTA	TGAACAAGGT	AACGGTGTA	120
AACGTGATTA	TCAACAAGCG	ATAAACCTTT	ACCTTAAACA	TATCAACAGA	ATGGATCACA	180
TCAGTCCCC	CAGTTTTGTG	GCTCTGGGTG	ATATCTATTC	TCTGGGATTS	GGGGTAGAGA	240
AAAACCCACA	ACTGGCTGAA	AAATGGTATC	AAAAAGCGAT	AGATGCAGCT	AATACACAAC	300
ATAACCAGGA	AATAAATCAT	TAAACGACAA	CACTTAATAC	CATATTGTGA	AGATGTTTCAG	360

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ACATGGCGGA ATTCCCCTAT TCTTTGTTGG CGCTTACAAC AGACTATATT CCGCCATATC 420
 TGTCTTTATT GTGTATAAAC CATCGATACT GATGTTTGAT AGTGCTAAAT AATCATTGGC 480
 GCAATCACAA AGCCTAATGC CACTCCAGCA ATAATTCCCC CCAACCCAGG CAGCATAAAT 540
 GG 542

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GAACCACTTA GCGGCAGCTA TCGGGAATCG CCTGCTGAAA GACGGTCAGA CAGTGATTGT 60
 GGTACCGTG GCTGATGTTA TGAGTGCCCT GCACGCCAGC TATGACGATG GGCAGTCAGG 120
 CGAAAAATTT TTGCGGGAAC TGTGCGAAGT GGATCTGCTG GTTCTTGATG AAATTGGCAT 180
 TCAGCGCGAG ACGAAAAACG AAGCAGGTGG TACTGCACCA GATTGTTGAT CGCCGGACAG 240
 CGTCGATGCG CACGTGGGGA TRCTGACAAA CCTGAACTAT GAGGCCATGA AAACATTGCT 300
 CGGCGARCGG ATTATGGATC RCATGACCAT GAACGCGCGG CGATGGGTGA ATTTTAACTG 360
 GGAGACTGGC GTCCGAATGT CG 382

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGTCCCGCAC CCGGAAATGG TCAGCGAACC AATCAGCAGG GTCATCGCTA GAAATCATCC 60
 TTAGCGAAAG CTAAGGATTT TTTTATCTG AATTCTAGCC AGATCCCCGC TGATTTATGC 120
 TGGTTA 126

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

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ACCCCCAGCC TAGCTGGGGG TTTTCTGTGC AAAAAAATC CCGGCATAAT GGCCGGGATT	60
TGCGAGCTTT CCCACTATTT CTTGATTCCT AAACGGAACA TATCAGTTGG GAATAAAGGT	120
TGTATTATCA CTTTCATCATT ANAAATGAAT AATTTGGGCG ATAAAGCTGT TACGTCATAG	180
ATATTTTCAG CGATTAATCT TAGANTTGAC CTAAAACTG GAATACTTGC ATCATCTGCA	240
AAGACAAACA TGTCATCG	258

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AACCAGCGGT TCGCATCATC TCATCCCACT GACTCTCCGC TTTTGACAGA TCTGCATATC	60
CTCGGGCCAA CTTATCCAGT ACTCCGTAGT TTGCCGATTT ATTCACCCGC CAGAACACCG	120
CCTCACCTGC ATCGGCAAGC CGGGGGGAAA ACTGATACCC CAGTAGCCAG AACAGACCGA	180
AAATAATATC GCTGCTACCC GCAGTGTCTG TCATGATTTT AACTGGATTC AGCCCTGTCT	240
GCTGCTCAAG AAGTCCTTCC AGTACAAAAA TCGAATCCCG TAATGTACCG GGTACCACAA	300
TGCCATGGAA CCCAGAGTAC TGATCAGATA CGAATTATAC CAGGTGATGC CTCGTCCAGA	360
ACCAAATAT TTTCTGTTAG ATCCTGAGTT GATGGTCTT	399

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AAATAACATC AACATACATT TGA CTGCGG GGGAAACGTT TACGGAGTCT TCATACTGGC	60
ACTTTTTTAT GCTGCTGACT ACTCTTCGTC ATCGCCATCA ACATGCGCAC GAATCAGCGC	120
CATAAACGGT TTGCCAAAGC GTTCCAGCTT GCGCATCCCA ACGCCGTTAA CGCTGAGCAT	180
TTCGCTGGCG GTGATCGGCA TCTGTTGAGC CATCTCAATC AAGGTTGCGT CGTTAAACAC	240
CACGTACGSC GGGACATTAC TTTTCATCGGC TATCGATTTA CGCAGTTTGC GTAATTNGGC	300
GAACAGTTTG CGATCATAGT TGNCGCCGAN CGATNTCTGC ATCGCTTTTCG GTTTGAGCGC	360
CACGATACGC GGCACGGCAA TTGCAAAGAG GATTGCGCGC GCAGCACCGG GCGCGCGGCC	420
TCTGTCAATT GTAGGGCAGA ATGCTGGGCA ATATTTTGCG TCACCAGGCC GAGGTGAATC	480

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AGCTGGCGGA TCACGCTCAC CCAATGTTCA TGGCTTTTAT CACGGCCCAT GCCATAGACT	540
TTCAGTTTGT CATGACCATA GTCGCGGATA CGCTGGTTAT TAGCACCACG AATCACTTCC	600
ACCACATAAC CCATCCCCAA CCGCTGATTC ACACGACCAA TGGTGGAAAG GGCAATCTGA	660
GCATCGGTTG AACCGTCGTA CTGTTTCGGC GGATCGAGGC AGATATCGCA GTTCNCCGCA	720
CGGCTCCTGA CGCCCTTCGC CAAAA	745

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

AGAATGGCGG CTTCTTGCCC CCCTTTGCCC CGGTCCTGAC TAGCATGGCT GGAGTCCAGT	60
GTCCAGGCCA CGACCATGCT CATCATGGAA GCAGCTTTTG TAGTACANTC GCAGCTTATT	120
TTCCTGGAAC GAAATGTCTG GCATCGTGGT GCATAACATA ACCCCCAATG CCCAGCAGAT	180
GCACAGAAGG TTCTAGAATC GCCCACTGAT ATCCCATACA AAATTTACCA AACGTGTTC	240
GTATTTCTCG TATAAATAAT GTCTCTATGG TGACGTTCTA GACTTCAAAC CCACTTTTTG	300
AATTTGATGA TGTGCTCCTA ATCTCTTCAG GAATGTAACG CCCTTGTTT ACAGCTACCA	360
ATACACTGGA GGTATACTTA TCTGCAACTG GATGAACTAG ATGTACTTGA GCAAACATTT	420
CATAAGCTCG ACGACAGTT	439

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CTGGAAAGCG ACGTTGATGG ATTAATGCAG TCGGTAAAAC TGAACGCTGC TCAGGCAAGG	60
CAGCAACTTC CTGATGACGC GACGCTGCGC CACCAANTCA TGGAACGTTT GATCATGGAT	120
CAAMTCATCC TGCAGATGGG GCAGAAAATG GGAGTGAAAA TCTCCGATGA GCAGCTGGAT	180
CAGGCGATTG CTAACATCGC GAAACAGNAC AACATGACGC TGGATCAGAT GCGCACCGTC	240
TGGCTTACGA TGGACTGAAC TACAACACCT ATCGTAACCA GATCCGCAAA GAGATGATTA	300
TCTCTGAAGT GCGTAACAAC GAGGTGCGTC GTCGNATCAC CATCCTGCCG	350 -

(2) INFORMATION FOR SEQ ID NO: 134:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```
CCCCAAGATT GCTAACAAAT GCGCGTTGTT CATGCCGGAT GCGGCGTGAC CGCCTTATCC      60
GGCCTACGAA ACCGCAAGAA TTCAATATAT TGCAGGAGCG GTGTAGGCCT GATAAGCGTA      120
GCGAWTCAGG CAGTTTTGCG TTTGCCCCGA ACCTTAGGGG ACATTTAGCG ACCCCATTTA      180
TTTCTCACTT TTCCGCCTCA TCATCGCGCG TTAATTTCTT TCATGAATCA CGCTTTACAA      240
TATCCAGCGC GCGCANAAAC GTACTGGCAG GGATCTGAAT TTTCTCCAG CAGCACAATC      300
AAATCGACAG CCAGTTTGAC ATCGTCAAGG GGCATTTTCC CAGTGACATA ATCTCTCCAT      360
TGCTAAGCGG GTTAAACGC GCTAACCTGT TTCGATTTTT      400
```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```
CTATCCTTAT GACCACCCAA CTACNTCATT TACACCCAAA CCAGCGATCT GAATAAAGAA      60
GCGATTGCCC AGTTACGACT GGGCGGAAAA TGCGCGTAAG GATGAAGTAA AGTTTCAGTT      120
GAGCCTGGCA TTTCCCTGTG GCGTGGGATT TTAGGCCCCGA ACTCGGTGTT GGGTGCCTCT      180
TATACGCAAA AATCCTGGTG GCAACTGTCC AATAGCGAAG AGTCTTCACC GTTTCGTGAA      240
ACCAACTACG AACCGCAATT GTTCCTCGGT TTTGCCACCG ATTACCGTTT TGCAGGTTGG      300
ACTGCGCGAT GTGGAGATGG GGTATAACCA CGACTCTAAA CGGGCGTTCC GACCCGACCT      360
CCCGCAGCTG GAACCGCCTT TATACTCGCC TGATGGCAGA AAACGGTAAC TGGCTGGTAG      420
AAGTGAAGCC GNGGTATGTG GTGGGTAATA CTGACGATAA CCC      463
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(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

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TTGGTCAGCC GTACCTGAAT GGGGGCTGAT GCCCGGCTGG TTAATGGCAG GTGGTCTGAT	60
CGCCTGGTTT GTCGGTTGGC GCAAACACG CTGATTTTTT CATCGCTCAA GCGGGCCGT	120
GTAACGTATA ATGCGGCTTT GTTTAATCAT CATCTACCAC AGAGGAACAT GTATGGGTGG	180
TATCAGTATT TGGCAGTTAT TGATTATTGC CGTCATCGTT GTA CTGCTTTT TTGGCACCAA	240
AAAGCTCGGC TCCATCGGTT CCGATCTTGG TCGGTCGATC AAAGGCTTTA AAAAAGCAAT	300
GAGCGATGAT GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC	360
TATCGCCGAT AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACGCGAAGCC	420
TACGNTAAAG AGCAGGTGTA ATCCGTGTTT GATATCGGTT TTAGCGNACT GCTATTGGTG	480
TTCATCATCG GCCTCGTCGT TCTGGGGGCG CAACGACTGC CTGTGGCGGT AAAAACGGTA	540
GCGGGCTGGA TTCGCGCGTT GCGTTCCTG GCGACAACGG TGCA	584

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GCAGGCAGGA GGAAGTCCCC AGTGATACGG TTATTCGTGA TGGCGGAGGG CAGAGCCTTA	60
ACGGACTGGC GTTGAACACC ACGCTGGATA ACAGAGTTGA GCATTGGNTA CACGGGGGAG	120
GGAAAGCAGA CGTTACAATT ATTAACCAGG ATGTTTACCC AGACCATAAA ACATGGCGGA	180
TTGGCAACCG NAACCATCGT CAACACCGTT GCAGAAGKTG GTCCGGAGTC TGAAAATGTG	240
TCCAGCGGTC AGATGGTCGG AGGGACGGCT GAATCCACCA CCATCAACAA AAATGGCCGG	300
CAGTTATCTG GTCTTCGGGG ATGGCACGGG ACACCCTCAT TTGCGCTGGT GGTGACCAGA	360
CGGTACACGG AGAGGCACAT AACACCCGAC TGGAGGGAGG TTAACCAGTA TGTACACAAC	420
GGTGGCACGG CAACAGAGAC GCTGATAAAC CGTGATGGCT GGCAGGTGAT TAAGGAAGGA	480
GGGAAGTGCC GGCGCATTAC CACCATCAAN CCNGAAAAGG GAAANCT	527

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GTCAGTCTCT GGGGAAGTG CGTGTTCCGA CCGGGGAAAT GTGGTGGAGA AAGTTATTGA	60
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AGGGGCTTAC GAGGTGTTGG GGGTTTTTGA CCGGATTGAG GAAAAGCGTG ATGCCATGCA 120
 GTCGCTGATT CTGCCGCCAC CGGACGCCAG GCGCTGGCAC AGGCGGCACT GACTTACCGT 180
 TATGGTGACG AACMTCARCC CGTCACCACC GCCGACATTC TGACACCACG ACGCCGGGAR 240
 GATTACGGTA AGGACCTGTG GAGTGCTTAT CAGACCATTC AGGAGAATAT GCTGAAAGGC 300
 GGAATTTCCG GTCGCAGTGC CAGAGGAAAA CGTATCCATA CCCGTGCCAT TCACAGCATC 360
 GACACCGACA TTAAGCTCAA CCGCGCATTG TGGGTGATGG CTGAAACGCT GCTGGAGAGT 420
 ATGCGCTGAT GCCGTTTCCN T 441

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGAGCGAGAT GAACTTCGAG GGCGGTGTGA GCCAGTCGGC TTACGAGACA CTGGCGGCGC 60
 TTAATCTGCC GAAACCGCAG CAAGGGCCGG AAACCATTAA TCAGGTTACC GAGCATAAGA 120
 TGTCAGCTGA GTAAGCCTGT ATGCCGGATA AGGCGCTCGC GCCNATTCCG ATGAAATAAG 180
 GCGCATCGGG CCTGAAGGAA AGCCGTATGN ATACACCCGC AGCCCGCATC CGGCAAGTTA 240
 CAACAAATAA CCTTTAACCA TGCTTTTTGA TGTTTTTCAG CAATACCCCG CGGCGATGCC 300
 CATACTGGCA ACCGTGCGGA GGGATTGATC ATCGGCAGTT TTTTGAATGT GGTGATTGG 360
 GCGTTACCCC ATCATGCTGC GCCAACAAT GGCGGAGT 398

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GCCGAACAGA CACAGCAATA TGAACCTGTC CAGCGCAGAC GCTTGCTGAT TAATGCTCTG 60
 AACAAAAGGC GAAGAATGGC AAATCCTGCG ATCAGCAAAG TCAGCGCACC GACTATCTGT 120
 AACATAGTCA CTCCGTGATG AATATCATGT GTATTGTGAA TGCCAGTGAA TGTGGCACTG 180
 AAGCGTTTGC ACCTGTCCGG GTCCCGGTCA TGATGACCGS AACAGAGAGA CAATGCCGAA 240
 TTATCAGAAG GTCACATTCA GTGTGCTTGG GCCGTTATAA CCTTCAGCGC TGCTGCCGCT 300
 GACGCTGTGG GCATAACCGG CCTGAACGCC CAGGGTGATA TTTTCCCGGA CACGGGCTTC 360

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CAGTCCGGCC TGCAGCTCCA GTGACGTGCC ATTCCGGGAC GGTGAGAACG TCATGTTACT	420
GCCGGCTGCG GCTGTACCCA TGCTCATGTC TCCCCGGGAG CTGAAGGTGC GGATAACAGA	480
AGGCTGTACC CACCCGTTCA CCGGCAGTTC ACGCACACTG TGTTTTGCAC TGTCACGCAA	540
GGTGTACGG GATGAGGTGC CTTCANCAAA AGGTCATATT	580

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGCGGACATC CAGCGTCCG CCATCATCCA CACGGGTTCT GGTGGCTGTG TGTCCGGTCA	60
GCACATCCAG ACGGCCGCCA TTTTCCAGTA CGACATTATC AGCTTTACCC TCCACAACAG	120
AGAATGCTCC CAGGCGGTTT GTGCCGTTGA CGGTTGCAGC AGTGCTGGTA ACCAGTGCTC	180
CGCCCGTGTT CTGGGTGACA TCAGACGCTT TACCGCCGGC ATTCACCTGC AGCTTTCCTT	240
TCTGGTTGAT GGTGGTATGC GCGGCAGTTC CTCCTTCCTT AATCAMCTGC CAGCCATCAC	300
GGTTTATCAG CGTCTCTGTT GCCGTGCCAA CGTTGTGTAC ATACTGGTTA MCTCCCTCCA	360
GTCGGGTGTT AWGTGSCTCT CCGTGTANCG TCTGGTCANC AACACGCAA ATGANGGTGT	420
CCCGTGCCAT CCCCAGAGAC CAGTAA	446

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGAATACGTT AAGTCAGCAG ACCGGCGGAG ACAGTCTGAC ACAGACAGCG CTGCAGCAGT	60
ATGAGCCGGT GGTGGTTGGC TCTCCGCAAT GGCACGATGA ACTGGCAGGT GCCCTGAATA	120
ATATTGCCGG AGTTCGCCAC TGACCGGTCA GACCGGTATC AGTGATGACT GGCCACTGCC	180
TTCCGTCAAC AATGGATACC TGGTCCGTC CACGGACCCG GACAGTCCGT ATCTGATTAC	240
GGTGAACCCG AAAGTGGATR GTCTCGGACA GGTGGACAGC CATTTGTTN CCGGACTGTA	300
TGAGCTTCTT GGAGCGAAAC CGGGTCA	327

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>5</u> , line <u>8</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection (ATCC)	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 23, 1996	Accession Number 97726
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
DNA plasmid PAI-1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
<div style="border: 1px solid black; padding: 5px;"><div style="text-align: center; font-weight: bold; font-size: small;">For receiving Office use only</div><div style="margin-top: 10px;"><input type="checkbox"/> This sheet was received with the international application</div><div style="border-top: 1px solid black; margin-top: 10px; height: 40px; vertical-align: bottom;">Authorized officer</div></div>	<div style="border: 1px solid black; padding: 5px;"><div style="text-align: center; font-weight: bold; font-size: small;">For International Bureau use only</div><div style="margin-top: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border-top: 1px solid black; margin-top: 10px; height: 40px; vertical-align: bottom;">Authorized officer</div></div>